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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 24, 2002, 07:20:59; Search time 10173.5 Seconds (without alignments)
13311.631 Million cell updates/sec
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8209
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

A66553 A66553 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITHORS TITHORS TITHORS TITHORS TOURNALL SOURCE SOURCE SOURCE TOURNALL SOURCE SOURCE		Result Sc No.:
0		100 100 100 100 100 100 100 100 100 100
nce 3.1 3.1 vir vir vir ase ait		110.03.66.0.88.99.77.17.99.7.17.0.99.7.7.99.7.99.7.9.99.7.7.99.7.99.7.99.7.99.7.99.7.99.7.99.7.99.7.99.7.99.7.99.7.9.99.7.9
from GI:453 dogeno dogeno etroid es; 1- 1 to 8 D.N., TROVIR 97401 ECH LT cocatio ocatio organi		Hength 8209 8918 8918 8918 8918 8763 8763 8763 8763 8763 8763 8763 876
m / C		- DB - CB
p DNA p DNA lent W09740167. retrovirus. retrovirus retroviridae; malian type C virus porth,C., Lees,G.M. a A 3 30-OCT-1997; (GB) pualifiers taxon:61673"	ALIGNMENTS	A66553 A66552 PEN133816 PEN133817 PEN293657 PEN133818 BERY17713 AF014162 A66559 AF002804 PERENV2 PEN293656 SSU77599 AX052634 AX052635 AX052636 AX052636 AX052637 AR130475 AR130477 AR130477 AR130473 AR130474 AR13047
Mammalian group nd Smith,K		
29-MAR-1999 lian type C th,K.T.		Description A66553 Sequence 3 A66552 Sequence 2 AJ133816 Porcine e AJ23367 Porcine e AJ23367 Porcine e AJ133818 Porcine end AF03461 Sus scrof AF044162 Porcine end AF044162 Porcine end AF044162 Porcine end AF044162 Porcine end AF042804 Sequence Y1239 Porcine end AJ23656 Porcine end AJ23656 Porcine end AJ23656 Porcine end AJ23656 Porcine end AJ23657 Sequence AX052637 Sequence AX052637 Sequence AX052637 Sequence AX052638 Sequence AF034600 Sus scrof AX052638 Sequence AF036400 Sus scrof AJ28858 Porcine end AJ3845 Sus scrofa AJ005400 Sus scrofa AJ005410 Sus scrofa AJ005410 Sus scrofa AJ005410 Sus scrofa AJ0053326 Porcine e AF033260 Porcine e AF0333260 Porcine e AF033260 Porcine e AF03460 Porcine e AF04540 Porcine e AF04540 Porcine e AF04540 Porcine e AF04

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9t99t9tacgact9t999cccca9c9c9ctt99aataaaaatcctcttqctgtttgcatc 60
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//Lagis lation="Grrgsbulpeprytiksplvipecpvpligrdhitkmgaqisf"
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product="VIRAL CORE PROTEIN"

product="VIRAL CORE PROTEIN"

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TSAPPGAPVYEGPAGTRSRRGATPERTDEILIFLFTYGPPMPGGQLOFLOYWPFSS

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RKNYPGADGRPTQLQNEIDMGFPLTRGWDYNTAEGRESLKIYROALVAGLRGASRRP

RKNYPGADGRPTQLQNEIDMGFPLTRGWDYNTAEGRESLKIYROALVAGLRGASRRP
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KKLQRLEGLQEAELRDLVREABKVYYRRETEEEKEQRKEKEREEREERRDRRQEKNLT
KILAAVVEGKSSRERERDFRKIRSGPRQSGNLGNRTPLDKDQCAYCKEKGHWARNCPK
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           cggagcggacagacgagatcgcgatattaccgctgcgcacctatggccctcccatgccag
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2340	. gaaaactaaaagaaaaaaatcctgggtgatgggtgccacagggcaacggcagtatccat	2281	Ωу
2280	AACCAGTTGAGTTCCTGGTTGATACCGGAGCGGAGCATTCAGTGCTGCTACAACCATTA	N	DЬ
2280	aaccagttgagttcctggttgataccggagcggagcattcagtgctgctacaaccatta	Ν	Qy
2220 2220	aggggagacggggttcggaccccctccccgagcccagggtaactttgaaggtggagggc	\vdash \vdash	Фр
	actgccccaagaa ACTGCCCCAAGAA	2101 2101	Qу
10	ggacactgggcaa GGACACTGGGCAA	0 0	ОУ
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1980	AGAGAAGAATTTGACTAAGATCTTGGCCGCAGTGGTTGAAGGGAAGAGCAGCAGCAGGG AGAGAGAATtttaqqaaaattaqqtcaqqccctaqacaqtcaqqqaacctqqqcac	9 9	Q B
	aagagaagaatttgactaagatcttggccgcagtggttgaaggggaagagcagcagggaga	1921	Qy
1920 1920	agaaggaacagagaaaagaaaaggagagaagaaaggagaaggaaggaagcagc	1861 1861	Дb
98	TTACGTGATCTAGTGAGAGAGGCAGAGAAGGTGTATTACAGAAGGGAGACAGAAGAG	1801	DЬ
	acqtgatctaqtgagagaggcagagaaggtgtattacagaagggagacagaa	_	Qy
1800	ggcagtcggctctggatatcaggaagaaacttcagagactggaagggttacaggaggctg	1741 1741	Ωу
7	AAGCCTCAGTGGCCCTGGCCTTCATTG	1681	Db
1740	accentitigatectaceteagaggeecagaagecteagiggeeciggeetteatig	1681	Qy
1680 1680	agggaccgaacgaacctccctcggtatttcttgagaggctcatggaagccttcaggcggt	1621 1621	Фр
	CGGGTCTCCGGGGCGCCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAGGTGATGC	1561	Db
	gggtctccggggcgcctcaagacggcccactaatttggctaaggtaagagaggtgatgc	1561	Qy
1560 1560	gggactacaacacggctgaaggtagggagagcttgaaaatctatcgccaggctctggtgg 	1501	Ф
1500	ggcgacccacgcagttgcaaaatgagattgacatgggatttcccttgactcgccccggtt	1441 1441	pb VQ
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o o	1999a19a19t9teaaca9c19c19ca9acactcttca 	(C) (A)	Db dy
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1260 1320	GGGCCAATTGCAGCCCCTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTG	1201	
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20	ggacagcaggtatgcctttgcgactgcacacgtacacggggccatctataaacaaaqqq 4	4261	Qy
	- AGCTCATGGCCCTCACGCAAGCTTTGCGGCTGGCCGAAGGGAAATCCATAAACATTTATA 4	4201	Db
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0	- ACGGGACCCCCACGATCTGGCCAGCAGCCAGCCTGCCGGAAGGGAACTTCAGCGCAAAAGGCTG 4	4141	DЬ
00	. acgggacccgcacgatctgggccagcagcctgccggaaggaa	\vdash	Qy
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120	l ttctgcctgaagagactgatgaaccagtgactcatgattgccatcaactattgattg	3961	Qy
60	1 GCCTGCTTCTCACAGAGAGGGTCACTTTCGCTCCACCAGCCGGTCTCAACCCTGCCACTC 39	3901	Db
60	cctgcttctcacagagagggtcactttcgctccaccagccgctctcaaccctgccac	3901	Qy
000	ACATCG	3841	DЬ
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340	1 ACGCTGACAAATTGACTTTGGGACAGAATATAACTGTAATAGCCCCCCATGCATTGGAGA 38	378:	Db
340	gctyacaaattgactttgggacagaatataactgtaatagccccccatgcattggag	378:	Qy
		372	ДЬ
780	agccagtggttggcccgtatgtctgaaggctatcgcagctgtggccatactggtcaag	372	Qy
N		366	Db
720	ccaaaccctaggaccatggaggagacctgttgcctacctgtcaaagaagcttgatcct	366	Qy
560	1 TAACTAAACCCTTTACCCTTTATGTGGATGAGGCGTAAGGGAGTAGCCCGAGGAGTTTTAA 36	360	Db
560	actaaaccctttaccctttatgtggatgagcgtaagggagtagcccgaggagtttta	360	Qy.
600	AGGCATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCT	354	Db
600	ggcatttgatgctatcaaaaaggccctgctgagcgcacctgctctggccctccct	4	Qy
540	1 CCCCACTCTACCCGCTAACCAAAGAAAAAGGGGGATTCTCCTGGGCTCCTGAGCACCAGA 3	348	Db
4	cccactctacccgctaaccaaagaaaaagggggattctcctgggctcctgagcaccaga 3	4.8	Qy
	1 AGTTTTTGGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTGCGACCTTAGCAG 3	342	DЬ
480	gtttttggggacagctggattttgcagactgtggatcccgggggtttgcgaccttagcag 3	342	Qy
420	1 AGGCACGGAAGAAAACTGTAGTCCAGATACCGGCCCCAACCACCAGCCAAACAAGTGAGAG 3	336	Db

cttatctcgtacttttgaccacac 5580	77 - 77	5521 5521	Qy Db
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6720	. catagaaatcaatgtacatgggggtcccgaaataagcttaccctcactgaagtttccggg	6661	Qy
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6600	TICCAAGCCATCAACTCCACCGACCCTGATGCCACTTCTTCTTGTTGGCTTTGTCTATCC	6541	B 8
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	AACACAGCCGCCTAGCAACAGTACCACTGGATTGATTCCTACCAACACGCCTAG	6421	Дb
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6300	ATAGTTTTTTATTTATATGGCGGGGGAGCAGGGTCCACTTTAACCATTCGCCTTAGGAT		Db
6300	aatagtttttattatatggcgggggagcagggtccactttaacccattcgccttaggata	Ν	Qy
6240	AGTTTCACTGAAAGGAAAACAGGAAAATATTCAAAAGTGGATAAATGGTATGAGCTGGGG	6181	Db
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5880	GTGGCCTGAACTG	5821	Db
5880	gtgtcactgtaaatagcactcgaggtgttgctcctagaggcacctggtggcctgaactg	5821	Qy
5820	gacagorogaacococaragacorratecorrateoragorgamantamacocorgamacocococamagacorratecorratecorratecorrateacorrateacococamacocococamacocococamacocococococ	5761	Дb
	CCATCGCCTGGTTCCTTACTCTAACAATAACTCCCCAGGCCAGTAGTAAACGCCTTATA	7	Db
76	tecategeetggtteettaetetaacaataacteeccaggeeagtagtaaacgeettata	7	Qy
5700 5700	cgccacctcccgactcggggtggagagccgaaaagactgagaatccccttaagcttcgcc	5641 5641	Оу
5640	CAACGGCTGTGAAAGTCGAAGGAATCCCCACCTGGATCCATGCATCCCACGTTAAGCCGG	5581	Дb
5640	acqqctqtqaaaqtcqaaqqaatccccacctggatcccatgcatcccacgttaaqccgg	5581	Qy

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7740	aagttaataaaaagctctaaatgcccccgaattacagaccctgctggctg	7681 7681	Оу
68	ATGCAACCTAACCCTCCCAGAACCCAG		ДУ
62	TTCTGAGCCAAGGAGAACTGACCTCTAGCCTTCCCAGTTCTAAGATTAGAACTATTA	56	Db 4
7560 7620	TIGTTAGAGAACGAGTGAGTGCAGTCCAGATCATGGTACCTTAGGCAACAGTACCAAGG +++++==============================	50	Db C
56	tttgttagagaacgagttgagtgcagtccagatcatggtacttaggcaacagtaccaaggc	7501	Qy
7500	ctagtagtcctgctcctgttacttacagttgggccttgcttaattaa	7441 7441	Фр
44	TTTCTGCTCTGACGGGGCC	38	Db
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38	aagcttagaaaaaagttagagaggcgtcgaaggggaaagagaggctgaccaggggtggttt	32	Qy
7320	THAAAAGAAGATGTTGCTTCTATGTAGATCACTCAGGAGCCATCAGAGACTCCATGAAC	7261	Db
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7260	CtacagaaccggaggggattagatCtgctgttCtaagagaaggtgggttAllIIIIIIIIIIIIIIIIIIIIIIIIIIIII	7201	. Ob
20	CCTTAAAAGGAGTCTGTTAGCAACCTAGAAGAGTCCCTGACTTCTTTGTCTGAAGTGGT	14	Дb
20	gccttaaaggagtctgttagcaacctagaagagtccctgacttctttgtctgaagtggtt	7141	Qy
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7140		7081	Qy
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6780	aggggacatgcataggaaaagctcccccatcccaccaacacctttgctatagtactgtg	721	Qy
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                                                                               CGTGAGTGATTTGGGGTGTCGCCTCTTCCGAKCCCGGACGAGGGGGATTGTTCTTTTACT
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Sequence 2 from Patent W09740167.
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                                                                                                                                                                                                                                                                                                                           PORCINE RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses;
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                                                                                                                                                                             Conservative
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BIOTECH LTD (GB)
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                                                                                                                                                                                                                                                                                                                                                                                    endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                                                                             endogenous retrovirus.
                                                                                                                                                                                                                                          /organism="porcine endogenous retrovirus"
/db_xref="taxon:61673"
2061 c 2146 g 1820 t 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-MAY-1999) Toenjes R.R., Medical Biotechnology, Paul-Ehrlich-Institut, Paul-Ehrlich-Strasse 51-59, Hessen, D-63225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Czauderna,F., Fischer,N., Boller,K., Kurth,R. and Tonjes,R.R. Establishment and characterization of molecular clones of porcine endogenous retroviruses replicating on human cells J. Virol. 74 (9), 4028-4038 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toenjes, R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retroviruses; 1-Mammalian type C virus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; Retroid viruses; Retroviridae; Mammalian type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine endogenous retrovirus type C proviral gag, pol and env genes and LTR (class B, clone 33).
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                                                                              CTATTAACAAGACAAGAAGTGGGGAATGAAAGGATGAAAATGCAACCTAACCCTCCCAGA 8245
                                                                                                                                                                                                                                                                                                                                  TGTTGCCTTTGTTAGAGAACGAGTGAGTGCAGTCCAGATCATGGTACTTAGGCAACAGTA 8125
                                                                                                                                                                                                                                                                                                                                                          tgttgcctttgttagagaacgagtgagtgcagtccagatcatggtacttaggcaacagta 7553
                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGTTTGAAGGATGGTTCAACAGGTCTCCTTGGATGACCACCCTGCTTTCTGCTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catgaacaagcttagaaaaagttagagaggcgtcgaaggggaaagagggctgaccaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCAGCCTTAAAAGAAGAATGTTGCTTCTATGTAGATCACTCAGGAGCCATCAGAGACTC 7885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGGTTCTACAGAACCGGAGGGGATTAGATCTGCTGTTTCTAAGAGAAGGTGGGTTATG 7825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCCGAGCCTTAGAGGAGTCTGTTAGCAACCTAGAAGAGTCCCTGACTTCTTTGTCTGA 7765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAGGACCACAGCAGCTAGAGAAAGGACTTGGTGAGCTACATGCGGCCCATGACAGAAGA 7705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             teteegageettaaaggagtetgttageaacetagaagagteeetgaettetttgtetga 7193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccttgatgaatatgactatcggtataaccgaccaaaaagagaacccgtatcccttaccct 7013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-MAY-1999) Toenjes R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEN133817 8849 bp DNA CRL (Porcine endogenous retrovirus type C proviral gag, genesand LTR (class A, clone 42).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Langen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Czauderna, F., Fischer, N., Boller, K., Krach, U., Kurth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retroviruses; 1-Mammalian type C virus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Retroviridae; Mammalian
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1115. .2686
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RKNVPGADGRPTQLQNEIDMGFPLTRPGWDYNTAEGRESLKIYRQALVAGLRGASRRP
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                                                                                                                                                                                                                                                            /gene="gag"
                                                                                                                                                                                                                                                                                                                                      /note="gly4"
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                                                                                                                                                                                                                                                                                                                                                                          note="cap site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="porcine endogenous retrovirus"
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polyA_signal BASE COUNT 2355 Query Match Best Local Best Local Similarity Matches 5330; Conserv mat_peptide mat_peptide 528 GTGGTGTACGACTGTGGGCCCCCAGCGCGCTTGGAATAAAAATCCTCTTGCTGTTTGCATC 587 1 gtggtgtacgactgtggggccccagcgcgcttggaataaaaatcctcttgctgtttgcatc 60 tgttcttttactggcctttcatttggtgcgttggccgggaaatcctgcgaccacccctta 180 aagaccgcttctcgtgagtgatttggggtgtcgcctcttccgagcccggacgagggggat 120 AAGACCGCTTCTTGTGAGTGATTTGGGGTGTCGCCTCTTCCGAGCCCGGACGAGGGGGAT 647 TGTTCTTTTACTGGCCTTTCATTTGGTGCGTTGGCCGGGAAATCCTGCGACCACCCCTTA 707 CLRLHOTSOPLEA EEMRDDGTGRTGOLTWTRLTOGERKSEPT I FDEALHADLANK I OH
POUTILOY VDDLLLAGATKODCLEGTKALLELSDLGY RASAKKAQICRREVTY LGYS
LRGGORNITEARKKTVOG I PAPTTAKOV REFIGTAGFCRLWI I PEFATLAAD LY PLTKE
RGETSMAD BEIGO KA FDALKKALLENDTK PFTLY VDERRGVAROVLTOTIGDW
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VRKDLTD I PLTGEVLTWFTDGSSY VPESKRMAGAAV VDGTTTI WASSLDEGTSAOKAE
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VKPAKYGNKYLLYFUDTE SGWEAY PTKKETSTWYAKKILEEL FPREGIPKVIGSDNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caacagatacatcgtctaacccacctaggaactaaacacctgcagcagttggtcagaaca 4739
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                                 l (bases 1 to 0/03)
Krach,U., Fischer,N., Czauderna,F. and Tonjes,R.R.
Comparison of replication-competent molecular clones of porcine
Comparison of replication and class b derived from pig and
                                                                             polymerase; polyprotein.
porcine endogenous type C retrovirus.
porcine endogenous type C retrovirus
viruses; Retroid viruses; Retroviridae;
l (bases 1 to 8763)
                                                                                                                                                AJ293657.1 GI:14275841 env gene; envelope; gag gene; group specific
                                                                                                                                                                              and env gene, class
                        human cells
                                                                                                                                                                                                             Porcine endogenous
                                                                                                                                                                                                                           PEN293657
          Virol.
           75 (12),
                                                                                                                                                                                                                        8763 bp
                                                                                                                                                                                            bp DNA
  type C retrovirus
  B, clone 213.
             5465-5472 (2001)
                                                                                                                                                                                                          proviral
                                                                                              Gammaretrovirus.
                                                                                                                                                  antigen;
                                                                                                                                                                                                          gag
                                                                                                                                                                                                          gene,
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Submitted (31-JUL-2000) Toenjes R.R., Medical Biotechnology,
Paul-Ehrlich-Institut, Paul-Ehrlich-Str. 51-95, Langen, 632
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Toenjes, R.R.
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                                                /gene="env"
6112. .8085
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VTLLQVYDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLR
GGQRWLTEARKKTVVQIFAPTTAKQVREFLGTAGFCRLHIPGFBATLAAPLYPLTKEKG
EFSWAPEHQKAFDAIKKALLSAPALALDDVTKPFTLYVDERKGYARGYLTQTLGPWRR
PVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNLTVIAPHALENIVRQPP
DRWMTNARWTHYGSLLLTERVIFAPPAALNAPATLLPEETDEPVTHDCHQLLIEETGVR
KDLDTPLTGEVLTWFTDGSSYVVEGEKKMAGAAVDGCTRTIWASSLPEGTSAQKAEL
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ALHLFKRLAIIHCPGHQKAKDLISRGWQMADBVAKQAAQAVNLTHITHLTGENFOR
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/protoin_id="CAC39625.1"
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/gene="gag"
1077. .2651
/gene="gag"
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KKLQRLEGLQEAELRDLVREAEKVYYRRETEEEKEQRKEKEREERERRDRRQEKNLT
KILAAVVEGKSSRERERDFRKIRSGPRQSGNLGNRTPLDKDQCAYCKEKGHWARNCPK
                                                                                                                                                                                                                                      PFVLFRVRNTPGQFGLTPYELLYGGPPPLVEIASVHSADVLLSQPLFSRLKALEWVRQ
RAWKQLREAYSGEGDLQVPHRFQVGDSVYVRRHHAGNLETRWKGPYLVLLTTPTAVKV
                                                                                                                                                                                                                                                                                                                                                                   YTLEDWQEIKK IDQFSETPEGTCYTSYGKEILPHKEGLEYVQQIHRLTHLGTKHLQQL
VRTSPYHVLRLPGVADSVVKHCVPCQLVNANPSRIPPGKRLRGSHPGAHWEVDFTEVK
PAKYGNKYLLVFVDTFSGWVEAYPTKKETSTVVAKKILEEIFPRFGIPKVIGSDNGPA
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KQVPPQVIQLKASATPVSVRQYPLSREAREGIWPHVQRLIQQGILVPVQSPWNTPLLP
VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSALPPERNWYTVLDLKDAFFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="polymerase"
/protein_id="CAC39626.1"
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/translation="GRRGSDPLPEPRVTLKVEGQPVEFLVDTGAEHSVLLQPLGKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="complete
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/specific_host="Sus scrofa"
/specific=host="Sus scrofa"
/db_xref="taxon:70540"
/clone="$13"
/cell_line="px15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                           EGISTWIHASHVKLAPPPDSGWRAEKTENPLKLRLHRLVPYSNNNSPGQ"
                                                                                                                                                                                                                                                                                                                                  FVAQVSQGLAKILGIDWKLHCAYRPQSSGQVERMNRTIKETLTKLTTETGINDWIALL
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<2652. .623
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/gene="env"
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                 1093 tggtggagggacctgctgccgggactcggagccggagaggcgccaccccggagcggacag
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                                                                                                                                   1462 CTGGTATCTACCCCGAGATCGAGGAGCCGCCGACTTGGCCGGAACCCCAACCTGTTCCCC
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7221	AATCAATGTACATGGGGGTCCCGAAATAAGCTTACCCTCACTGAAGTTTCCGGGAAGGGG	7162	da
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-MAY-1999) Toenjes R.R., Medical Biotechnology, Paul-Ehrlich-Institut, Paul-Ehrlich-Strasse 51-59, Hessen, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEN133818 8750 bp DNA VRL Porcine endogenous retrovirus type C proviral genes and LTR (class B, clone 43).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Langen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endogenous retroviruses replicating on human cells J. Virol. 74 (9), 4028-4038 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses; 1-Mammalian type C virus group.
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AJ133818.1 GI:6688949
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ORIGIN

Query Match

DB 14;

Length 8750;

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6569 atgccacttcttcttgttggctttgtctatcctcagggcctccttattatgaggggatgg 6628 	Qу
6509 gacagagactottcagtotcatccagggagctttccaagccatcaactccaccgaccctg 6568 	Qу
	ДУ
ω ω	ОУ
ω ω	Оу
6269 cagggtccactttaaccattcgccttaggatagagacggggacagaaccccctgtggcaa 6328 	ДУ
σ N	Qу
6152 occcatcagacttagattatctaaagattagtttcactgaaaggaaaacaggaaaata 6209 	Qу ДЬ
6092 ttgtcaattccggcccgggcaagtacaaaatgatgaaactatataaagataagagctgct 6151 	Qу
6032 cctccaacgatggagactggaaatggccgatctctctccaggaccgggtaaaattctcct 6091 	ОУ

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                                                       TGGTGTACGACTGTGGGCCCCCAGCGCGCTTGGAATAAAATCCTCTTGCTTTTGCATCA
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porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian type
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Czauderna, F., Fischer, N., Boller, K., Kurth, R. and Tonjes, R.
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/gene="gag"
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KKLQRLEGLQEAELRDLVREAEKAYYGRETEEEKEQRKEKEREEREERRDRRQEKNLT
KILAAVVEGKSSRERERDFRKIRSGPRQSGNLGNRTPLDKDQCAYCKEKGHWARNCPK
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/db_xref="taxon:61673"
/tissue_type="kidney"
/cell_line="pK15"
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CTCTCATCCTGATCAGGAGCCCTATATCCTTACGTGGCAAGACTTGGCAGAAGATCCTCC
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GTTGLLTTNTPRNSPGVPVKTOQRLFSLIQGAFQAINSTDPDATSCWLCLSSGPPYY
EGMAKEGKFNVTKEHRNQCTWGSRNKLTLTEVSTGTGTGKAPPSHQHLCYSTVVYEQ
ASENQYLVPGYMRWAACNTGLTPCVSSSYFNQSKDFCVMQTVPRVYHPEEVVLDEY
DYRYNRPKREPVSLTLAVMLGLGTAVGVGTGTAALITGPQQLEKGLGELHAAMTEDLR
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cgtattgtaaagaaaaaggacactgggcaaggaactgccccaagaagggaaacaaaggac 2127
                                        caggccctagacagtcagggaacctgggcaataggaccccactcgacaaggaccagtgtg
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t 296	accettataacctettgagegecetecegeetgaaeggaaetggtacacagtattggae	2908	Qy
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C 25	ACCGGTTAGGAAGCCTGGGACCAATGATTATCG	2460	Db
ac 2847	atcccttqgaatactcccctgctaccggttaggaagcctgggac	2788	Qy
C 245	GAGAAGGAATTTGGCCGCATGTTCAAAGATTAATCCAACAGGGCATCCTAGTTCCTGTC	40	문 5
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C 2727	aactgaaggccagtgctacaccagtatcagtcagacagtaccccttgagtaggaggct 	2668	P 69
C 23	aagcctgggcagaaaccgcagggatgggtttggcaaagcaagttcccccacaggtactagg 	2280	Ωу
C 227	ATATTCTCCCCAAGTAAAGCCTGATCAAGATATACAGTCCTGGTTGGAGCAGTTTCCC	22	рb
c 260	tccc		Qy
.C 2219	CGA	\vdash	Db
c 2547	gtctgtgaataacaaacccatcactgtgttgaccctccaattagatgatgaatatcga	2488	Qy
g 2487 G 2159	gtagagacttactgaccaagatgggagctcaaatttcttttgaaccaaggaagaccagaa 	2428 2100	Qy Db
20	TGGGACGGTAACCCACTCGTTTCTGGTCATCCCTGAGTGCCCAGTACCCCTTCTA	2040	Db
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g 2367 2039	tgatgggtgccacagggcaacggcagtatccatggactacccgaagaaccgttgacttg	2308 1980	Qy Db
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230	gagcggagcattcagtgctgctacaaccattaggaaaactaaaagaaaaaaatcctgg	24	Qy
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5367 5038	5308 atgaattgctctacgggggaccccccccgttggcagaaattgcctttgcacatagtgctg	Оу
5307 4978	5248 tcctgccctttgtgctttttagggtgaggaacacccctggacagtttgggctgacccct	Qy Db
5247 4918	5188 ccattaaagagaccettaccaaattgaccacagagactggcattaatgattggatggctc 	Фр
5187 4858	5128 ggaaactgcattgtgcatacagaccccaaagctcaggacaggtagagaggatgaatagaa 	Qу
5127 4798	5068 atggtccagctttcgttgcccaggtaagtcagggactggccaagatattggggattgatt	Qу
5067 4738	5008 agaaaatactggaggaaatttttccaagatttggaatacctaaggtaatagggtcagaca 	φġ
5007 4679	4948 ccttttcaggatgggtagaggcttatcctactaagaaaga	Qy Db
4947 4619	4888 acttcactgaggtaaagccggctaaatacggaaacaaatatctattggtttttgtagaca 	Qy Db
4887 4559	4828 ccagaatacctccaggaaagagactaaggggaagccacccaggcgctcactgggaagtgg 	Qy
4827 4499	4768 gagtggctgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaatcctt	Оу
4767 4439	.708 gaactaaacacctgcagcagttggtcagaacatccccttatcatgttctgaggctaccag	ОУ
4707 4379	4648 toctgccccacaaagaaggttagaatatgtccaacagatacatcgtctaacccacctag	Qy Db
4647 4319	88 agatagaccagttctctgagactccggaggggacctgctatacctcatatgggaaggaa	Qy .
4587 4259	4528 cgcccaaagccccagaacccagacgacagtacaccctagaagactggcaagagataaaaa	Qy Db
4527 4199	4468 tggctgaccgggttgccaagcaggcagcccaggctgttaaccttctgcctataatagaaa	Qу
4467 4139	4408 ctattatacactgtcctggacatcagaaagccaaagatctcatatctagagggaaccaga (Qу
4407 4079	4348 taaagaacaaagaggaaattotaagcotattagaagcottacatttgccaaaaaggotag (Qу
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Sus scrofa
Direct Submission
Submitted (15-MAY-1998) Infectious Disease Unit, Massachusetts
General Hospital, 55 Fruit Street, Boston, MA 02114, USA
Sequence update by submitter
                                                                   Direct Submission
Submitted (16-DEC-1997) Infectious Disease Unit, Massachusetts
General Hospital, 55 Fruit Street, Boston, MA 02114, USA
3. (bases 1 to 7333)
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J. Virol. 72 (5), 4503-4507
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                                                                                                                                                                                                                                                                                                                                                                                      AAGACCGCTTCTTGTGAGTGATTTGGGGTGTCGCCTCTTCCGAGCCCGGACGAGGGGGAT 130
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  ctcagaccgtaaggactggaggactgtgatcagcagacgtgctaggaggatcacaggctg
                                                       GGCGTCTCTGTTCTGAGTGTCTGTTTTCGGTGATGCGCGCTTTCGGTTTGCAGCTGTCCT
                                                                                         ggcgtctctgttctgagtgtctgttttccggtgatgcccgctttcggttttcggttttcagctgtcct 300
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/protein_id="AAC16766.1"
/protein_id="AAC16766.1"
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/translation="MGQTVTTPLSLTLDHWTEVRSRAHNLSVQVKKGPWQTFCASEWP
/translation="MGQTVTTPLS"
/translation="MGQTVTS"
/translation="MG
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PSAPGCAPVVEGPAAGTRSRRGATPERFDEIAILPLRTYGPPWPEGQLODLQYWPESS
ADLYNWKTHHPPFSEDPORLTGLVESLMFSHQPTWDDCQOLLQTLFTTEERERLLEA
KKNVPCADGREPQLQNEIDMGFPLTREGWDYNTAEGRESLKIYRQALVAGLRGASRRP
TNLAKVREVMGGPNEPPSVFLERLMEAFRFTPFDPTSEAQKASVALAFIGQSALDIR
TNLAKVREVMGGPNEPPSVFLERLMEAFRFTPFDPTSEAQKASVALAFIGQSALDIR
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/db_xref="taxon:9823"
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ANFRIGHPQVTLLQYVDDLLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQJCRRE
VTYLGYSLRGGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAP
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/protein_id="AAC16767.1"
/db_xref="G1:313305"
/db_xref="G1:313305"
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TKMGAQISFEGGRPEVSVNNKPITVLTLQLDDEYRLYSPQVKPDQDIQSWLEQFDLYDVQ
AETAGMGLAKQVPPQVIQLKASATPYSVRQVPLSEAREGIWPIVQRLLQQGILVPVQ
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               1380 acaaccgaggagcgagagaattctgttagaggctagaaaaaatgttcctggggccgac 1439
                                                     1330 CTTATGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTC
                                                                                                                             1270 AAAACTAACCATCCCCCTTTCTCGGAGGATCCCCAACGCCTCACGGGGTTGGTGGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACCCTGGGGGACGCCCCGGGAGGGTGGGGAGGCCAGGGACGCCTGGTGGTCTCCTACT
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1860 gagaaggaacagagaaaagaa 	
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                                                                                                                                     Molecular sequences of swine retroviruses method of using Patent: US 6190861-A 2 20-FEB-2001; cocation/Qualifiers 1. .7333
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3032 gagagatccaggtacgggaagaaccgggcagctcacctggacccgactgccccaagggtt 3091
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                                                                                                                                                                                                                                                                     Patent: WO 9740167-A 1
Q ONE BIOTECH LTD (GB)
                                                                                                                                                                                                                                                                                                            1 (bases 1 to 3320) Galbraith,D.N., Haworth,C., Lees,G.M. and Smith,K.T.
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                  PORCINE RETROVIRUS
Patent: WO 9740167-A 1 30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                          porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian type
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1 from Patent W09740167 A66551
                                                                                                                                                                                                                                                                                                                                              retroviruses; 1-Mammalian type C virus
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844 c 832 g
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		accgctgactggagaagtgctaacctggttcactgacggaagcagctatgtggtggaagg 4111	tcatgattgccatcaactattgattgaggagactggggtccgcaaggaccttacagacat 4051 			AACTGTAATAGCCCCCATGCATTGGAGAACATCGTTCGGCAGCCCCCAGACCGATGGAT 920 yaccaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcactttcgc 3931		tategeagetgtggecataetggteaaggaegetgaeaaattgaetttgggaeagaatat 3811			gogtaagggagtagcccgaggagttttaacccaaaccctaggaccatggaggagacctgt 3691 			gggattctcctgggctcctgagcaccagaaggcatttgatgctatcaaaaaggccctgct 3571 	GIGGATCCCGGGGTTTGCGACCTTAGCAGCCCCACTCTACCCGCTAACCAAAGAAAAAGG 560		ggcccaaaccacagccaaacaagtgagagagtttttggggacagctggattttgcagact 3451	tttgcggggcgggcagcgatggctgacggaaggcacggaagaaaactgtagtccagatacc 3391	Cagagoctotgotaagaaggocoagatttugoaggagaaggtaacatacttygygyacag 		caaacaggactgcttagaaggtacgaaggcactactgctggaattgtctgacctaggcta 3271	ccaacaccctcaggtgaccctcctccagtacgtggatgacctgcttctggcggggagccac 3211 			
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AGACCC		ATTGTG	TTTTCG	rttcg	:ggagg	atggg	GGTAA.	TCCAG	tccag	letcgg	CCTGC	cctgc	caaag	IIIII GTTCT	cccad	cccaga	GGTTG	CTGTC	AGAGG?	agaggć	ceeee	AGGGA/	AGGAA(aggga <i>a</i>	aggaac 	TANGAGATOGCIGOO
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acttcaggcgacaaaggctaggctcatggccCCCCAGACCAGATCTGGGCCAGCAGCCGCCAGCAGCCGCCAGCAGCCGCCAGCAG	Oy 5132 actgcattgto	5012 aatactggag 2061 AATACTGGAG 5072 tccagctttc	1 AATACCTCCA 2 cactgaggta 1 CACTGAGGTA 2 ttcaggatgg 1	761 TANACACCTG 772 99ctgactc9 [y 4592 agaccagttc b 1641 AGACCAGTTC y 4652 gcccacaaa y 111111111 b 1701 GCCCCACAAA	12 Calabaccas 61 TATACACTGTC 61 TATACACTGTC 72 tgacagggttc 73 tgacaggggtTc 74 TGACCGGGTTC 75 TGACCGGGTTC 76 TGACCGGGTTC 77 TGACCGGGTTC 78 TGACAGCCCCAC	4292 cgtacacggg	Db 1161 TAAGAGGATGGC Qy 4172 gccggaaggaac
	acagaccccaaagctcaggacaggtagagaggatgaatagaaa	aaatttttccaagatttggaatacctaaggtaatagggtcagacc 	GAAAGAGACTAAGGGGAAGCCACCCAGGCGCTCACTGGAAGTGGA agccggctaaatacggaaacaaatatctattggtttttgtagacac		ctgagactccggagggacctgctatacctcatatgggaaggaa		atctataaacaaaggggttgcttacctcagcagggaggga	TGGGGCGCAGTGGTGGACGGACCCGCACGATCTGGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG

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                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-MAY-1999) Virology, Max-von-Pettenkofer-Institute, Pettenkofer-Str. 9a, Munich 80336, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blusch,J.H., Seelmeir,S. and von der Helm,K.
Evidence for extreme sequence homogeneity of the PERV A/B 5'
LTR/leace/jag/prot region by predicted targeted amplification from
                                                                                                                                                                                                                                                                                                                                                                                                                                             Blusch, J.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Sus scrofa domestica
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                                                                                                /note="gag protein produced by proteolytic
mature protease out of the precursor"
                                                                                                                                                                               /rpt_type=dispersed 587. .605
                             /product="gag-pol precursor"
/protein_id="AAF65926.1"
                                                                                                                                                                                                                                                                   /strain="breed Duroc x German
/sub_species="domestica"
/db_xref="taxon:9825"
           /db_xref="GI:7650140"
                                                               transl_except=(pos:2604.
                                                                                 /codon_start=]
                                                                                                                                                      /note="primer binding site for tRNA-Gly"
                                                                                                                                                                                                                /note="PERV A/B; porcine endogenous retrovirus
/rpt_family="perv"
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KPRKPGPRILALGEKNKHSAEKVEPSPRIYPEIEEPPTWPEPDPPPPAQGAVRG
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AUTHORS
Haworth, C., Galbraith, D.N.,
  Lees, G.M.
   and
   Smith, K.T
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TCCGGCCCGGGCAAGTACAAAATGATGAAACTATATAAAGATAAGAGCTGCTCCCCATCA
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porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian
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97478526
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porcine endogenous retrovirus.
Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 1-Mammalian type C virus group.
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Le Tissier,P., Stoye,J.P., Takeuchi,Y., Patience,C.
Two sets of human-tropic pig retrovirus
Nature 389 (6652), 681-682 (1997)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	A66553	RESULT 1
/organism="porcine endogenous retrovirus" /db_xref="taxon:61673"	18209	Location/Qualifiers	Q ONE BIOTECH LTD (GB)	Patent: WO 9740167-A 3 30-OCT-1997;	PORCINE RETROVIRUS	Galbraith, D.N., Haworth, C., Lees, G.M. and Smith, K.T.	1 (bases 1 to 8209)	retroviruses; 1-Mammalian type C virus group.	Viruses; Retroid viruses; Retroviridae; Mammalian type C	porcine endogenous retrovirus	porcine endogenous retrovirus.		A66553.1 GI:4538106	A66553	Sequence 3 from Patent WO9740167.	A66553 8209 bp DNA PAT 29-MAR-1999		

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gtgcaggaaacctcgagactcggtggaagggaccttatctcgtacttttgaccacaccaa
                                                                                     2168
                                                                                                                                                                                        Conservative
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GFSWARBHOKAEDAIKKALLSAPALALPDVTKFFLLVUDERKGVARGVLTQTLGFWRR
PVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGONITVIAPHALENIVROPP
DRWMTNARMTHYQSLLLTERVTFAPPAAINPATLLPEGTDEPVTHDCHQLLIEETGVR
KDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELM
ALTQALKILAEGKSINIYDSRYAFATAHVHGAIYKORGLETSAGREIKKEEILSLLE
ALHLERRLAIHGPGHQKAKDLISRGNOMADEVAKQAQAVNLLPIETFXAPEPRRO
YTLEDWOEIKKLDQFSETPEGTCYTSYGKEILPHKEGLEYVQQIHRLTHLGTKHLQQL
VRTSPYHVLRLPGVADSVVKHCVPCQLVNANPSRIPPGKRLRGSHPGAHWEVDFTEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="GRRGSDPLPEPRVTLKVEGQPVEFLVDTGAEHSVLLQPLGKLKE
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EQGRPEVSVNNKPITVLTLQLDDEYRLYSPQVKEDQDLQSWLEGPPQAWAETAGMGLA
KQVPPQVIQLKASATPVSVRQYPLSREAREGINPHVQRLQQGILVPVQSPWNTPLLP
VRKPGTNDYREVQDLAEVNKRVQDIHETVPNPYNLLSALPPERNWYTVLDKDAFFCLL
RLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFRIQHPQ
VTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="VIRAL CORE PROTEIN"
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/TDVGWPSEGTENSEIILAVKALIFQTGPGSHDQEFYLLTWQQLAEDPPWVKPWLN
/TDVGWPSEGTENSEIILAVKALIFQTGPGSSSYLPBDGGADLAGTPTCSFPPLSSTGCCEG
KPRKPGPRILALGEKNKHASEKVERSSSYLPBDGGADLAGTPTCSFPPLSSTGCCEG
TSAPPGAPVVEGPAAGTRSRRGATPERTDEIAILPLRTYGPPMPGGGLOPLQYWPFSS
                                                                                                                                                                                                                                                                                                                               NKLRKKLERRRREREADOGWFEGWFNRSPWMTTLLSALTGPLVVLLLLLTVGPCLINR
FVAFVRERVSAVQIMVLRQQYQGLLSQGETDL"
1 2064 c 2154 g 1823 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLTIRLRIETGTEPPVAMGPDKVLAEQGPPALEPPHNLPVPQLTSLRPDITQPPSNS
TTGLIPTNTPRNSPGVPVKTGQRLFSLIQGAFQAINSTDPDATSSCWLCLSSGPPYYE
GMAKERKFNVTKEHRNQCTWGSRNKLTLTEVSGKGTCIGKAPPSHQHLCYSTVVYEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MHPTLSRRHLPTRGGEPKRLRIPLSFASIAWELTLTITPOASSK RLIDSSNPHRPLSLTWLIIDPDTGVTVNSTRGVAPRGTWWPELHFCLRLINPAVKSTP PNLYRSYGFYCCPGTEKEKYCGGSGESFCRRWSCVTSNDGDWKWPISLDDTGVTVRSTSTROYAPRGTWYPELHFCLLINPAVKSTP STALLBERKYGKYGKYKOKWYSLGNSFLLYGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="REVERSE TRANSCRIPTASE"
/protein_id="CAB39348.1"
/db_xref="GI:4538108"
                                                                                                                                                                                                                                                                                                                                                                                                 SENQYLVPGYNRWWACNTGLTPCVSTSVFNQSKDFCVMVQIVPRVYYHPEEVVLDEYDYRYRYRPKREPVSLTLAVMLGLGTAVGVGTGTAALITGPQQLEKGLGELHAAMTEDLRA
LKESYSNLEESLTSLSEVVLQNRRGLDLLFLREGGLCAALKEECCFYVDHSGAIRDSM
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/db_xref="GI:4538109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIPTWIHASHVKPAPPPDSGWRAEKTENPLKLRLHRLVPYSNNNSPGQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAKYGNKYLLVFVDTFSGWVEAYPTKKETSTVVAKKILEEIFPRFGIPKVIGSDNGPA
FVAQVSQGLAKILGIDWKLHCAYRPOSSGQVERMNRTIKETLTKLTTETGINDWAALL
PFVLFRVRNIPGQFGLTPYELLYGGEPPLAEJAFAHSADVLLSGPLFSRIKALEWRG
RAWKOLREAYSGGDLQVPHRFQVGDSVYVRRHRAGNLETRWKGPYLVLLTTPTAVKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGNKGPKVLALEEDKD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KILAAVVEGKSSRERERDFRKIRSGPRQSGNLGNRTPLDKDQCAYCKEKGHWARNCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKLQRLEGLQEAELRDLVREAEKVYYRRETEEEKEQRKEKEREEREERRDRRQEKNLT
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RKNVPGADGRPTQLQNEIDMGFPLTRPGWDYNTAEGRESLKIYRQALVAGLRGASRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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TITLE
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388 cacctcccgactcggggtggagagccgaaaagactgagaatccccttaagcttcgcctcc
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                                CGGCTGTGAAAGTCGAAGGAATCCCCACCTGGATCCATGCATCCCACGTTAAGCYGGCGC
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A66552
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Viruses; Retroid viruses; Retroviridae; Mammalian type
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Q ONE BIOTECH LTD (GB)
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Galbraith, D.N., Hawo
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                                                                                                                                                                                                                                                     Submitted (04-MAY-1999) Toenjes R.R., Medice Paul-Ehrlich-Institut, Paul-Ehrlich-Strasse
                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 8750)
Czauderna,F., Fischer,N., Boller,K., Kurth,R. and Tonjes,R.R. Establishment and characterization of molecular clones of por endogenous retroviruses replicating on human cells
                                                                                                                                                                                                                                        Langen,
                                                                                                                                                                                                                                                                                                                                        Toenjes, R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine endogenous retrovirus type C proviral gag, genes and LTR (class B, clone 43).
AJ133818
                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retroviruses; 1-Mammalian type C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       porcine endogenous retrovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                            Virol. 74 (9), 4028-4038 (2000)
                                                                                                                                                                                                                                             GERMANY
                                                                                          /strain="type C"
/db_xref="taxon:61673"
                                                                                                                                        /proviral
                                                                                                                                                            /organism="porcine endogenous retrovirus"
                                                                      /clone="43"
                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                       Medical Biotechnology,
trasse 51-59, Hessen, D-63225
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SFEGGFPEVSVNINKEITVLTIQLDEYRIZISPOKPODDIOSRILEGPPOAMBLIANGWAL
SFEGGFPEVSVNINKEITVLTIQLDEYRIZISPOKPODDIOSRILEGPPOAMBLIAGMG
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LPVRKPGTNDYRPVQDLEEVNKRODIIHPTVPNPYNLLSALIPPERNWYTVLDLKDAFF
CLR.HPTSOPLFAEWRODGTGRTGQLTWTRLEQGEKNSPTIFDEALHRDLANFRIOH
POVTLLOYVDDLLLAGANTKODCLEGTRALLLELSDLGYRASAKKAQICRERTYYLGYS
LRGGORWLTEARKKTVVQIPAPTTAKOVRETIGTAGFCRLWIPGGATLAALPZYPLTKE
KGEESWAPEHQKTEDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTOTLGPW
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PDDRWMTNARMTHYOSLLTTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETG
VRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVOGTTHTWASSLPEGTSAQKAB
LWAALTQALRABECKSINIYTDGSRYAPAALNPATLLYBETDEPVTHDCHQLLIEETG
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LEBALHLPKRLAIIHCPGHQKAKDLISTGKGAAVAILVKDAAVAILVEITETGTRKHLO
QUVRTSPYHVLRLPGVAADSVVKHCVPCOLVNANPSRYPBGRKLRGSHPGAHREVDFTE
VKPAKYGNKYLLVFVDTFSGWVEAYPTKETSTVVAKKILEEIFPREGIFVULGSDNG
PAFVAQVSOGLAKILGTUWKLHCAYRPOSSGQVERMINTIKETLTKLTTTTTAV
KVBGISTWIHASHVKLAPPDSGWFARETENPLKLRLHRLVPYSNINSPGOMPTLSH
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WHLPTRGGEPKRLRIPLSFASTAWETLTTTTPOASSKRLDSSNRHPELSLTWLI IDP
DTGVTVNSTRGVAPRGTWWPELHFCLRLINAAVKSTPPNLVRSYGFYCCPGTSKEKYC
GGSEESGCRWSCVTSNUGDWKMPISLOPTVPRKYGGGAKSTLIRLIETGTBPPVAVG
POKVLARGOPPALEPPHNLPVPLITSLADITOPPSNCTTGLIPNTPRNSGGYPVKF
GORLFSLIOGAROA INSTIDDTATSSCWICLSSAPPYVEGGAKGTLIRLIETGTBPPVAVG
FORKVLARGOPPALEPPHNLPVPLITSLGADTOPSNCTTGLIPNTPRNSGGYPVKF
GORLFSLIOGAROA INSTIDDTATSSCWICLSSAPPYVEGGMAKERK WONTKEHRMOCTW
                                                                                                                                                     /product="Env
6099. .8069
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GSRNKLTLTEVSGKGTCIGKAPPSHOHLCYSTVVYEQASENQYLVPGYNRWWACNTGL
TPCVSSSVFNQSKDFCVMVQIVPRVYYHPEEVVLDEYDYRYNRPKREPVSLTLAVMLG
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1064. .2635
/gene="gag"
1064. .2635
/gene="gag"
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KGNKOPKVLALEEDKDGRRGSDPLPEPRVALKVEGOPVEFLVDTGAEHSVLLQPLGKL
KEKKSWVMGATGOROYPWTTRRTVDLAVGRVTHSFLVIPECPVPLLGRDLLTKMGAQI
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RKNVPGADGRPTQLQNEIDMGFPLTRPGWDYNTAEGRESLKIYRQALVAGLRGASRRP
TNLAKVREVWQGPNBPPSVFLERLMEAFRRFTPFDPTSEAQKASVALAFIGQSALDIR
KKLQRLEGLQEAELRDLVREAEKVYYRRETEBEKEQRKEKERBEREERRDRRQEKNLT
                                                                                                                              /gene="env"
                                                                                                                                                                                                  function="retroviral envelope"
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KPRKPGPRILALGEKNKHSAEKVEPSPRIYPEIEEPPTWPEPQPVPPPPYPAQGAVRG
PSAPPGAPVVEGPAAGTRSRRGATPERTDEIAILPLRTYGPPWPGGQLQPLQYWPFSS
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632. .649
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                                                                                                                                                                                                                                                                                                                                                  function="retroviral"
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	961 aagtggataaatggtatgagctggggaatagtttttaataataatgcgggggagcagg 961 aagtggataaatggtatgagctggggaatagttttttaataatatgcgggggggagcagg 	Qу
tcaa TCAA	901 tcagacttagattatctaaagataagtttcactgaaaaaggaaaacaggaaaatat 	ph VQ
ccca CCCA	841 aattccggcccgggcaagtacaaaatgatgaaactatataaagataagagctgctc 	ОУ
gtc	781 aacgatggagactggaaatggccgatctctctccaggaccgggtaaaattctccttt 	Оy
TCC	721 gagaaatactgtgggggttctgggggaatccttctgtaggagatggagctgcgtcacc	Qу
laa AA	661 agcacacctcccaacctagtccgtagttatgggttctattgctgcccaggcacagaga 	Оу
A – a	601 agaggcacetggtggcetgaactgcatttetgcetecgattgattaacecegetgtta	Qy Db
G = 6	541 tggctgattattgaccctgatacgggtgtcactgtaaatagcactcgaggtgttgctc 	Qу
S = S	481 caggccagtagtaaacgccttatagacagctcgaacccccatagacctttatcccctac	Qу
$\tilde{\Omega} - \tilde{\Omega}$	421 ctgagaatccccttaagcttcgcctccatcgcctggttccttactctaacaataactcc	Qу
D - 0	361 tccatgcatcccacgttaagctggcgccacctcccgactcggggtggagagccgaaaag	Qу Db
> — a	301 cttatctogtacttttgaccacaccaacggctgtgaaagtcgaaggaatctccacctgg	Ωу
$\tilde{o} - \tilde{o}$	241 gagattcagtctatgttagacgccaccgtgcaggaaacctcgagactcggtggaaggga 	Qy Db
G – G	181 agotocgggaggcotactcaggagagagagacttgcaagttccacatcgcttccaagtt	Qy Db
o o	121 cccagcctttgttctctaggctcaaggcgctcgagtgggtgaggcaacgagcgtggaag 	Qy Db
4-4	61 acgggggaccccccccgttggtagaaattgcttctgtacatagtgctgatgtgctgctt 	Qy Db
H-H	1 tgotttttagggttaggaacacccctggacagtttgggctgaccccctatgaattgctc 	Qу
Gap	ry Match 59.6%; Score 1763; DB 14; Length 8750; t Local Similarity 99.2%; Pred. No. 0; ches 2913; Conservative 0; Mismatches 23; Indels 0;	Que Bes Mat

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KEYWORDS
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 Patent:
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                  Detection of retroviral subtypes based
                                Stoye, J.P. and Weiss, R.A.
                                                                porcine endogenous retrovirus porcine endogenous retrovirus Viruses; Retroid viruses; Ret
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KEYWORDS SOURCE

ORGANISM

porcine endogenous retrovirus. porcine endogenous retrovirus

ACCESSION DEFINITION LOCUS RESULT

Porcine endogenous Y12239

PERENV2

3482 bp

retrovirus env gene, RNA

3482 bp.

14-OCT-1997

VERSION

Y12239.1 env gene.

GI:2576324

PERENV2

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                                                     CTTATCTCGTACTTTTGACCACACCAACGGCTGTGAAAGTCGAAGGAATCTCCACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Le Tissier,P., Stoye,J.P., Takeuchi,Y., Patience,C. and Weiss,R.A. Two sets of human-tropic pig retrovirus
Nature 389 (6652), 681-682 (1997)
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/db_xref="Sprembe:041173"
/db_xref="Sprembe:041173"
/translation="MHPTLSWRHLPTRGGEPKRLRIPLSFASIAWFLTLTITPQASSK
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PNLVRSYGFYCCGGTEKEKYGGGSGESFCRWSCVTSNDGDWKWFISLODRYKFSEFVN
SGPGKYKVMKLYKDKSCGSPSDLDYLKISFTEKGKOENIQKWINGMSWGIVFYKYGGGA
GSTLTIRLRIETGTEPPVAVGPDKVLAEGGPPALEPPHULPVPQLTSLRPDITQPPSN
GTTGLIFNTFRRSPGVVVKTGGRLESLIGARPQAINSTDPDATSSCWICLSSGPPYV
EGMAKEKFNVTKEHRNQCTWGSRNKLTLTEVSGKGTCIGKAPPSHQHLCYSTVVYEQ
ASENQYLVPGYNRWWACNTGLTPCVSTSVFNQSKDFCVMVQIVPRVYXHPEEVVLDEY
DYRYNREKREPVSLTLAWNLGLGTAVGYGTGTAALTTGPPQLEKGGELHAAWTEDLR
ALEESYSNLEBSLTSLSEVVLQNRRGLDLLFLREGGLCAALKEECCFYVDHSGAIRDS
MSKLRERLERREREADQGWEEGWFNKSPWNTTLLSALTGPLVVLLLILLTVGPCLIN
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/protein_id="CAA72928.1"
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/specific_host="Sus scrofa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            taccatcctgaggaagtggtccttgatgaatatgactatcggtataaccgaccaaaaaga 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toagtottoaaccaatocaaagatttgtgtgtgtcatggtccaaaatcgtcccccgagtgtac 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTACCTGGTTATAACAGGTGGTGGGCATGCAATACTGGGTTAACCCCCCTGTGTTTCCACC 2167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtacctggttataacaggtggtgggcatgcaatactgggttaaccccctgtgttttccacc 1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaacccgtatcccttaccctagctgtaatgctcggattagggacggcggttggcgtagga 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGTCTTCAACCAATCCAAAGATTTCTGTGTCATGGTCCAAATCGTCCCCGAGTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcaggagccatcagagactccatgaacaagcttagaaaaaagttagagaggcgtcgaagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Czauderna, F., Fischer, N., Boller, K., Kurth, R. and Tonjes, R.R. Establishment and characterization of molecular clones of porcine endogenous retroviruses replicating on human cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           env gene; gag gene; pol gene.
porcine endogenous retrovirus.
porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-MAR-1998) R.R. Toenjes, Paul-Ehrlich Institut, Paul-Ehrlich Str. 51-59, P.O.Box 1740, D-63207 Langen, FRG
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BASE COUNT
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Best Local :
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                                            301 ottatotogtacttttgaccacaccaacggctgtgaaagtcgaaggaatctccacctgga 360
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             acagaccctgctggctgccagtaaataggtagaaggtcacacttcctattgttccagggc
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CCAGACCCTGCTGCCAGTAAATAGGTAGAAGGTCACACTTCCTATTGTTCCAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 8918)
Czauderna, F., Fische
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Viruses; Retroid viruses; Retroviridae; Mammalian
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genes and LTR (class B,
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                                                                                                                                                                                                                                                                                                                                                                                                                          endogenous retroviruses replicating on human cells J. Virol. 74 (9), 4028-4038 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
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                                                                                        /gene="gag"
1154 . . 2725
/gene="gag"
                                                                                                                                                             /note="cap: 710...727
                                                                                                                                                                                           545
                                 /product="Gag protein" join(1154. .2725,2729. .6/

/note="viral polypeptide"
                                                                                                                                     /note="gly4"
1154. .2725
                                                                                                                                                                                                                                                                          /proviral
                                                                                                                                                                                                                                                                                                        1. .8918
/protein_id="CAB65339.1"
/db_xref="GI:6688946"
                                                                                                                                                                                                                    /note="grown
                                                                                                                                                                                                                                  /clone="33"
                                                                                                                                                                                                                                              /db_xref="taxon:61673"
                                                                                                                                                                                                                                                             /strain="type C"
                                                                                                                                                                                                                                                                                        organism="porcine endogenous"
                           /codon_start=
                                                                              function="retroviral capsid"
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polyA_signal
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ACGGGGGACCCCCCCCTTGGTAGAAATTGCTTCTGTACATAGTGCTGATGTGCTGCTTT 5945
                                                                                                                         TGCTTTTTAGGGTTAGGAACACCCCTGGACAGTTTGGGCTGACCCCCTATGAATTGCTCT
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8212. .8918
8811. .8816
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LMALTQALRLAGKSINIYTDSRYAFATAHVIGAIYKQRGLLTSAGREIKNKEEILSL
LEALHLPKRLAIIHCPGHQKAKDLISRGNQMADFVAKQAQAVNLJLPIIETPKAPEPR
RQYTLEDWQEIKKIDQPSETPBGTCYTSYGKEILPHKEGLEYVQQIIHRLTHLGTKHLQ
QLVRTSEYHVLRLEGVADSVVKHCVPCQLVNANPSRIPPGKRLRGSHPGAHWEVDFTE
VKPAKYGNKYLLVFVDTFSGWYFYKKETSTYVAKKILEELFRRGIPKTGINDWIA
LLPFVLGYNAQVSQGLAKILGIDWKLHGAYPYKKETSTYVAKKILELTKITTFTGINDWIA
LLPFVLFRVRNTPGQFGLTPYELLYGGPPLVEIASVHSADVLLSQDLFSRLKALEWV
RQRAWKQLREAYSGEGDLQVPHREQVGDSVYVRRHRGNLLTTWKKGPYLVLLTPTAN
RQRAWKQLREAYSGEGDLQVPHREQVGDSVYVRRHRGNLTTRWKKGPYLVLLTPTAN
VEGTSTWITTSHVYIN DEDDCGTON
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LAKQVPPQVIQLKASATPVSVRQYPLSREAREGIWPHVQRLIQGILVPVQSPWNTPL
LPVRKPGTNYXRPVQDLTEVNKRVQDIHPTVPNPYNLLSALPPERNWYTVLDLKDAFT
CLRLHPTSQPLFAFEWNDPGTGRTGQLTWTRLPGGFKNSPTIFDEALHRDLANFRIQH
PQVTLLYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Env protein" 6189. .8162
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6189. .8162
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KGEFSWAPEHQKAFDAIKKALLSAPALALPDYTKFTLYVDERKGVARGVLTQTLGPW
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PPDRWMTNAKMTHYOSLLLTERVTFAPPAALNPATLLPETDEPVTHDCHQLLIETG
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TEDVGWPSEGTFNSEIILAVKAIIFQTGPSSHPDQEPYILTWQDLAEDPPWVKPWLN
KPRKPGPRILALGEKNKHSAEKVEPSPRIYPELEEPPTWPEPQPVPPPPYPAGGAVRG
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YQGLLSQGETDL"
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RKNVPGADGRPTQLQNEIDMGFPLTRPGWDYNTAEGRESLKIYRQALVAGLRGASRRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="retroviral protease and polymerase"
product="pol protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="pol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="retroviral envelope"
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99.2%;
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Pred. No. 0;
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B Qy Вb QY

aggacag 1260	ggattgattcctaccaacacgcctagaaactccccaggtgttcctgttaagac	1201	Qy
TACCACT 7025	AACCTCGCTGCGGCCTGACATAACACAGTCGCCTAGCAACGG	6966	Db
taccac	tyccccaattaacctcyctycyycctyacataacacayccycctaycaacay	1141	Qy
Ğ=	AAAGTACTGGCTGAACAGGGGCCCCCGGCCCTGGAGCCACCGCATAA	6906	Db
cttgcc	ccgataaagtactggctgaacaggggcccccggccctggagccaccgcataa	1081	Qy
aatggga 1080 AGTGGGA 6905	tccactttaaccattcgccttaggatagagacggggacagaaccccctgtggc	1021 6846	ДУ
AGCAGGG 68	AGTGGATAAATGGTATGAGCTGGGGAATAGTTTTTTATAAATATGCGGGGG	7	Db
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TATTCAA 67		2	Db
tatto	caqacttaqattatctaaaqataaqtttcactqaaaaaqqaaaacaqqaaaa	901	Qу
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CACCTCC 6605	gagada Lacig 199999 tict99999aatccttctgtaggagatggaggtgggt 	6546	Db 49
AGAGAAA 65	CACACCTCCCAACCTAGTCCGTAGTTATGGGTTCTATTGCTGCCCAGGCAC	o oc) b
agagaaa 720	agcacacotocoaacotagtocgtagttatgggttotattgctgcccaggcac	66	Qy S
TGTTAAA 6485	AGAGGCACCTGGTGGCCTGAACTGCATTTCTGCCTCCGATTGATT		Db 53
A+++>>> 660		9	0
	tggctgattattgaccctgatacgggtgtcactgtaaatagcactcgaggtgtt	541 6366	Qy Db
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ccctac	aggccagtagtaaacgccttatagacagctcgaacccccatagacctttatc	481	Qу
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gaaaaga 4	ccatgcatcccacgttaagctggcgccacctcccgactcggggtggagagcc	361	Qy
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acctgga 3	atctcgtacttttgaccacaccaacggctgtgaaagtcgaaggaatctcc	30:	Qy
Jaagggac 300 BAAGGGCC 6125	gagattcagtctatgttagacgccaccgtgcaggaaacctcgagactcggtgg 	241 6066	Qy Db
CCAAGTGG 6065	AGCTCCGGGAGGCCTACTCAGGAGAAGGAGACTTGCAAGTTCCACATCGCTTC	6006	Дb
caagtt	gctccgggaggcctactcaggagagagagacttgcaagttccacatcgctt	181	Qy
)tggaagc 180 TGGAAGC 6005	cccagcctttgttctctaggctcaaggcgctcgagtgggtgagcaacgagcg	121 5946	Qy Db

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1 (bases to 8763)
1 (comparison of replication-competent molecular clones of porcine comparison of replication and class b derived from pig and
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porcine endogenous type C retrovirus
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus
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CDS gene

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BASE COUNT 2301
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KKSWVMGATGQRQYPWTTRRTVDLAVGRVTHSFLVIPECPVPLLGRDLLTKMGAQISF
EQGRPEVSVNNKPITVLTLQLDDEYRLYSPQVKPDQDTQSWLEQFPQAWAETAGMGLA
KQVPPQVTQLKASATPVSVRQYPLSREAREGIWPHVRLIQQGTLVPVQSPWNTPLLP
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Submitted (16-JUL-1997) Q-One
Glasgow G20 OXA, UK
                                                                                                                                                                                                                                                                                                            porcine endogenous retrovirus.
porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian type
                                                                                                                                                                                                                                                                                                                                                                                         cds
                                                                                                                                                                                                                     Haworth, C., Galbraith, D.N., Lees, G.M. and
                                                                                                                                                                                                                                 Unpublished 2 (bases 1
                                                                                                                                                                                                                                                           Porcine endogenous retrovirus (PoEV) Env sequence
                                                                                                                                                                                                                                                                       1 (bases 1 to 1971)
Haworth,C., Galbraith,D.N., Lees,G.M. and Smith,K
                                                                                                                                                                                                                                                                                               retroviruses, 1-Mammalian type C virus
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                                                                .1971
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                                                                                                                                                                                                                        Smith, K.T
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NKLHKKLERRREREBADGGWFBGMFNRSPMMTFLLSALITGPLVVLLLLTVGPCLINR
FVAFVRERVSAVQIMVLRQQYGGLLSQGETDL"
30 a 490 c 482 g 469 t

9y 383 99c9ccacctcccgactcgggttggagagccgaaaagactgagaatccccttaagct
ggcgccacctcccgactcgggttggagagccgaaaagactgagaatcccctttaagcttcg [
20 20 20 20 80 80 63 83 83 83 84 90 90
383 383 200 80 80 80 80 80 80 80 80 80
20 20 20 20 1443 80 80 80 80 80 80 80 80 80 80 80 80 80
183 20 20 20 20 80 80 80 63 63 23
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2243 ttgcctttgttagagaacgagtgagtgcagtccagatcatggtacttaggcaacagtacc 2302

2242

1816 2182

1876

1817

2183

1757

ggtttgaaggatggttcaacaggtctccttggatgaccaccctgctttctgctctgacgg

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2062 1696	003 cagcettaaaagaagaatgttgettetatgtagateaeteaggagecateagagaeteea 		U D
2002 1636	943 tggttctacagaaccggaggggattagatctgctgtttctaagagaaggtgggttatgtg 	ОУ 19 Db 15	U 0
1942 1576	883 tccgagccttaaaggagtctgttagcaacctagaagagtccctgacttctttgtctgaag 	Qy 18 Db 15	ם מ
1882 1516	823 caggaccacagcagctagagaaaggacttggtgagctacatgcggccatgacagaagatc 	Qy 18 Db 14	п n
1822 1456	763 ctgtaatgctcggattagggacggcgttggcgtaggaacagggacagctgccctgatca 	р р	п О
1762 1396	703 ttgatgaatatgac 	Qy 13 Db 13	пΩ
1702 1336	643 atttgtgtgtcatggtccaaatcgtcccccgagtgtactaccatcctgaggaagtggtcc 	Qу 16 ДЬ 13	υ 0
1642 1276	N G	Qy 1:	по
1582 1216	.523 ctgtggtttatgagcaggcctcagaaaatcagtatttagtacctggttataacaggtggt 	Qy 15 Db 11	п ^
1522 1156	63 ccgggaaggggacatgcataggaaaagc 	Qy 1,	п ~
1462	4 0		н ^
1402	343 tatcctcagggcctccttatta 	Qy 1 Db	H ^
976	283 gagctttccaagcca 	Qy 1 Db	
128 916		Qy 1 Db	
856		Db	-

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence update by submitter
On May 16, 1998 this sequence version
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-MAY-1998) Infectious Disease General Hospital, 55 Fruit Street, Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-DEC-1997) Infectious Disease General Hospital, 55 Fruit Street, Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
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 	t DLKDAFFCLRLHPTSQPLFTFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDI
                                                                                                                                                                                                        KKLQRLEGLQEAELRDLVREAEKVYYRRETEEEKEQRKEKEREEREERBRDRRQEKNLT
KILAAVVEGKSSRERERDFRKIRSGPRQSGNLGNRTPLDKDQCAYCKEKGHWARNCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus but represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Cetartiodactyla; Suina; Suidae;
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7070

ATGCGGACCTCCGGAGCTATTTTAAAATGATTGGTCCACGGAGCGCGGGCTCTCGATATT

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Submitted (04-MAY-1999) Toenjes R.R., Medical Biotechnology,
Paul-Ehrlich-Institut, Paul-Ehrlich-Strasse 51-59, Hessen, D-63225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genesand LTR (class A, AJ133817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 1-Mammalian type C virus group.
1 (bases 1 to 8849)
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2 (bases 1
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1115, .260
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             /protein_id="CAB65340.1"
/db_xref="G1:6688948"
/db_xref="G1:6688948"
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PSAPPCAPVVEGPAAGTASRRCATPERSTDEATLILATYGPMPEGQLLQCYWPFSE
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ADLYNWKTNHPPFSEDPQRLTGLVESLMFSHQPTWDDCQQLLQTLFTTEERERILLEA
                                                                                                                                                                                                                                                         /note="
1115. .
RKNVPGADGRPTQLQNEIDMGFPLTRPGWDYNTAEGRESLKIYRQALVAGLRGASRRP
                                                                                                                                         /product="Gag protein"
join(1115. .2686,2690. .6
/note="viral polypeptide"
                                                                                                                                                                                                                                                                                                      /note="cap site"
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                                                                                                                                                                                                                                                                                                                                                                       /clone="42"
                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:61673"
                                                                                                                                                                                                                                                                                                                                                                                                    /strain="type C"
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polyA_signal {
BASE COUNT 2355 a 7877 GTTAGAGAGGCGTCGAAGGGAAAGAGAGGCTGACCAGGGGTGGTTTGAAGGATGGTTCAA 7936 2142 caggtctccttggatgaccaccctgctttctgctctgacggggcccctagtagtcctgct 2201 2082 gttagagaggcgtcgaaggggaaagaggctgaccaggggtggtttgaaggatggttcaa 2141 7937 CAGGTCTCCTTGGATGACCACCCTGCTTTCTGCTCTGACGGGGCCCCTAGTAGTCCTGCT mat_peptide mat_peptide Local agtgagtgcagtccaggatccatggtacttaggcaacagtaccaaggccttctgagccaagg AGTGAGTGCAGATCATGGTACTTAGGCAACAGTACCAAGGCCTTCTGAGCCAAGG 676; Similarity Conservative /gene="env" 8182. .8849 8742. .8747 a 2191 c /gene="pol" 6150. .8129 /gene="env" /product="Env protein" 6150. .8129 YCGNPQDEFCKOWSCITSNDGNWKWPVSOQDRVSYSFVNNPTSYNOFNYGHGRWKDWQ GRVQKDYRNKQISCHSLDLDYLKISFTEXGKOENIQKWVNGISWGIVYYGGSGRKKGS VLTIRLRIETQMEPVAIGPNKGLAEQGPPIGEQRESPNPSDYNTTSGSVPTEPNITI KTGAKLFESLIGGAFQALNSTTPEATSSCWLCLASGPPYYEGMARGGKFNVTKEHEDDC TWGSQNKLTLTEVSGKGTCIGMVPPSHQHLCNHTEAFNRTSESQYLVPGYDRWWACNT KVERIPTWIHASHVKPAPPDSGWKAEKTENPLKLRLHRVVPYSVNNSSSMHPTLSRR HLPIRGGKPKRLKIPLSFASIAWFLTLSITPQVNGKRLVDSPNSHKPLSLTWLLTDSG TGININSTQGEAPLGTWWPELYVCLRSVIPGLNDQATPPDVLRAYGFYVCPGPPNNEE RQYTLEDWQEIKKIDQFSETPEGTCYTSYGKEILPHKEGLEYVQQIHRLTHLGTKHLQ QLVRTSPYHVLRLPGVADSVVKHCVPCQLVNANPSRIPPGKRLRGSHPGAHWEVDFTE VKPAKYGNKYLLVFVDTFSGWVEAYPTKKETSTVVAKKILEEIFPRFGIPKVIGSDNG RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALĒNIVRQ PDRWMTNARWTHYQSLLLTERVTFAPPALNPATLLPEETDEPVTHDCHQLLILEETG VRKDLTDIFDIGEVITWFDGSSYVVEGKRMAGAAVUDGTRTIWASSLPEGTSAQKAE LMALTQALRLAEGKSINIYTDSSRYAFATAHVHGAIYKQRGLLTSAGREIKNKEEILSL function="retroviral protease and polymerase" /product=-Pol protein" 2690. .6271 QQYQGLLSQGETDL" 2690. .6271 PAFVAQVSQGLAKILGIDWKLHCAYRPQSSGQVERMNRTIKETLTKLTTETGINDWA LLPFVLFRVRNTPGQFGLTPYELLYGGPPPLVEIASVHSADVLLSQPLFSRLKALEWV LRGGQRWLTBARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKE KGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW KKLQRLEGLQEAELRDLVREAEKVYYRRETEEEKEQRKEKEREEREERRDRRQEKNLT KILAAVVEGKSSRERERDFRKIRSGPROSGNLORTPILDKDQCAYCKEKGIWARNCPK KGNKGPKVLALEEDKOGREGSDPLPEBRYTLKVEGQPVEELVDTGAEHSVLLOPLGK KEKKSWVMGATGQRQYPWTTRRTVDLGVGRVTHSFLVIPECPVPLLGRDLLTKMGAQI ${\tt GWFEGWFNRSPWMTTLLSALTGPLVVLLLLLTVGPCLINRFVAFVRERVSAVQIMVLR}$ VLQNRRGLDLLFLKEGGLCVALKEECCFYVDHSGAIRDSMSKLRERLERRRREREADQ GLTPCVSTLVFNQTKDFCVMVQIVPRVYYYPEKAVLDKYDYRYNRPKREPISLTLAVM RQRAWKQLREAYSGEGDLQVPHRFQVGDSVYVRRHRAGNLETRWKGPYLVLLTTPTAV PQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYS CLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDLANFKIQH LPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSALPPERNWYTVLDLKDAFF SFEQGRPEVSVNNKPITVLTLQLDDEYRLYSPQVKPDQDIQSWLEQFPQAWAETAGMG LGLGVAAGVGTGTAALITGPQQLEKGLSNLHRIVTEDLQALEKSVSNLEESLTSLSEV LEALHLPKRLAIIHCPGHQKAKDLISRGNQMADRVAKQAAQAVNLLPIIETPKAPEPR LAKQVPPQVIQLKASATPVSVRQYPLSREAREGIWPHVQRLIQQGILVPVQSPWNTPL function="retroviral envelope" 21.2%; 0; 2281 Score 626; Pred. No. 0; Mismatches g 2022 DB 14; μ, Length 8849; Indels 0; Gaps 8116 2321 8056 2261 7996 0;

В Qy 밁 Š Db Qy

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cctgttacttacagttgggccttgcttaattaattaggtttgttgcctttgttagagaacg
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                                              CAGGTCTCCTTGGATGACCACCCTGCTTTCTGCTCTGACGGGGCCCCTAGTAGTCCTGCT 2057
                                                                                                         GTTAGAGAGGCGTCGAAGGGAAAGAGAGAGGCTGACCAGGGGTGGTTTGAAGGATGGTTCAA 1997
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Stoye, J.P. and Weiss, R.A.
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Viruses; Retroid viruses; Ret
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1 from Patent WO9853104.
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1 573 c 575 g
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                                                                                                                                                                                                                                                                                                                                                      COUNCIL (GB);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1-Mammalian type C virus group
                                                                                                                                                                      0;
                                                                                                                                                                                 Score 457; DB 6;
Pred. No. 3.6e-252;
                                                                                                                                                                                                                                                                                                                                                                                                     subtypes based upon envelope
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                        STOYE JONATHAN PAUL (GB); WEISS ROBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroviridae; Mammalian type
                                                                                                                                                                                                                                                                599 t
                                                                                                                                                                                                Length 2462;
                                                                                                                                                                      Indels
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                                                                                                                                                                   Gaps
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-APR-1997) J.P. Stoye, National Institute Research, Virology, The Ridgeway Mill Hill, London, NW7 revised by author 16-SEP-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2462)
Stoye, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   porcine endogenous retrovirus
Viruses; Retroid viruses; Retroviridae; Mammalian type
retroviruses; 1-Mammalian type C virus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Le Tissier,P., Stoye,J.P., Takeuchi,Y.,
Two sets of human-tropic pig retrovirus
Nature 389 (6652), 681-682 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y12238
Y12238.1 GI:2576322
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                                                                                                                                                                   /gene="env"
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/codon_start=1
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/prottin_id="CAA72927.1"
/prottin_id="CAA72927.1"
/prottin_id="CAA72927.1"
/db_xref="g1:2576323"
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/db_xref="sPTREMBL:041172"
/db_xref="
                                SPNPSDYNTTSGSVPTEPNITIKTGAKLFSLIQGAFQALNSTTPEATSSCWLCLASGP
PYYECHARGKENVTKEHRDQCTWGSQNLLTLTEVSGKGTCIGNPPYPSHQHLCNHTEA
FNRTSESQLLVPGYDGWAACNTGLTPCVSTLVFNQTKDFCVLWYQIVPRVYYYEKAVL
DEYDYRYNRPKREPISLTLAVMLGLGVAAGVGTGTAALITGPQQLEKGLSNLHRIVTE
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211. .2193
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211. .2193
DLQALEKSVSNLEESLTSLSEVVLQNRRGLDLLFLKEGGLCVALKEECCFYVDHSGAI
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/db_xref="taxon:61673"
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ORIGIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              2082 gttagagaggcgtcgaagggaaagaggctgaccaggggtggtttgaaggatggttcaa 2141
                                                                                                             2442 ctctaaatgcccccgaattacagaccctgctggctgccagtaaataggtagaaggtcaca
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                                                                                                 CTCTAAATGCCCCCGAATTCCAGACCCTGCTGGCTGCCAGTAAATAGGTAGAAGGTCACA
                                                  GGGAATGAAAGGATGAAAATGCAACCTAACCCTCCCAGAACCCAGGAAGTTAATAAAAAG
                                                                                                                                                            gggaatgaaaggatgaaaatgcaacctaaccctcccagaacccaggaagttaataaaaag
                                                                                                                                                                                                  AGAAACTGACCTCTAGCCTTCCCAGTTCTAAGATTAGAACTATTAACAAGACAAGAAGTG
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LINRFVAFVRERVSAVQIMVLRQQYQGLLSQGETDL"
a 573 c 575 g 599 t
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99.8%;
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Pred. No. 3.6e-252;
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Search completed: February Job time: 28485 sec 24, 2002, 07:32:50

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                      Score
                 8209
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2967
2682
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Match Length DB
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117.9
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ALIGNMENTS

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AAV09700
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   CDS
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                                                                                                                                                                                                                                                                                                AAV09700 standard; DNA; 8209 BP.
                                        CDS
                                                                                                       misc_feature
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                                                                                                                                                                                   Porcine retrovirus.
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Best Local Similarity
Matches 8209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA sequence encodes the porcine retrovirus (POEV) virion core polypeptide (GAR), polymerase (POL) and envelope (ENV) proteins and also includes the Long Terminal Repeat (LT). These proteins can be used to develop viral vaccines, antisense nucleic acids, ribozymes and other antiviral agents. They can also be used in xeno-transplantation technology and as diagnostic tools.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding porcine retrovirus expression product useful to develop products for use in vaccines, diagnosis and
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gctc	igatga atga	 ataa	ggct	tgtt:	lili tgag tgtt	 tgctg atgag	IIIII laaggg tqctq	lgact lgact	gact	atacc	tacag	iiii	igcca iggct	gcca [[]]	cagga cagga	 	cgaa cgaa	cgaa	acttaa cttaa	ac	cgaac	yacca gacca	garra.
acca	CCAAC	ctgta ctgta	HHH tegea		ijiii gtaa ccta	IIII gege	 gatt ggatt	tgga	tgga	99ccc	tttgc	Caga	caga	caaa 	tccaa tccaa	Caag	ggag ggag tcaa	ggag	aaga 	cctta	ctta	gtaca gtaca	† V
ccgc	geeeg 11111	latago atago	igetg 	HIII	 ggag	IIIII acct	ictec	cccg	cccg	caacc	36666 11111 36666	loct.	agga	agga	Caccc	IIIII	igat lgat	igat	tgcctt	taacc	aac	ggact 	
tete	Catga	1111	1111 1111	 aaag	agcc	ctct	19990	ggtt ggtt	gggtt	acago 	2999ca 999ca	gcta	tgct	ctgct	tcagg		IIII aggt	aggt ette	cttc	tettg	tett	tgaga	
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gcca) 	ttgg ttgg	ggtca ggtca	tgat	lagti agti	IIIII	igcac	ctta	cctta	aagtg	tggct 11111 tggct		gtac	ggtad	ctcct	++++++++++++++++++++++++++++++++++++++	agaa	lagat agaa	.gagat	HIII	cctc	caat	
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Оy Дb Qy DЬ

DЪ Qy

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y 6961 gaatatgactatcggtataaccgac 	6781 gtttatgagcaggcctcagaaatcg 6841 tgcaatactgggttaaccccctgtg 6841 tgcaatactgggttaaccccctgtg 6841 tgcaatactgggttaaccccctgtg 6901 tgtgtcatggtccaaatcgtccccc 6901 tgtgtcatggtccaaatcgtccccc	b 6601 tcagggcctccttattatgaggggatch b 6601 tcagggcctccttattatgaggggatch b 6601 tcagggcctccttattatgagggatch y 6661 catagaaatcaatgtacatggggtc y 6661 catagaaatcaatgtacatgggggtc	6361 ccccoggccctgagccaccgcataac 61 cccccggccctggagccaccgcataac 6361 cccccggccctggagccaccgcataac 6421 gacataacacagccgcctagcaacagt 6421 gacataacacagccgcctagcaacagt 6421 gacataacacaggccgcctagcaacagt 6481 aactccccaggtgttcctgttaagacc 6481 aactccccaggtgttcctgttaagacc 6481 aactccccaggtgttcctgttaagacc 6481 aactccccaggtgttcctgttaagacc 6481 aactccccaggtgttcctgttaagacc 6541 ttccaagccatcaactccaccgaccc	6121 atgatgaaactatataaagataagagct
	cagtatitagiacotggttataacaggtgg1gggccagtatitagiacotggttataacaggttgttcaaccaatccaaagatttugtttcaaccaatccaaagatttugtttcaacctaagttttll	tgyctaaagaaagaaatcaatgigaccaaagag [rettgccggtgcccaattaacctcgctgcggcct 6 acttgccggtgcccaattaacctcgctgcggcctaga 6 gtaccactggattgattcctaccaacacgcctaga 6 fll	ttgctccccatcagacttagattatctaaagata

Porcine retrovirus; PoEV; POL protein; ENV protein; GAG protein;

Porcine retrovirus DNA encoding, GAG, POL and ENV.

19-MAY-1998 (first entry)

AAV09699;

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RESULT
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AAV09699 standard; DNA;

8196

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                                                                                                                                                                                                       Matches 8192;
                                                                                                                                                                     Query Match
121 ggcctttcatttggtgcgttggccgggaaatcctgcgaccaccccttacacccgagaacc 180
           133 ggcctttcatttggtgcgttggccgggaaatcctgcgaccaccccttacacccgagaacc 192
                                                                                                                                                                                           Sequence 8196 BP; 2165 A; 2061 C; 2147 G; 1820 T; 3 other;
                                                                                                                                                                                                                      This DNA sequence encodes the porcine retrovirus (PoEV) virion core polypeptide (GAG), polymerase (POL) and envelope (ENV) proteins. These proteins can be used to develop viral vaccines, antisense nucleic acids, ribozymes and other antiviral agents. They can also be used in
                                                                                                                                                                                                                xeno-transplantation technology and as diagnostic tools.
                                                                                                                                                                                                                                                                                      Claim 4; Fig 2; 69pp; English.
                                            61 cgtgagtgatttggggtgtcgcctcttccgagcccggacgagggggattgttcttttact 120
                                                       73 cgtgagtgatttggggtgtcgcctcttccgagcccggacgagggggggattgttcttttact 132
                                                                                                  13 tgtgggccccagcgcgcttggaataaaaatcctcttgctgtttgcatcaagaccgcttct 72
                                                                                                                                                                                                                                                                                                                 xeno-transplantation
                                                                                                                                                                                                                                                                                                                           Polynucleotide encoding porcine retrovirus expression product
                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-535851/49.
                                                                                                                                                                                                                                                                                                                                                                             Galbraith DN, Haworth C, Lees GM,
                                                                                                                                                                                                                                                                                                                                                                                                     (IMUT-) IMUTRAN LTD.
(QONE-) Q-ONE BIOTECH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1997;
19-APR-1996;
                                                                                      1 tgtgggccccagcgcgcttggaataaaaatcctcttgctgttttgcatcaagaccgcttct 60
                                                                                                                                                     Match 95.0%;
Local Similarity 99.9%;
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                                                                                                                                                                                                                                                                                                                   to develop products for use in vaccines, diagnosis
                                                                                                                                             Conservative
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96GB-0008164
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 Mismatches

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Pred. No. 0;
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                             1201 agcccctccagtattggcccttttcttctgcagatctctataattggaaaactaaccatc 1260
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                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                                                                                                                                                                                                                                                                           Defective retroviral genome isolated from PK-15 cell line
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The present invention relates to a method for screening a cell or tissue for the presence or expression of a retrovirus (RV), comprising contacting a target nucleic acid from the cell or tissue with a second nucleic acid from the present invention (e.g. the present sequence or a graft transplantation risk. Screening of animals allows the elimination of domors with active replication of known viruses. Inactive proviruses of domors with active replication of known viruses. Inactive proviruses of potential human pathogens derived from swine in a manner not in the outbred human organ donor population and is important to can be detected and inactivated, allowing Claim 1; Fig 2; 127pp; English. or miniature swine retroviral genome Assessing risk of endogenous retroviruses in clinical practice and in xenotransplantation, comprises using probe sequences derived from swi identification and elimination from swine possible

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development of human xenotransplantation.

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                                                                           4752..6722
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4738..6725
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/note= "putative ENV coding region (partial) as
_____described in the specification"
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598..2169
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found in PK-15 cells containing the putative coding regions for viral GAG, POL and ENV proteins. There are a few in frame stop codons and apparent frame shifts in the given coding sequence which alter features apparent frame shifts in sequence and PCR fragments generated from the of the translation. This sequence and PCR fragments generated from the sequence (see AAT74812 TA482) could be used to screen organs for the presence of porcine retroviruses prior to xenotransplantation fransplantation can increase the likelihood of retroviral activation if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of transmitting infection to graft recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intact and infectious proviruses are present. The porcine retroviral sequence can be used to generate probes to determine the level (e.g. sequences) of intact (i.e. potentially replicating) porcine provirus copy number) of intact (i.e. potentially replicating) porcine provirus sequences in a strain of xenograft transplantation donors. It can be used to detect mutations, genetic lesions or viral recombinants and to used to detect mutations, genetic lesions of activated retrovirus. Using determine the histological localisation of activated retrovirus. Using replymerase Chain Reaction DNA Quantitation (pDQ) on blood mononuclear polymerase Chain Reaction bnA Quantitation (pDQ) on blood mononuclear cells, infectivity titration and susceptibility testing can be performed. Ultimately animal donors without intact porcine retroviral sequences or a lower copy number of viral elements could be selected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7393 BP; 2004 A; 1801 C; 1896 G; 1692 T; 0 other;
                                                                                                                                                                                                                                                                                                                      Match 36.1%;
Local Similarity 99.8%;
                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 gtggtgtacgactgtgggccccagcgcgcttggaataaaaatcctcttgctgtttgcatc 70
                 421 gtcggtcagaggaccgagttctgttgttgaagcgaaagcttcccccttccgcgggccgtccg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 aagaccgcttcttgtgagtgatttggggtgtcgcctcttccgagcccggacgaggggat 130
431 gtcggtcagaggaccgagttctgttgttgaagcgaaagcttccccctccgcggccgtccg 490
                                                                              371 ccaccctgggggacgccccgggaggtggggagagccagggacgcctggtggtctcctact 430
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           1500 tgggactacaacacggctgaaggtagggagagcttgaaaatctatcgccaggctctggtg 1559
                                                     1450 gggcgacccacgcagttgcaaaatgagattgacatgggatttcccttgactcgccccggt
                                                                  1440 gggcgacccacgcagttgcaaaatgagattgacatgggatttcccttgactcgccccggt 1499
                                                                                                          atttgtcagttcaggttaagaagggaccttggcagactttctgtgcctctgaatggccaa 720
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                                                                                                                       acaaccgaggagcgagagagttctgttagaggctagaaaaaatgttcctggggccgac 1439
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                                    2590 atacagtectggttggageagtttececeaageetgggeagaaacegeagggatgggtttg
                                                      2580 atacagtcctggttggagcagtttccccaagcctgggcagaaaccgcagggatgggtttg
                                                                                                            2530 accetecaattagatgatgaatategaetatatteteeecaagtaaageetgateaagat 2589
                                                                                                                                2520 accetecaattagatgatgaatategaetatatteteeceaagtaaageetgateaagat 2579
                                                                                                                                                                                                        2460 atttcttttgaacaaggaagaccagaagtgtctgtgaataacaaacccatcactgtgttg 2519
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3490 gccccactctacccgctaaccaaagaaaaaggggg 3524
                              3480 gccccactctacccgctaaccaaagaaaaaggggg 3514
                                                   3430 gagtttttgggggacagctggattttgcagactgtggatcccgggggtttgcgaccttagca 3489
                                                                      3420 gagtttttggggacagctggattttgcagactgtggatcccgggggtttgcgaccttagca 3479
                                                                                                                 3370 gaggcacggaagaaactgtagtccagataccggccccaaccacagccaaacaagtgaga 3429
                                                                                                                                3360 gaggcacggaagaaactgtagtccagataccggccccaaccacagccaaacaagtgaga
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RESULT 5
AAV09698
ID AAV09698;
XX
AC AAV09698;
XX
DT 19-MAY-1998 (first entry)
XX
XX
DF Porcine retrovirus pol and env DNA.
XX
XX
KW Porcine retrovirus; PoEV; POL protein; ENV protein; vaccine;
KW diagnosis; xenotransplantation; prophylactic; therapeutic; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA sequence encodes the porcine retrovirus (POEV) polymerase (POL) and envelope (ENV) proteins. These proteins can be used to develop viral vaccines, antisense nucleic acids, ribozymes and other antiviral agents. They can also be used in xeno-transplantation technology and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-535851/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic tools.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xeno-transplantation
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3332 tttgcggggcgggcagcgatggctgacggaggcacggaagaaaactgtagtccagatacc 3391
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agttggagattcagtctatgttagacgccaccgtgcaggaaacctcgagactcggtggaa
                                                                                                              9t9gaagcagctccgggaggcctactcaggaggagacttgcaagttccacatcgcttcca
                                                                                   gtggaagcagctccgggaggcctactcaggaggagacttgcaagttccacatcgcttcca
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                                                                                                                                                                                                    gctgctttcccagcctttgttctctaggctcaaggcgctcgagtgggtgaggcagcgagc 5431
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Qy В

Вb QΥ Дb γ 밁 Qy B Q DЪ

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5699 cctccatcgcctggttccttactctaaccaataactccccaggccagtagtaaacgcctta 5758

cctccatcgcctggttccttactctaacaataactccccaggccagtagtaaacgcctta

5639 ggcgccacctcccgactcggggtggagagccgaaaagactgagaatccccttaagcttcg 5698

ggcgccacctcccgactcggggtggagagccgaaaagactgagaatccccttaagcttcg

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В

Qy DЬ

DЬ Ş DЪ Qy 망 QΥ 밁 Ş 밁 Qγ

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Matches 1949;
                                 Query Match
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                                                            Sequence 1974 BP; 534 A; 489 C; 483 G; 468 T; 0 other:
                                                                                            This sequence encodes the porcine retrovirus envelope (ENV) protein isolated from the human cell line Raji. Such viral proteins can be u to develop viral vaccines, antisense nucleic acids, ribozymes and ot antiviral agents. They can also be used in xeno-transplantation
                                                                                                                                                                                            Polynucleotide encoding porcine retrovirus expression product useful to develop products for use in vaccines, diagnosis and
                                                                                       technology and as diagnostic tools.
                                                                                                                                                             Claim 6; Fig 4; 69pp; English.
                                                                                                                                                                                       xeno-transplantation
                                                                                                                                                                                                                                       P-PSDB; AAW39274.
                                                                                                                                                                                                                                                 WPI; 1997-535851/49
                                                                                                                                                                                                                                                                           Galbraith DN,
                                                                                                                                                                                                                                                                                               (IMUT-) IMUTRAN LTD
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19-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porcine retrovirus
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                   Local Similarity
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       Conservative
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96GB-0008164
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1..1974
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/product= ENV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "envelope protein"
                18.3%;
99.7%;
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       0;
                Score 1499;
Pred. No. 0
     Mismatches
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                            DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pig endogenous retrovirus; PERV-A; envelope protein; PERV-B; subtype; probe; primer; detection; retrovirus; human tissue; xenotransplant; primary porcine tissue; human cell line; porcine cell line; ss.
                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                  endogenous retrovirus
                                                                                                                                                                 911..2884
               /product= envelope_protein
                                                                                            /*tag=
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Claim 3; Page 21-23; 36pp; English.
                                                                                                       Newly isolated nucleic acid probe capable of hybridising to either the PERV-A or PERV-B env gene - useful in the detection of retroviruses, and their subtypes, in a sample of porcine/human
                                                                                                                                           P-PSDB; AAW85452.
                                                                                                                                                  WPI; 1999-045324/04.
                                                                                                                                                                               (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                             16-MAY-1997;
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                                                                                                                                                                 Weiss RA;
                                                                                                                                                                                            97GB-0010154
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envelope genes. Probes and primers can be derived from the envelope (env) genes of PERV-A and PERV-B. The probes and primers are used in a method to detect retroviruses in a sample of porcine/human tissue, cultivated in the presence of a porcine cell line, or human tissue from a patient with a xenotransplant. Subtype of PERV in a sample containing one of the PERV env genes can also be determined. The present sequence encodes a Pig endogenous retrovirus (PERV)-B envelope protein. PERV exists in two different subtypes, PERV-A and PERV-B. The differences are reflected in sequence divergence in the

Sequence 3482 BP; 927 A; 854 C; 867 G; 834 T; 0 other;

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             6059 cgatctctctccaggaccgggtaaaattctcctttgtcaattccggcccgggcaagtaca 6118
                                                                                                                                           5939 gtagttatgggttctattgctgcccaggcacagagaaagagaaatactgtggggggttctg 5998
                                                                                                                            1230 gtagttatgggttctattgctgcccaggcacagagaaaagagaaatactgtgggggttctg
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PERV env protein coding sequence SEQ ID NO:

27-MAR-2001 (first entry)

xenotransplantation; infectious agent; vaccine;

Porcine endogenous retrovirus.

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gcttggaataaaaatcctcttgctgtttgcatc 3482
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             gcttggaataaaaatcctcttgctgtttgcatc 8187
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                                                                     tccgcactcggggccgcagtcctctacccctgcgtggtgtacgactgtgggccccagcgc 8154
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The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the transplant recipient.

Sequence 4402 BP; 1259 A; 1085 C; 1111 G; 947 T; 0 other;

10.3%;

Pred. No. 0; Score 848;

DB 22;

Length 4402;

Claim 16; Page 105-106; 144pp; English.

swine cells -

Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as

(MAYO-) MAYO MEDICAL VENTURES

24-MAY-1999;

99US-0135631

24-MAY-2000; 2000WO-US14296

30-NOV-2000 WO200071726-A1

WPI; 2001-032041/04 Federspiel MJ;

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WO200071726-A1
                                                                    Xenotransplantation; infectious agent;
                                                                               PERV env protein coding sequence
                                                         Porcine endogenous retrovirus
                                                                                             27-MAR-2001
                                                                                                                    AAC67021 standard; DNA; 6076
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(MAYO-) MAYO MEDICAL VENTURES

24-MAY-1999;

99US-0135631.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as
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Sequence 7362 BP; 1997 A; 1821 C; 1881 G; 1663 T; 0 other;

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                                                                                                 Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such
                                                                                                                                                      WPI; 2001-032041/04.
                                                                                                                                                                           Federspiel MJ,
                                                                                                                                                                                                                      24-MAY-1999;
                                                                                                                                                                                                                                                                 30-NOV-2000
                                                                                                                                                                                              (MAYO-) MAYO MEDICAL VENTURES
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                                                                                                                                                                                                                                                                                     WO200071726-A1
                                                                                                                                                                                                                                                                                                        Porcine endogenous retrovirus
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The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the

transplant

Claim 16; Page 101-104; 144pp; English.

such as

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3942 geteteaaccetgeceactettetgeetgaagagaetgatgaaccagtgaetcatgattge
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Pred. No. 1.8e-297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC67032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                               Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such a
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                                                                                                                                                                                                            Sequence 6076 BP; 1619 A; 1505 C; 1598 G; 1354 T; 0 other;
                                                                                                                                                                                                                                                          The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from
                                                                                                                                                                                                                                                                                                           Claim 16; Page 117-119; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAYO-) MAYO MEDICAL VENTURES
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                                                                                                                                                                                                                                               the infectious agent, and then introducing these cells into the
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Pred. No. 7.7e-278;
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	ctctgg	41	Db
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RESULT 12 AAT74884 ID AAT748: XX

AAT74884 standard; cDNA; 7892 BP

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Query Match
Matches 2204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miniature swine retrovirus cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine retrovirus.
                                                                                            infectious proviruses are present. The porcine retroviral sequence can be used to generate probes to determine the level (e.g. copy number) of intact (i.e. potentially replicating) porcine provirus sequences in a strain of xenograft transplantation donors. It can be used to detect mutations, genetic lesions or viral recombinants and also to determine the histological localisation of activated retrovirus. Using polymerase chain Reaction DNA Quantitation (PDQ) on blood mononuclear cells, infectivity titration and susceptibility testing can be performed. Ultimately animal donors without intact porcine retroviral sequences or a lower copy number of viral elements could be selected.
                                                                                                                                                                                                                                          containing the putative coding regions for viral GAG, POL and ENV proteins. This sequence and PCR fragments generated from it (see AAT74812-T74882) can be used to screen organs for the presence of porcine retroviruses prior to xenotransplantation. Transplantation can increase the likelihood of retroviral activation if intact and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1995;
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                                                                                                                                                                                                                                                                                                                This cDNA sequence represents a porcine retrovirus from miniature swine
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW32096-W32098.
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                                                                                                                                                                                                                                                                                                                                                                            transmitting infection to graft recipient
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                                                                     Sequence
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98.7%;
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               3993 catgattgccatcaactattgattgaggagacttggggtccgcaaggaccttacagacata
                                                           3930 ccaccagccgctctcaaccctgccactcttctgcctgaagagactgatgaaccagtgact
                                                                                                                      3870 accaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcacgttcgct
                                                                                                                                      3873 accaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcactttcgct
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5133 ctgcattgtgcatacagaccccaaagctcaggacaggtagaggatgaatagaaccatt 5192
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                                          tcaggatgggtagaggcttatcctactaagaaagagacttcaaccgtggtggctaaaaaa
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Qy 밁 δÃ В

3093 aagaactccccgaccatctttgacgaagccctacacagggacctggccaacttcaggatc

2973 gatgcettettetgeetgagattacaceceaettageeaaceaetttttgcettegaatgg 3032

gatgccttcttctgcctgagattacaccccactagccaaccactttttgccttcgaatgg 3029

Matches 2204; Query Match

Conservative

0,

Mismatches

30;

0;

Gaps

0;

Length 8132; Indels

Local Similarity

8.6%; 98.7%;

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RESULT 13
AAF77727
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                                                                                          The present invention relates to a method for screening a cell or tissue for the presence or expression of a retrovirus (RV), comprising contacting a target nucleic acid from the cell or tissue with a second nucleic acid from the present invention (e.g. the present sequence or a fragment thereof). The method is useful for RV detection and to assess graft transplantation risk. Screening of animals allows the elimination of donors with active replication of known viruses. Inactive proviruses can be detected and inactivated, allowing identification and elimination of potential human pathogens derived from swine in a manner not possible in the outbred human organ donor population and is important to the development of human xenotransplantation.
                                                                    Sequence 8132 BP; 2248 A; 1977 C; 2037 G; 1870 T; 0 other
                                                                                                                                                                                                                                                                                                                       or miniature swine retroviral genome -
                                                                                                                                                                                                                                                                                         Claim 1; Fig 3; 127pp; English.
                                                                                                                                                                                                                                                                                                                                             Assessing risk of endogenous retroviruses in clinical practice and
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-256211/26.
P-PSDB; AAB73285, AAB73286, AAB73287.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fishman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-1996;
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Score 704; Db 2...
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Qy 3273 agagcctct Db 3270 agagcctct Qy 3333 ttgcggggc Qy 3393 gccccaacc Qy 3393 gccccaacc Qy 3453 tggatcccc Qy 3450 tggatcccc Qy 3450 tggatcccc Qy 3573 agcgcacc Qy 3633 cgtaaggg Qy 3633 cgtaaggg Qy 3633 cgtaaggg Qy 3630 glallill Db 3630 gctacggac Qy 3631 actgtaagg Qy 3633 cctacact Qy 3753 atcgcagc Qy 3753 atcgcagc Qy 3753 actgcagc Qy 3753 actgcagc Qy 3753 actgcacc Qy 3753 actgcacc Qy 3873 acccaacg Qy 3933 ccaccac
273 agagcctctgctaa;
273 agagcctctgctaag
3273 agagcctctgctaaga
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3273 agagcctctgctaa
3273 agagcctctgctaaga
Qy 3153 caacacctcaggtgacc

AAC67022 ID AAC6

AAC67022 standard; DNA; 4918 BP.

RESULT 14

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                                                                                                                                                                  5010 atactggaagaaatttttccaagatttggaatacctaaggtaatagggtcagacaatggt 5069
                                                      5130 ctgcattgtgcatacagaccccaaagctcaggacaggtagaggatgaatagaaccatt 5189
                                                                  5133 ctgcattgtgcatacagaccccaaagctcaggacaggtagagaggatgaatagaaccatt 5192
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          3875 caacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcactttcgctcc 3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4918 BP; 1382 A; 1173 C; 1183 G; 1180 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 109-111; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as swine cells -
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                                                                                                                                                                                                                                                                                                                                    79 attctcctgggctcctgagcaccagaaggcatttgatgctatcaaaaaggccctgctgag 138
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caacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcacgttcgctcc
                                                      cgcagctytggccatactggtcaaggacgctgacaaattgactttgggacagaatataac
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                                                                                                                                                                                                                                                                                             CGCACCTGCTCTGGCCCTCACCTGACGTAACCTAAACCCCTTTACCCTTTATGTGGATGAGCG 3634
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                               aggatgggtagaggcttatcctactaagaaagagacttcaaccgtggtggctaagaaaat 1578
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                                                                                                                                                                                                                                                                                                                    Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as
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                                                                      Sequence 7873 BP; 2200 A; 1913 C; 1962 G; 1798 T; 0 other:
                                                                                                                                                                                                          transplant recipient.
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Search completed: February 24, 2002, 07:42:18 Job time: 16843 sec

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Disclosure; Page 98; 144pp; English.

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ALIGNMENTS

Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as swine cells -Xenotransplantation; infectious agent; vaccine; ds. BP. Porcine endogenous retrovirus (MAYO-) MAYO MEDICAL VENTURES AAC67007 standard; DNA; 633 99US-0135631. 24-MAY-2000; 2000WO-US14296. (first entry) PERV-MSL LTR SEQ ID NO; 7. WPI; 2001-032041/04. WO200071726-A1. Federspiel MJ; 24-MAY-1999; 27-MAR-2001 30-NOV-2000 AAC67007; AAC67007/c RESULT X AX X E

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               The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as
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                                                                                                                                          100.0%; Score 18; DB 22; Length 633; 100.0%; Pred. No. 2.4; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 22; Length 704; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                   Sequence 633 BP; 170 A; 125 C; 147 G; 191 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 704 BP; 187 A; 162 C; 158 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Xenotransplantation; infectious agent; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 97-98; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Fr.
0;
                                                                                                                                                                                                                                                                                                         AAC67006 standard; DNA; 704 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2000; 2000WO-US14296.
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                                                                                                                                                                                                                        497 CCACAGTCGTACACCACG 480
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                                                                                                                                                                                                       1 ccacagtcgtacaccacg 18
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                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001 (first entry)
                                                                                                                                                              Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                IamAl LTR SEQ ID NO: 6.
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                                                                         transplant recipient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-032041/04.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentiifed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1999;
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                                                                                                                                                Query Match
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The present sequence encodes a Pig endogenous retrovirus (PERV)-B envelope protein. PERV exists in two different subtypes, PERY-A and PERV-B. The differences are reflected in sequence divergence in the envelope genes. Probes and primers can be derived from the envelope (env) genes of PERV-A and PERV-B. The probes and primers are used in a method to detect retroviruses in a sample of porcine/human tissue, particularly primary porcine tissue and human cell lines that have been cultivated in the presence of a porcine cell line, or human tissue from a patient with a xenotransplant. Subtype of PERV in a sample containing one of the PERV env genes can also be determined.
                                                                                                                                                                                                                                            Pig endogenous retrovirus; PERV-A; envelope protein; PERV-B; subtype; probe; primer; detection; retrovirus; human tissue; xenotransplant; primary porcine tissue; human cell line; porcine cell line; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newly isolated nucleic acid probe capable of hybridising to either the PERV-A or PERV-B env gene - useful in the detection of retroviruses, and their subtypes, in a sample of porcine/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                     Pig endogenous retrovirus (PERV)-B envelope (env) gene region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
911..2884
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AAV82749 standard; DNA; 3482 BP.
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ID AAC67022 standard; DNA; 4918
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                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 Pig endogenous retrovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stoye JP, Weiss RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045324/04.
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Best Local Similarity
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                                                                                                                        25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                  4781 CCACAGTCGTACACCACG 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4918 BP; 1382 A; 1173 C; 1183 G; 1180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 109-111; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant recipient.
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                                                                                                                                                                                                                              PERV env protein coding sequence SEQ ID NO: 21.
                                                                                                                                                                                                                                                                                                      AAC67021 standard; DNA; 6076
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                                                                                                                                                           WO200071726-A1
                                                                                                                                                                                                       Xenotransplantation; infectious agent; vaccine; ds
                                                                                                                                                                               Porcine endogenous retrovirus
           WPI; 2001-032041/04.
                                  Federspiel MJ;
                                                                                    24-MAY-1999;
                                                                                                          24-MAY-2000; 2000WO-US14296.
                                                           (MAYO-) MAYO MEDICAL VENTURES
                                                                                                                                                                                                                                                                                                                                                                                                                             Match 100.0%; Score 18; Local Similarity 100.0%; Pred. No. 2.
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Query Match Matches

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Length 6076; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 107-109; 144pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6076 BP; 1613 A; 1512 C; 1609 G; 1342 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                 Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such swine cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1999;
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                                                                                               The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                  Claim 16; Page 117-119; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-032041/04.
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Sequence 6076 BP; 1619 A; 1505 C; 1598 G; 1354 T; 0 other;
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                                                               transplant recipient.
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                                                                                                                                                                                                                                                                                                                                                                                          such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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δÃ

1 ccacagtcgtacaccacg 18

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AAC67019/c
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                                                                                                                                                                    QУ
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AAF77726/C
ID AAF77726 standard; DNA; 7333 BP.
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                27-MAR-2001
                                                        AAC67019;
                                                                          AAC67019 standard; DNA; 7362 BP
                                                                                                                                                                                                                                                                 The present invention relates to a method for screening a cell or tissue for the presence or expression of a retrovirus (RV), comprising contacting a target nucleic acid from the cell or tissue with a second fragment thereof). The method is useful for RV detection and to assess of donors with active replication of known viruses. Inactive proviruses of potential human pathogens derived from swine and inactivated, allowing identification and elimination in the outbred human organ donor population and is important to the development of human xenotransplantation.
                                                                                                                                        7279 CCACAGTCGTACACCACG 7262
                                                                                                                                                                                                                                                Sequence 7333 BP; 1984 A; 1788 C; 1885 G; 1676 T;
Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 2; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 or miniature swine retroviral genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-256211/26.
P-PSDB; AAB73282, AAB73283, AAB73284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          xenotransplantation, comprises using probe sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assessing risk of endogenous retroviruses in clinical practice and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fishman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-1996;
                                                                                                                                                                                        Local Similarity 100.
hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6190861-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retrovirus; graft transplantation; xenotransplantation; PK-15 cell line;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Defective retroviral genome isolated from PK-15 cell line.
                                                                                                                                                     1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF77726;
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                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0572645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0766528
                                                                                                                                                                                        100.0%; 9
100.0%; F
htive 0;
                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                      0;
                                                                                                                                                                                                           Length 7333;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived from swine
                                                                                                                                                                                    0;
                                                                                                                                                                                 Gaps
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RESULT 9
AAT74883/c
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                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Matches
              mat_peptide
                                                             CDS
                                                                                            mat_peptide
                                                                                                                              Key
                                                                                                                                                 Porcine retrovirus.
                                                                                                                                                                      activated virus; PCR; ss.
                                                                                                                                                                                       Retrovirus; porcine; GAG protein; POL protein; ENV protein;
                                                                                                                                                                                                               Porcine retrovirus cDNA (defective).
                                                                                                                                                                                    xenotransplantation;
                                                                                                                                                                                                                                            09-FEB-1998
                                                                                                                                                                                                                                                                  AAT74883;
                                                                                                                                                                                                                                                                                   AAT74883 standard; cDNA; 7393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7362 BP; 1997 A; 1821 C; 1881 G; 1663 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as swine cells -
                                                                                                                                                                                                                                                                                                                                           682 CCACAGTCGTACACCACG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplant recipient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 101-104; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-032041/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Federspiel MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAYO-) MAYO MEDICAL VENTURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenotransplantation; infectious agent; vaccine; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200071726-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERV env protein coding sequence SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                        1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                       (first entry)
/*tag=
            2320..3522
                /note= "putative POL coding region (partial)
    described in the specification"
                                                                                         598..2169
                                                                                                  /*tag=
                                                                                                                 Location/Qualifiers 598..2172
                                            /*tag=
                                                         2320..4737
                                                               /note= "putative GAG protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0135631.
                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                          infectious; provirus; organ transplant; donor;
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                          Length 7362;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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DA X
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                                                                                 AAC67023/c
                                                                                              RESULT 10
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                   Query Match
   27-MAR-2001
                                  AAC67023;
                                                         AAC67023 standard; DNA; 7873 BP
                                                                                                                                         7339 CCACAGTCGTACACCACG 7322
                                                                                                                                                                                                                                                                                                                                                              intact and infectious proviruses are present. The porcine retroviral sequence can be used to generate probes to determine the level (e.g. copy number) of intact (i.e. potentially replicating) porcine provirus sequences in a strain of xenograft transplantation donors. It can be used to detect mutations, genetic lesions or viral recombinants and to detect mutations genetic lesions or viral recombinants. Using the histological localisation of activated retrovirus. Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA sequence represents a defective purified swine retrovirus found in PK-15 cells containing the putative coding regions for viral GAG, POL and ENV proteins. There are a few in frame stop codons and apparent frame shifts in the given coding sequence which alter features of the translation. This sequence and PCR fragments generated from the sequence (see AAT74812-T74882) could be used to screen organs for the presence of porcine retroviruses prior to xenotransplantation.
                                                                                                                                                                                                                                                                         Sequence 7393 BP; 2004 A; 1801 C; 1896 G; 1692 T; 0 other;
                                                                                                                                                                                                                                                                                                   Polymerase Chain Reaction DNA Quantitation (PDQ) on blood mononuclear cells, infectivity titration and susceptibility testing can be performed. Ultimately animal donors without intact porcine retroviral sequences or a lower copy number of viral elements could be selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of transmitting infection to graft recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Fig 2; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-332804/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW32091-W32095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fishman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9721836-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                   1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                       18;
                                                                                                                                                                                                    Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0572645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US19680
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4738..6725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /"Lag= e
/note= "putative POL protein (partial)"
4332.4748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4752..6722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "putative POL protein (partial)"
3516..4328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "ENV protein (partial)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "putative ENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                    0,
                                                                                                                                                                                                                 Score 18; DB Pred. No. 2.7;
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the specification"
                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                  0;
                                                                                                                                                                                                                             Length 7393;
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                 0,
                                                                                                                                                                                               Gaps
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AAT74884/C
ID AAT748
XX
     RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                            mat_peptide
                                                     CDS
                                                                                          mat_peptide
                                                                                                                    CDS
                                                                                                                                                       Porcine retrovirus.
                                                                                                                                                                                  activated virus; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                          7708 CCACAGTCGTACACCACG 7691
                                                                                                                                                                                        Retrovirus; porcine; GAG protein; POL protein; ENV protein; xenotransplantation; infectious; provirus; organ transplant
                                                                                                                                                                                                                                 Miniature swine retrovirus cDNA.
                                                                                                                                                                                                                                                        09-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                     AAT74884;
                                                                                                                                                                                                                                                                                                            AAT74884 standard; cDNA; 7892 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7873 BP; 2200 A; 1913 C; 1962 G; 1798 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 112-115; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such swine cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant recipient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-032041/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAY-2000; 2000WO-US14296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Federspiel MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenotransplantation; infectious agent; vaccine; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERV env protein coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                       /*tag= a
585..2156
                         /note= "putative GAG protein"
2307..5744
/*tag= c
2307..5741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0135631
/note= "putative POL protein"
                                                                              /*tag=
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                       infectious; provirus; organ transplant; donor;
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 22;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7873;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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AAT74811/c
ID AAT74811 standard; cDNA; 8060 BP
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intact (i.e. potentially replicating) porcine provints sequences in a strain of xenograft transplantation donors. It can be used to detect mutations, genetic lesions or viral recombinants and also to determine the histological localisation of activated retrovirus. Using Polymerase Chain Reaction DNA Quantitation (PDD) on blood mononuclear cells, infectivity titration and susceptibility testing can be performed. Ultimately animal donors without intact porcine retroviral sequences or a lower copy number of viral elements could be selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              containing the putative coding regions for viral GAG, POL and ENV proteins. This sequence and PCR fragments generated from it (see AAT74812-T74882) can be used to screen organs for the presence of porcine retroviruses prior to xenotransplantation. Transplantation can increase the likelihood of retroviral activation if intact and infectious proviruses are present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of transmitting infection to graft recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9721836-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This cDNA sequence represents a porcine retrovirus from miniature swine containing the putative coding regions for viral GAG, POL and ENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Fig 3; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW32096-W32098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-332804/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fishman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7892 BP; 2191 A; 1915 C; 1980 G; 1806 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infectious proviruses are present. The porcine retroviral sequence can be used to generate probes to determine the level (e.g. copy number) of
                                                                             Retrovirus; porcine; GAG protein; POL protein; ENV protein; xenotransplantation; infectious; provirus; organ transplant; donor; activated virus; Tsukuba-1; PCR; ss.
                                                                                                                                                                                11-FEB-1998 (first entry)
                  Key
                                                                                                                                              Porcine retrovirus Tsukuba-1 cDNA.
                                                                                                                                                                                                               AAT74811;
                                                 Porcine retrovirus.
                                                                                                                                                                                                                                                                                                                                19 CCACAGTCGTACACCACG 2
                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0572645
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5620..7533
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                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7892;
                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     0;
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PR
YX
PA
YX
PI
DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                            for porcine retroviruses prior to xenotransplantation. Transplantation can increase the likelihood of retroviral activation if intact and infectious proviruses are present. The porcine retroviral sequence can be used to generate probes to determine the level (e.g. copy number) of intact (i.e. potentially replicating) porcine provirus sequences in a strain of xenograft transplantation donors. It can be used to detect mutations, genetic lesions or viral recombinants and to determine the histological localisation of activated retrovirus. Using Polymerase Chain Reaction DNA Quantitation (PDQ) on blood mononuclear cells, infectivity titration and susceptibility testing can be performed. Ultimately animal donors without intact porcine retroviral sequences or with a lower copy number of viral elements could be selected.
                                                                                                                                                                                                                                               This sequence represents the purified porcine retroviral cDNA sequence of Tsukuba-1 and contains the putative coding regions for viral proteins GAG, POL and ENV. This sequence and PCR fragments generated from the sequence (see AAT74812-T74882) could be used to screen organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09721836-A1.
                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-332804/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fishman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                          transmitting infection to graft recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US19680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0572645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4871..8060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3112..4686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86..2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "putative POL protein (partial)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "putative GAG protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "putative ENV protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D)
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Sequence 8060 BP; 2233 A; 1959 C; 2012 G; 1856 T; 0 other;
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В
AAF77725/c
                                                                                                     RESULT 13
                                                                                                                                                             Matches
                                                                                                                                                                     Best
                                                                                                                                                                           Query Match
                                                                                                                             2546 CCACAGTCGTACACCACG 2529
                                                                      AAF77725;
                                                                                      AAF77725 standard; cDNA; 8060 BP
                                      Tsukuba-1 cDNA
                                                      23-MAY-2001 (first entry)
                                                                                                                                                                     Local Similarity
                                                                                                                                            1 ccacagtcgtacaccacg 18
                                                                                                                                                              18;
                                                                                                                                                              Conservative
                                                                                                                                                                     100.0%;
                                                                                                                                                               0;
                                                                                                                                                                      Score 18; DB 18; Length 8060; Pred. No. 2.7;
                                                                                                                                                               Mismatches
                                                                                                                                                                0,
                                                                                                                                                                 0;
                                                                                                                                                                 0;
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Tsukuba-1; retrovirus; graft transplantation; xenotransplantation; ss.

Porcine retrovirus

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RESULT 14
AAF77727/c
ID AAF777
                                                                                                                                                                                                                                                                                                                                                                                                망
                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
P-PSDB; AAB73285, AAB73286, AAB73287
              WPI; 2001-256211/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for screening a cell or tissue for the presence or expression of a retrovirus (RV), comprising contacting a target nucleic acid from the cell or tissue with a second nucleic acid from the present invention (e.g. the present sequence or a fragment thereof). The method is useful for RV detection and to assess graff transplantation risk. Screening of animals allows the elimination of donors with active replication of known viruses. Inactive proviruses of potential human pathogens derived from swine in a manner not possible in the outbred human organ donor population and is important to the development of human xenotransplantation.
                                      Fishman JA;
                                                                                       14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                         2546 CCACAGTCGTACACCACG 2529
                                                             (GEHO ) GEN HOSPITAL CORP
                                                                                                              13-DEC-1996;
                                                                                                                                                                  US6190861-B1
                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                    Retrovirus; graft transplantation; xenotransplantation; miniature swine;
                                                                                                                                                                                                                                              Nucleotide sequence of a retovirus found in miniature swine.
                                                                                                                                                                                                                                                                           23-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                            AAF77727 standard; DNA; 8132
                                                                                                                                                                                                                                                                                                        AAF77727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8060 BP; 2233 A; 1959 C; 2012 G; 1856 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or miniature swine retroviral genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assessing risk of endogenous retroviruses in clinical practice and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xenotransplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-256211/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fishman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6190861-B1
                                                                                                                                                                                                                                                                                                                                                                                                        1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                      95US-0572645
                                                                                                              96US-0766528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0572645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0766528
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8060;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 15
AAV09699/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                   10-FEB-1997;
19-APR-1996;
                                                                                                                                                                                                                  CDS
                         (IMUT-) IMUTRAN LTD
                                                                                            18-APR-1997;
                                                                                                                      30-OCT-1997
                                                                                                                                                W09740167-A1
                                                                                                                                                                                                                                                                                                                                                                                  Porcine retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; diagnosis; xenotransplantation; prophylactic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                  Porcine retrovirus; PoEV; POL protein; ENV protein; GAG protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine retrovirus DNA encoding, GAG, POL and ENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV09699 standard; DNA; 8196 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8080 CCACAGTCGTACACCACG 8063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                graft transplantation risk. Screening of animals allows the elimination of donors with active replication of known viruses. Inactive proviruses can be detected and inactivated, allowing identification and elimination of potential human pathogens derived from swine in a manner not possible in the outbred human organ donor population and is important to the development of human xenotransplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8132 BP; 2248 A; 1977 C; 2037 G; 1870 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contacting a target nucleic acid from the cell or tissue with a second nucleic acid from the present invention (e.g. the present sequence or a fragment thereof). The method is useful for RV detection and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assessing risk of endogenous retroviruses in clinical practice and in xenotransplantation, comprises using probe sequences derived from swine or miniature swine retroviral genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for screening a cell or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 3; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ccacagtcgtacaccacg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the presence or expression of a retrovirus (RV), comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                96GB-0008164
                                                                97GB-0002668
                                                                                          97WO-GB01087
                                                                                                                                                                                                                  5606..7576
                                                                                                                                                                       /note= "envelope protein"
                                                                                                                                                                                       /product= ENV protein
                                                                                                                                                                                                                            /product= POL protein
                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                   2143..5733
                                                                                                                                                                                                                                                                                           /note= "virion core polypeptide
                                                                                                                                                                                                                                                                                                           /product= GAG protein
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                      /*taq=
                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB;
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0;

(QONE-) Q-ONE BIOTECH LTD

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PI Galbraith DN, Haworth C, Lees GM, Smith KT;

XX

XX

XX

XX

XX

POlynucleotide encoding porcine retrovirus expression product -
PT useful to develop products for use in vaccines, diagnosis and
PT veno-transplantation

XX

Claim 4; Fig 2; 69pp; English.

XX

CC This DNA sequence encodes the porcine retrovirus (PoEV) virion core
CC polypeptide (GAG), polymerase (POL) and envelope (ENV) proteins. These
CC proteins can be used to develop viral vaccines, antisense nucleic acids,
CC ribozymes and other antiviral agents. They can also be used in

XX

XX

Sequence 8196 BP; 2165 A; 2061 C; 2147 G; 1820 T; 3 other;

Query Match

Best Local Similarity 100.0%; Score 18; DB 18; Length 8196;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

1 ccacagicgtacaccacg 18

Qy 1 ccacagicgtacaccacg 18
Qy 1 ccacagicgtacaccacg 18
Qy 1 ccacagicgtacaccacg 18
Qy 1 ccacagicgtacaccacg 18
Qy 1 ccacagicgtacaccacg 18
Search completed: February 24, 2002, 03:05:32

Job time: 19498 sec
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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                     a
                                                                 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-171-553B-1
3320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     February 24, 2002, 02:56:31; Search time 197.25 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
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Copyright (c) 1993 - 2000 Compugen Ltd.
Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
    DB
4 US-08-766-528-2
3 US-08-716-528-3
4 US-08-766-528-3
4 US-08-766-528-1
3 US-08-766-528-1
3 US-09-316-781-7
4 US-09-376-781-7
5 US-09-277-716-31
5 US-09-278-000-1
5 US-08-798-000-1
5 US-09-232-197-66
6 US-09-232-197-66
6 US-09-232-197-66
6 US-09-11-745-3
6 US-09-11-745-3
6 US-09-11-745-3
6 US-09-011-745-3
6 US-09-011
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3811.949 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                         Sequence 2, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 3, Appli
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Sequence 6, Appli
                                                sequence 66, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 24, Appli
Sequence 278, Appli
Sequence 278, Appli
Sequence 278, Appli
Sequence 278, Appli
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              Sequence
                                 Sequence
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Qy

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                   CGTTGGCAGAAATTGCCTTTGCACATAGTGCTGATGTGCTGCTTTCCCAGCCTTTGTTCT
                                                                                            c9tt9gcagaaatt9ccttt9cacatagt9ctgatgt9ct9ctttcccagcctttgttct 2443
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                                                                                                                                                     GGAACACCCCTGGACAGTTTGGGCTGACCCCCTATAAATTGCTCTACGGGGGACCCCCCC
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APPLICANT: Stoye, Jonathan P
APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
TITLE OF INVENTION: specific sequences
FILE REFERENCE: 4238/75168
FILE REFERENCE: 4238/75168
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CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                             2759 tggttccttactctgtcaataactcctcaagttaatggtaaacgccttgtgggacagcccg
421 attaacagcactcaaggggaggctcccttggggacctggtggcctgaattatatgtctgc
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                    attaacagcactcaaggggaggctcccttggggaacctggtggcctgaattatatgtctgc 2938
                                                                                        aactcccataaacccttatctctcacctggttacttactgactccggtacaggtattaat
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                                                                                       ; MOLECULE TYPE: CDNA US-08-766-528-3
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               Matches 2204;
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                  REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NERAL INFORMATION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 74
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/572,645 FILING DATE: 14-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version
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                                                                                                                          TOPOLOGY:
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               0;
                              Score 704; DB 4;
Pred. No. 2.8e-299;
               Mismatches
                                           DB 4; Length 8132;
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               Gaps
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8060 base pairs
                                                                                                                                                                                                                                                                                                                    Matches 1395;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
262 aaacaggactgottagaaggtacgaaggcactactgotggaattgtotgacotaggctac
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TOPOLOGY: lir
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralasses
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STATE: Massa
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                      accgctgactggagaagtgctaacctggttcactgacggaagcagctatgtggtggaagg
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                                                                                       GGCCGAAGGGAAATCCATAAACATTTATACGGACAGCAGGTATGCCTTTGCGACTGCACA
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US-09-376-781-7; Sequence 7, Application

US/09376781

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TITLE OF INVENTION: Detection of retroviral sultitle OF INVENTION: Specific sequences
FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 197-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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; ORGANISM: Porcine
US-09-111-085-3
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Best Local Similarity
Matches 521; Conserv
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gacccttaccaaattgaccacagagactggcattaatgattggat
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Pred. No. 1.7e-131;
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                                                                                                           Sequence 1, Application US/09075272 Patent No. 6136598
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APPLICANT: Patience, Clive
APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods
Patent No. 6261806
TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
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CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
                                                                                     GENERAL INFORMATION:
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                    APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: MILLER, A. DUSTY APPLICANT: WOLGAMOT, GREG APPLICANT: BONHAM, LYNN TITLE OF INVENTION: MUS DUNN
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nes 435; Conserv
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                                                                                                                                                                                                                                                               aagcaaataagctgtca 3258
                                                                                                                                                                                                                                                                                                                           tctcagcaagacagagtaagttactcttttgttaaccaatcctaccagttataatcaattt 3181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcctttgcaagcaatggagctgcataacttctaatgatg-ggaattggaaatggccagtc 312:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggttttacgtttgcccaggacccccaaataatgaagaatattgtggaaatcctcaggatt 3062
                                                                                                                                                                                                                                        aagcaaataagctgtca 437
                                                                                                                                                                                                                                                                                                                                                                      aattatggccatgggagatggaaagattggcaacagcgggtacaaaaagatgtacgaaat 3241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gatcagtaatccctggtctcaatgaccaggccacaccccccgatgtactccgtgcttacg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatcagtaatccctggtctcaatgaccaggccacaccccccgatgtactccgtgcttacg 3002
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                                                                                                                                                                                                                                                                                                                                                                                                              tctcagcaagacagagtaagttactcttttgttaacaatcctaccagttataatcaattt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcttttgcaagcaatggagctgcataacttctaatgatgaggaattggaaatggccagtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 265; DB 4; 99.5%; Pred. No. 6.5e-107;
  MUS DUNNI ENDOGENOUS RETROVIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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US-09-352-990-7
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                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09352990
Patent No. 6253090
GEMERAL INFORMATION:
APPLICANT: Famodu, Layo O.
APPLICANT: OTOZCO, Buddy
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
                                                                                                                                 SEQ ID NO 7
LENGTH: 836
              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                    FILE REFERENCE: BB-1191
CURRENT APPLICATION NUMBER: US/09/352,990
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,866
                                                                                                                                                                                    EARLIER FILING DATE: July 15, 1998 NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                     SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFONMUNICATION INFORMATION: TELEPHONE: (206) 467-9600 TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcac
CITY: San Francisco
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REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
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30; Conser
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100.0%; Pr
              100.0%;
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                                 0.9%;
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              Score 30; DB 4; L; Pred. No. 0.00053;
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0;
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Mismatches
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hes 0;
                               Length 836;
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; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert B) US-09-277-716-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08798000 Patent No. 5766945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER FILING DATE: 1998-10-07
EARLIER FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Szént-Gyorgyi, Christopher APPLICANT: PROLUME, LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bryan, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LOCATION: (7)..(720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1279
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3291 tcactaaaaaaaaaaaaaaaaaaaaaaaa 3320
                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Miller, A. Dusty
TITLE OF INVENTION: 10A1 RETROVIRAL PACKAGING CELL LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1237 tcactaaaaaaaaaaaaaaaaaaaaa 1266
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                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 12-FEB-1997
                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                  CLASSIFICATION:
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13-FEB-1996
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                     US 60/011,564
                                                                                                           . US/08/798,000
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US-08-798-000-1

Sequence 1, Application US/08798000 Patent No. 5766945

GENERAL INFORMATION:

APPLICANT: Miller, A. Dusty
TITLE OF INVENTION: 10A1 RETROVIRAL PACKAGING CELL LINES

CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor

STREET: Two Embarcac CITY: San Francisco NUMBER OF SEQUENCES:

COMPUTER READABLE FORM:

COUNTRY: USA ZIP: 94111-3834

STATE:

CA

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US-09-248-335-27
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US-09-248-335-27
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MCGONIGLE,
APPLICANT: MCGONIGLE
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word Version 7.0A SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.98;
Best Local Similarity 100.08;
Matches 29; Conservative
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                                                                                              Query Match 0.9%; Score 29; DB 3; Best Local Similarity 100.0%; Pred. No. 0.0014;
                                                                               Matches
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 74
1109 cactaaaaaaaaaaaaaaaaaaaaa 1137
                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                         LENGTH: 1198
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                                      3292 cactaaaaaaaaaaaaaaaaaaaaaa 3320
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LENGTH: 735 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 CATTGTGCATACAGACCCCAAAGCTCAGG 124
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STRANDEDNESS: both
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REFERENCE/DOCKET NUMBER: 14538A-002010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415-576-0300
                                                                             Conservative
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Pred. No. 0.001;
                                                                               Mismatches
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                                                                                                                Length 1198;
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CURRENT APPLICATION DATA:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66, Application US/09232200A Patent No. 6288213
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Best Local :
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APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
                                                                                                                                                                                           LENGTH: 23:
TYPE: DNA
                                                                                                                                                                                                                                                               NUMBER OF SEQ
                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/110,941
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LENGTH: 1234 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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29;
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12-FEB-1997
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                                                                                        score 29;
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0.0013;
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Matches

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Best Local Similarity

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GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Portion of ; OTHER INFORMATION: construct US-09-011-745-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Mus musculus US-09-232-197-66
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                                                                                                                                                                                                    ; SEQ ID NO 3
; LENGTH: 7308
; TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
LENGTH: 2338
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                Query Match
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APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MA
                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: PCT/GB96/02061 EARLIER FILING DATE: 1996-08-23
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                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: GB9517263.1
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                                                                                                                                                                             ORGANISM: Artificial Sequence
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Pred. No.
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0.0012;
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Search completed: February 24, 2002, 07:23:41 Job time: 16030 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-766-528-2
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US-09-376-781-10
US-09-376-781-45-4
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1	atch cal Simi 3507;	ON-766-528-2 ON-766-528-2 ON-766-528-2 ON-766-528-2 APPLICANT: Jay A. Fishman TITLE OF INVENTION: MOLECULAR S TITLE OF INVENTION: AND METHODS NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02109-1875 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: PATENTION LATA: APPLICATION NUMBER: US/08/766 FILING DATE: APPLICATION NUMBER: US/08/766 FILING DATE: 14 -DEC-1995 ATTORNAME: LOUIS MYETS REGISTRATION NUMBER: WS/08/766 FILING DATE: 14 -DEC-1995 ATTORNAME: APPLICATION INFORMATION: NAME: LOUIS MYETS REGISTRATION NUMBER: WS/08/766 FILECOMMUNICATION INFORMATION: TELEFAN: (617)227-7400 TELEFAN: (617)227-7400 TELEFAN: (617)227-5941 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 7333 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	
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+ +	ore 2967; Ded. No. 0; Mismatches	USE OF USE OF CP	09-078-294-3 09-376-781-23 09-368-364-3 09-357-251-1 08-728-259A-10 08-713-000-6 08-713-000-6 08-713-000-6 08-702-344-18 08-605-106-3 09-346-601-9 09-466-800-7 09-664-800-7 09-664-800-7 09-665-509-7 09-661-509-7 09-661-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7 09-681-509-7	
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cggacc CGGACC	gggaaaca 3GGAAACA	aggacc AGGACC	lggaaaattaggt GGAAAATTAGGT	taag AAG	aagaaaa AAGAAAA	gagas GAGAS	ggatatca GATATCA	CCTACCTC	creed	ggcgcctcaa GGCGCCTCAA	EGAA	gcaa GCAA	agaga AGAGA	agcct AGCCT	CTTTCTC	CCCTC	yagatogo	
ccctcc	aaggaccga \AAGGACCGa	:aaggaccagtgtgcgtatt AAGGACCAGTGTGCGTATT	ttaggt TAGGT	PCTTC	ggaga GGAGA	aggca AGGC/	aggaagaaa !AGGAAGAAA(95-3	gaco GACO	gtag AG	aatgag \ATGAG	aattctg ATTCTG	>tctcaccagcctacttgggatgattgtcaaca 		ttgcagcccctccagtattg 	gcgata GCGATA	
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etttgaa ETTTGAA	igaag GAAG	laggacac AGGACAC	agggaa AGGGA <i>I</i>	gaagag GAAGAG	gaaagacgt: GAAAGACGT(yaaggga SAAGGGA	agggtt AGGGTT	tggccct	iga:	jgtaa GTAA	S = S	cttga CTTGA	atgtteet NTGTTCCT	rgctgca rGCTGCA	cggggttg; cGGGGTTG;	tgcagatci GCAGATCI	CTATGGCCC	
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GENERAL INFORMATION:
APPLICANT: Stoye, Jor
APPLICANT: Weiss, Rob
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE REFERENCE: 4238
CURRENT APPLICATION N
CURRENT FILING DATE:
EARLIER APPLICATION N
EARLIER FILING DATE:
EARLIER FILING DATE:
EARLIER FILING DATE:
SAFTWARE:
NUMBER OF SEQ ID NOS:
SOFTWARE: PATENTIN VESEQ ID NOS:
SEQ ID NO 3
LENGTH: 3482
TYPE: DNA
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CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: specific sequences FILE REFERENCE: 4238/75168
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                                                         1290 gggaatccttctgtaggagatggagctgcgtcacctccaacgatggagactggaaatggc 1349
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Sequence

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APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TETERONES. AG 17127-77400
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SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS

TITLE OF INVENTION: AND METHODS OF USE
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
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3330 TTGCGGGACGGCAGCGATGGCTGACGGAGGCACGGAAGAAAACTGTAGTCCAGATACCG
                   3333 ttgcggggcgggcagcgatggctgacggaggcacggaagaaaactgtagtccagataccg 3392
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CITY: Boston
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/766,528
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(617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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4353 aacaaagaggaaattctaagcctattagaagccttacattt	Qy
b 4290 GTACATGGGCCATCTATAAACAAAGGGGGTTGCTTACCTCAGCAGGGAGGG	D
4293 gtacacgg	ΩУ
b 4230 GCCGAAGGGAAATCCATAAACATTTATACGGACAGCAGGTATGCCTTTGCGACTGCACA	1d
4233 gccgaagggaaatccataaac	уо
4170 CCGGAAGGAACTTCAGCACAAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTGCGGCT	Db
4173 ccggaaggaacttcagcgcaaaaggctgagctcatg	γQ
4110 AAGAGGATGGCTGGGCGGCGGTGGTGGACGGACCCGCACGATCTGGGCCAGCAGCAGCCT	שמ
4113 aagaggatggctggggggggggtggtggacgggaccggaccggatctggg	УО
4050 CCGCTGACTGGAGAAGTGCTAACCTGGTTCACTGGACGGAAGCAGCTATGTGGTGGAAGG	Db
4053 ccgctgactggagaagtgctaacctggttcactg	Qy
3990 CATGATTGCCATCAACTATTGATTGAGGAGCTGGGGTCCGCAAGGACCTTACAGACAT	DЬ
3993 catgattgccatcaactattgattgagga	у
3930 CCACCAGCCGCTCTCAACCCTGCCACTCTTCTGCCTGAAGAGACTGATGAACCAGTGAC	DЬ
3933 ccaccagccgctctcaacc	ОУ
3870 ACCAACGCCCGCATGACCCACTATCAAAGCCTGCTTCTCACAGAGAGAG	Db
3873 accaacycccycatyacccactatcaaaycctycttctcac	ОУ
3810 ACTGTAATAGCCCCCCATGCATTGGAGAACATCGTTCGGCAGCCCCCAGACCGATGGAT	Db
3813 actgtaatagccccccatgcattggagaacatcgttcggcagcccccagaccgatgg	Qy
3750 ATCGCAGCTGTGGCCATACTGGTCAAGGACGCTGACAAATTGACTTTGGGACAGAATA	Db
3753 atcgcagctgtggccatactggtcaaggacgctgacaaattgactttgggacagaatat	Qy
3690 GCCTACCTGTCAAAGAAGCTCGATCCTGTAGCCAGTGGTTGGCCCATATGCCTGAAGGC	Db
3693 gcctacctgtcaaagaagcttgatcctgtagccagtggtttggccggtatgtctgaagg	Qy
3630 CGTAAGGGAGTAGCCCGGGGAGTTTTAACCCAAACCCTAGGACCATGGAGAAGACACCTG	Дb
3633 cgtaagggagtagcccgaggagttttaacccaaaccctaggaccatggaggagacct	Ωу
3570 ACCCACCTGCTCTGGCCCTCCCTGACGTAACCTAAACCCTTTACCCTTTATGTGGATGA	Db
3573 agcgcacctgctctggccctccctgacgt	Qy
3510 GAATTCTCCTGGGCTCCTGAGCACCAGAAGGCATTTGATGCTATCAAAAAGGCCCCTGCT	Db
3513 ggattotootgggotootgagoaccagaaggo	Qу
3450 TGGATCCCGGGGTTTGCGACCTTAGCAGCCCCACTCTACCCGCTAACCAAAGAAAAAGG	Db
3453 tggatcccggggtttgcgaccttagcagccccactctacccg	Qy
3390 GCCCCAACCACAGCCAAACAAATGAGAGAGTTTTTGGGGACAGCTGGATTTTGCAGACT	Db
3393 gccccaaccacagccaaacaagtg	Qy

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4473 gaccgggttgccaagcaggcagcccaggctgttaaccttctgcctataatagaaacgccc 4532

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i, ORGANISM: Porcine retrovirus
US-09-11T-085-1
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                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                     Sequence 1, Application US/09111085 Patent No. 6100034
                                                                         APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
TITLE OF INVENTION: Specific sequences
FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
                         TYPE: DNA
                                      LENGTH:
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US-08-766-528-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,96
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MOLECULAR SEQUENCE OF TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 74
                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 60
                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
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99.8<del>8</del>;
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Pred. No. 4.1e-187;
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Best Local Sin
Matches 1395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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atcgcagctgtggccatactggtcaaggacgctgaccaaattgactttgggac-agaatat
                                                                                                                                                                            gccccaaccacgccaaacaagtgagagagtttttggggacagctggattttgcagactg
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                                               GCCTACCTGTCAAAGAAGCTCGATCCTGTAGCCAGTGGTTGGCCCATATGCCTGAAGGCT
                                                                gcctacctgtcaaagaagcttgatcctgtagccagtggttggcccgtatgtctgaaggct
                                                                                                                CGTAAGGGAGTAGCCCGGGGAGTTTTAACCCCAAACCCTAGGACCATGGAGAAGACCTGTC
                                                                                                                              cgtaagggagtagcccgaggagttttaacccaaaccctaggaccatggaggagacctgtt
                                                                                                                                                                                                                                           GAATTCTCCTGGGCTCCTGAGCACCAGAAGGCATTTGATGCTATCAAAAAGGCCCCTGCTG
                                                                                                                                                                                                                                                               ggattctcctgggctcctgagcaccagaaggcatttgatgctatcaaaaaaggccctgctg
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Pred. No. 6.7e-152;
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6275

ATCGCAGCTGTGGCCATACTGGTCAAGGACGCTGACAAATTGACTTTGGGACAAGAATAT

6334

Query Match Best Local Similarity

3.4%; 100.0%;

Score 278; Pred. No.

4.le-110;

DB 4;

Length

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; NUMBER OF SEQ
; SOFTWARE: Pate
; SEQ ID NO 10
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Art.
FEATURE:
; OTHER INFORMA;
; OTHER INFORMA;
; OTHER INFORMA;
; OTHER INFORMA;
                                                                                                                         APPLICANT: Banerjee, Papia T.
APPLICANT: Pattence, Clive
APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Sw.
Patent No. 626.1806
TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION UMBER: 60/097,015
EARLIER APPLICATION SUMBER: 60/097,015
EARLIER APPLICATION SUMBER: 60/097,015
SEARLIER APPLICATION SUMBER: 50/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
LENGTH: 278
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                    FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Nucleotide OTHER INFORMATION: sequence of part of POEV env gene corresponding OTHER INFORMATION: residues 6057-6333 of WO 97/40167 for comparise
                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09376781
                                                                                                                                                                                                                                                                                                                                     Swine Retrovirus and
                    corresponding to for comparison.
                                                                                                                                                                                                                                                                                                                                     Methods
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Matches

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US-09-075-272-1

"Sequense 1, Application US/09075272"
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                                                                                                                                                                                                                                                                                                                                                                  1.0%;
Best Local Similarity 99.3%;
Matches 136; Conservative
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TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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EARLIER FILING DATE: 1998-08-18
NUMBER OF SEO ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Nucleotide OTHER INFORMATION: sequence of part of PERV-B env gene corresponding OTHER INFORMATION: to residues 1350-1623 of GenBank Accession No. 6261806 OTHER INFORMATION: Y12239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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TYPE: DNA
                                                                                                                                     6177 gataagtttcactgaaa 6193
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                                                                                                               gataagtttcactgaaa
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5. 6261806
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Pred. No. 1.4e-27
0; Mismatches
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                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Miller, A. Dusty
TITLE OF INVENTION: 10A1 RETROVIRAL PACKAGING CELL LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/041
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 145:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5154 caaagctcaggacaggtagagaggatgaatagaac 5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5249 CAAAGCTCAGGACAGGTAGAGGATGAATAGAAC 5283
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 60/046,140
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 8655 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BOUNDAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                          STREET: Two Embarcac
CITY: San Francisco
                                                                                                            ZIP: 94111-3834
                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 0.4%; Score 35; DB 3;
Local Similarity 100.0%; Pred. No. 9.5e-(
nes 35; Conservative 0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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EDNESS: single
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                                                                                                                                                                                                Two Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: TOWNSEND and TOWNSEND and CREW Two Embarcadero Center, 8th Floor
                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
  PatentIn Release #1.0, Version #1.25
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thes 0;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/798,000

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
TELEFAX: 415-576-0300
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,564
FILING DATE: 13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Miller, A. Dusty TITLE OF INVENTION: 10A1 RET NUMBER OF SEQUENCES: 3
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1234 base pair
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5136 cattgtgcatacagaccccaaagctcagg 5164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                           NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,9
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/798,000 FILING DATE: 12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity tes 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12 CLASSIFICATION:
             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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TELEFAX: 415-576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/011,564 FILING DATE: 13-FEB-1996
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                                nucleic acid
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                                               1234 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend and Townsend and Crew LLP
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1997
               both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10A1 RETROVIRAL PACKAGING CELL LINES
                                                                                                                                                                           31,990
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US-09-011-745-3
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                                      SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09011745 Patent No. 6165715
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Best Local Similarity 100.0%; F
Matches 29; Conservative 0;
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                                                                              EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                 APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
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APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
                                                                                                                                                                        EARLIER APPLICATION NUMBER: PCT/GB96/02061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: GB9517263.1
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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                      LENGTH: 7308
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Pred. No. 0.0036;
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; OTHER INFORMATION: Description of Artificial Sequence: Portion ; OTHER INFORMATION: construct US-09-011-745-2
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Best Local Similarity
Watches 29; Conserve
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                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08258420 Patent No. 5710037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09011745
Patent No. 6165715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/011,745 CURRENT FILING DATE: 1998-06-22 EARLIER APPLICATION NUMBER: PCT/GB96/02061 EARLIER FILING DATE: 1996-08-23 EARLIER APPLICATION NUMBER: GB9517263.1 EARLIER FILING DATE: 1995-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Expression systems FILE REFERENCE: 09/011,745
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cosset, Francois-Loic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 7616
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
CCMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                     5339 cattgtgcatacagaccccaaagctcagg 5367
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                                                                                                                                                                                                                                    APPLICANT: Nienhuis, Arthur W. APPLICANT: Vanin, Elio F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5136 cattgtgcatacagaccccaaagctcagg 5164
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                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR and Retroviral Vect NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100 hes 29; Conservative
                                                                                              CITY: Roseland
STATE: New Jersey
                                                             COUNTRY: UZIP: 07068
                                                                                                                                       STREET:
                                                                                                                                                          ADDRESSEE:
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                                                                                                                                   6 Becker Farm
                                                                                USA
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                                                                                                                                                          Carella, Byrne,
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100.0%; Pred. No.
ative 0; Mismatcl
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                                                                                                                                                          Bain, Gilfillan, Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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US-08-258-420-13
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Patent No.
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INFORMATION FOR SEQ ID NO:
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SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 10-JUN-1994
                         REFERENCE/DOCKET NUMBER: 930049.424C4 / 1147.005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-3520
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 6013517man J.
REGISTRATION NUMBER: 35,235
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                             FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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P.O. Box 8097
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Chada, Suni
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(510) 655-3542
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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 8332 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid

TOPOLOGY: linear

US-08-850-961-1

Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5136 cattgtgcatacagaccccaaagctcagg 5164

Db 5232 CATTGTGCATACAGACCCCAAAGCTCAGG 5260

Search completed: February 24, 2002, 07:30:07

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score greater than or equal to the score of the result being printed,
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yacccc yaccccc yggagg 	conser Conser ttagggt	ASSULT 1 JS-09-111-085-3 Sequence 3, Application Patent No. 6100034 GENERAL INFORMATION: APPLICANT: Stoye, Jona APPLICANT: Weiss, Robi TITLE OF INVENTION: De TITLE OF INVENTION: De TILE REFERENCE: 4238// CURRENT APPLICATION NU CURRENT FILING DATE: J EARLIER APPLICATION NU CURRENT FILING DATE: J EARLIER APPLICATION NO COMMENCE TO SEQ ID NOS: SOFTWARE: PATENTIN Very SEQ ID NO 3	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                          TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
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TITLE OF INVENTION: MOLECULAR SEQUENCE
TITLE OF INVENTION: AND METHODS OF USE
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                                                                                                                                                              REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pair
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
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CITY: E
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                    NAME: LOUIS Myers
REGISTRATION NUMBER:
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TOPOLOGY: li
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                                                                              Sequence 1, Application US/09111085 Patent No. 6100034
                                                                GENERAL INFORMATION:
             APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
TITLE OF INVENTION: specific
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                                                                                                                                            Patent No. 6261806
TITLE OF INVENTION: Use
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09376781 Patent No. 6261806
                                   CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
                                                                                                                                                                           TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods
                                                                                                                                                                                                     APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive APPLICANT: Andersson, Goran K.
                                                                                                                           FILE REFERENCE: 61750-267
SOFTWARE: PatentIn Ver. 2.0
                     NUMBER OF SEQ ID NOS: 33
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Best Local
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EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
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CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                    ctaatcgcttatctggattctgtaaaac 2445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agaaactgacctctagccttcccagttctaagattagaactattaacaagacaagaagtg 2237
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Pred. No. 4.6e-195;
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; OTHER INFORMATION: to resi;
; OTHER INFORMATION: Y12239.
US-09-376-781-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of TITLE OF INVENTION: Use FILE REFERENCE: 61750-267 CURRENT APPLICATION NUMBER: US/09/376,781 CURRENT FILING DATE: 1999-08-18 EARLIER FILING DATE: 1999-08-18 EARLIER FILING DATE: 1998-08-18 NUMBER: 60/097,015 EARLIER FILING DATE: 1998-08-18 NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 10
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                               Query Match
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LENGTH: 276
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Andersson, Goran K.
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                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:Nucleotide OTHER INFORMATION: sequence of part of PoEV env gene corresponding to OTHER INFORMATION: residues 6057-6333 of WO 97/40167 for comparison.
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
OTHER INFORMATION: sequence of part of PERV-B env gene corresponding
OTHER INFORMATION: to residues 1350-1623 of GenBank Accession No. 6261806
                    861 caaaatgatgaaactatataaagataagagctgctccccatcagacttagattatctaaa 920
                                                                                                           801 gccgatctctctccaggaccgggtaaaattctcctttgtcaattccggcccgggcaagta 860
61 caaaatgatgaaactatataaagataagagctgctccccatcagacttagattatctaaa 120
                                                                                                                                                                                                 Watch 4.6%; Score 137; DB 4; Local Similarity 100.0%; Pred. No. 5.1e-52;
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99.5%;
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Pred. No. 1.7e-56;
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                                                                                                                                                                                                                      Length 278
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921 gataagtttcactgaaa 937

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US-08-766-528-1
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Sequence 1, Application US/08766528
Patent No. 6190861
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
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APPLICANT: JAY A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF SEQUENCES: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                         2906 ggaataaaaatcctcttgctgtttgcatcaaaaaaaaa 2943
                                                                                                                                                                                                                                                                                                             8035 CACTCGGGGCCGCAGTCCTCTACCCCTGCGTGGTGTACGACTGTGGGCCCCCAGCGCGCTT 8094
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                                                                                                                                                                                                                                     8095 GGAATAAAATCCTCTTGCTGTTTGCATCAAAAAAAA 8132
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LENGTH: 8132 base pairs
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGI
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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NAME: Louis Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
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; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide; OTHER INFORMATION: sequence of the 3' end of the PERV-D env region. US-09-376-781-24
                                                                                                                                                                                                                                                                        Patent No. 6261806
TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-376-781-24
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; sequence 24, Application US/09376781
; Patent No. 6261806
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                                                                                                                                         SEQ ID NO 24
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                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/097,015
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/376,781 CURRENT FILING DATE: 1999-08-18
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive APPLICANT: Andersson, Goran K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                             EARLIER FILING DATE: 1998-08-18 NUMBER OF SEQ ID NOS: 33
                                                                                                                                                            SOFTWARE:
                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                   TYPE: DNA
                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 8060 base pairs
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 35,965
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CITY: Boston
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                                                                                                                                                            PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preu....
netive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Goran K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 91; DB 4; Length 8060; 100.0%; Pred. No. 1.5e-31;
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; LENGTH: 1736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-360-197-13
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US-09-376-781-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-376-781-25
                                                                                                                                                                                            TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of Patent No. 6261806
Patent No. 6261806
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 05/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 28; DB 4; Length 1736; Best Local Similarity 100.0%; Pred. No. 0.0023; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13
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CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION UMBER: 09/129,758
PRIOR APPLICATION NUMBER: 09/129,758
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
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APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Deweille, Jan R.
                                                                                                                                                      SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive APPLICANT: Andersson, Goran K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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              OTHER INFORMATION: Description of Artificial Sequence:Contiguous OTHER INFORMATION: compilation of SEQ ID NOS: 18, 22, and 24.
                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1709 tgcatcaaaaaaaaaaaaaaaaaaaa 1736
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                                                                                                                               LENGTH: 2000
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Lazdunski, Michel
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100.0%; Pred. No. 0.0023;
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; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide; OTHER INFORMATION: consensus sequence of PERV-D. US-09-376-781-30
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TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 11, Appl:
; Patent No. 614356;
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EARLIER APPLICATION NUMBER: 60/076,544
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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Best Local Similarity
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APPLICANT: Patience, Clive
APPLICANT: Andersson, Goran K.
APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of
                                                                                                                                                                              APPLICANT: Randall, Douglas D.
APPLICANT: Johnston, Mark L.
APPLICANT: Johnston, Mark L.
APPLICANT: Miernyk, Jan A.
APPLICANT: Luethy, Michael H.
APPLICANT: Luethy, Michael H.
APPLICANT: MOONEY, Brian P.
TITLE OF INVENTION: USE OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND
TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS
FILE REFERENCE: UMO 1482
CURRENT FILING DATE: 1998-06-30
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: 60/051,291
EARLIER FILING DATE: 1997-06-30
EARLIER FILING DATE: 1997-06-30
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                                                                                                                                 EARLIER APPLICATION NUMBER: 60/055,255 EARLIER FILING DATE: 1997-08-01
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5. 6261806
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100.0%; Pred. No. 0.0023;
tive 0; Mismatches 0
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100.0%; Pred. No. 0.0023;
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RESULT 14
US-09-248-335-35
; Sequence 35, Applic
; Patent No. 6096504
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Best Local Similarity
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Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (516) 743-43 INFORMATION FOR SEQ ID NO:
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                                                                                                              2931 catcaaaaaaaaaaaaaaaaaaaa 2956
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                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nunberg, Andrew N.
APPLICANT: Beremand, Phillip D.
TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
TITLE OF INVENTION: COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2930 gcatcaaaaaaaaaaaaaaaaaa 2956
                                                                                              305 CATCAAAAAAAAAAAAAAAAAAA 280
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                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 09-APF
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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            Application US/09248335
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                                                                                                                                                              Conservative
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(516) 743-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                               DNA (genomic)
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                                                                                                                                                             100.0%; P
tive 0;
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                                                                                                                                                                           0.9%; Score 26;
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US-08-725-532A-2/c
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; Patent No. 6020179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: maize US-09-248-335-35
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CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                 IMMEDIATE SOURCE:
                                                                      MOLECULE TYPE:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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CITY: Palo Alto
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Copyright (c) 1993 - 2000 Comp
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Query Best Match	RESULT US-08: Patew Pate	22222222222222222222222222222222222222
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•	CGCTGACTGGAGAAGTGCTAACCTGGTTCACTGACGGAAGCAGCTATGTGGTGGAAGGT 4	rgctgactggagaagtgctaacctggttcactgacggaagcagctatgtggtggaagg		atgattqccatcaactattqattqaqqqqqqqtqqqqqtcqqqaqqqc++acaqacata 110	CCACCAGCCGCTCTCAACCCTGCCGTCTTCTGCCTGAAGAGACTGATGAACCAGTGACTGAC	1940 1940	accaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcactttcgct 981 	CTGTAATAGCCCCCCATGCATTGGAGAACATCGTTCGGCAGCCCCCAGACCGATGGAT	gcagcccccagaccgatgga	œ	togcagotgtggccatactggtcaaggacgctgacaaattgactttgggacagaatat	GCCTACCTGTCAAAGAAGCTCGATCCTGTAGCCAGTGGTTGGCCCATATGCCTGAAGGCT 3749	cctacctgtcaaagaagcttgatcctgtagccagtggttggcccgtatgtctgaagg	AGACCTGTC 36	gtaagggagtagcccgaggagttttaaccccaaaccctaggaccatggaggagacctg	6	gcgcacctgctctggccctccctgacgtaactaaaccctttaccctttatgtggatgag 6		gattotoctgggctcctgagcaccagaaggcatttgatgctatcaaaaaggccctgctg 621	G d	ggatcccgqqqtttqcqaccttaqcaqccccactctacccqctaaccaaaagaaaaaggg %61		CCCCBBCCBCCBCBACBBCCBACTCBCCCCCCCCCCCCC	TGCGGGACGGCAGCGATGGCTGACGGAGGACAGAAAAACTGTAGTCCAGATACCG 3389	GAGCCTCTGCTAAGAAGGCCCAGATTTGCAGGAGAGAGGTAACATACTTGGGGTACAGT 33	agagcctctgctaagaaggcccagatttgcaggagagaggtaacatacttggggtacagt 381	AACAGGACTGCTTAGAAGGCACGAAGGCACTACTGCTGGAATTGTCTGACCTAG	gcttagaaggtacgaaggcactactgctggaattgtctgacctaggcta	2 2 2 3	aacaccctcaggtgaccctcctccagtacgtggatgacctgcttctggcgggagccacc 2		agaacteeeegaeeatetttgaegaageeetaeaeagggaeetggeeaaetteaggate 201	AGAGATCCAGGTACGGGAAGAACCGGGCAGCTCACCTGGACCCGACTGCCCCAAGGGTTC 3089	or saturable to the contract of the contract o	GATGCCTTCTTCTGCCTGAGATTACACCCCACTAGCCAACCACTTTTTGCCTTTCGAATGG 3029

GENERAL INFORMATION:
APPLICANT: Jay A.

Jay A. Fishman

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

LAHIVE & COCKFIELD,

ADDRESSEE:

TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE

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                                                                                                                                                                                                                                                                                        5910 TCT-----GACCTCACCCCCAGATATCCTCCATGCTCACGGATTTTATGTTTGCCC 5960
                                                                                                                                                                                                                                                                                                           2959 teteaatgaceaggeeacacececegatgtactcegtgettacgggttttacggtttgeee 3018
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                                                                                                                                                                                                                                                   6081 AAGTTTTTCTTATGTCAACACCTATACCAGCTCTGGACAATTTAATTACCTGACCTGGAT 6140
                                                                                                                                           6021 GAACTGTGTAACCTCTAATGATGGATATTGGAAATGGCCAACCTCTCAGCAGGATAGGGT 6080
6141 TAGAACTGGAAGCCCCAAGTGCTCTCCTTCAGACCTAGATTACCTAAAAATAAGTT 6196
                                3199 atggaaagattggcaacagcgggtacaaaaagatgtacgaaataagcaaataagct 3254
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US-08-766-528-1

Sequence 1, Application US/08766528 Patent No. 6190861

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                 5615 AAGAACTCCCCGACCATCTTTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATC
                                                                                                                                                      5735 AAACAGGACTGCTTAGAAGGCACGAAGGCACTACTGCTGGAATTGTCTGACCTAGGCTAC 5794
                                                                                         5855 TTACCGGACCGCCACCGATGGCTGACGGAGGCACGGAAGAAAACTGTAGTCCAGATACCG 5914
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                                                                                                                     322 agagcctctgctaagaaggcccagatttgcaggagagaggtaacatacttggggtacagt 381
                                                                                                                                                                      262 aaacaggactgcttagaaggtacgaaggcactactgctggaattgtctgacctaggctac 321
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STRANDEDNESS: single
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442 gccccaaccacagccaaacaagtgagagatttttggggacagctggattttgcagactg 501
                                            382 ttgcggggcggggcagcgatggctgacggaggcacggaagaaaactgtagtccagataccg 441
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RESULT 3 US-08-766-528-2

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014	7954	2480	894	420	7834	2360	7774	2300	7714	2240	7654	2180	7594	2120	7534	2060	7474	2000	7414	194	735	188	729	182	723	176	717	170	711	16	70	15	69
<u>, , , , , , , , , , , , , , , , , , , </u>		80 cgtggaagcagctccgggaggcctactcaggaggaggagttccagttccaggaggaggaggaggaggaggaggaggaggaggaggag		20 tactactttccccccccarresanarTGCTTCTGTACATAGTGCTGAT		60 aattgctctacggggacccccccqttqqcaqaaattqcctttqccacttccttn	7	00 tgccctttgtgctttttagggtgaggaacacccctqqacagtttqqqqqtqacccctt	14 TTAAAGAGACCCTTAC	240 ttaaagagacccttaccaaattgaccacagagactggcattaattgattg	654 AACTGCATTGTGCATACAGACCCCAAAGCTCAGGACAGGTAGAGGAGGATGAATAGAACC	180 aactgcattgtgcatacagaccccaaagctcaggacaggtagagagggtgaataaata	594 GTCCAGCTTTTGTTGCCCAGGTAAGTCAGGGACTGGCCAAGATATTGGGGATTGATT	120 gtocagotttogttgoccaggtaagtoagggactggocaagatattggggaffnaffna	٠	060 aaatactggaggaaatttttccaagatttggaatacctaaggtaatagggfcagacaa	47	000 tttcaggatgggtagaggcttatcctactaagaaagagacttcaagcggctggagcg	4	940 tcactgaggtaaagccggctaaatacggaaacaaatatctaffggffffffff	354 GAATGCCTCCAGGGAAGAGACTAAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGA	880 gaatacctccaggaaagagactaaggggaagccacccaggcgctcactgaraagtaca	TGGCTGACTCGGTGGTCAAACATTGTGTCCCTGCCAGCTGGTTAATGCTAATGCTTGTCTTGCCTGCTAATGCTTGTCTTGCCTGCTAATGCTTAATGCTTGTCTTGCCTGCTAATGCTTAATGCTTAATGCTTGTTGCCTGCC	820 tggctgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaatgctaat	234 CTAAACACCTGCAGCAGTTGGTCAGAACATCCCCTTATCATGTTCTGAGGCTACCAGG	760 ctaaacacctgcagcagttggtcagaacatccccttatcatqttctgaggctaccac	1	701 gccccacaaagaagggttagaatatgtccaac-agatacatcqtctaacccacctag	115 AGACCA	641 agaccagttctctgagactccggaggggacctgctatacctcatatronasacrass		.581 caaagccccagaacccaqacqacaqtacaccctagaagactagaagactagaagactagaagactagaagactagaagactagaagactagaagactagaagaagactagaagaagactagaagaagaagaagaagaagaagaagaagaagaagaaga	995 TGACCGGGTTGCCAAGCAGGCAGCCCAGGGTGTTAACCTTCTGCCTATAATAC
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MOLECULE TYPE: CDNA
US-08-766-528-2
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TELEPHONE: (617)227-7400
TELEPAX: (617)227-9941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pairs
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Best Local Similarity 95.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MOLECULAR SEQUENCE TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                1411 gaaattctaagcotattagaagcottacatttgocaaaaaggottagctattatacactgt 1470
                                                                                                                                                                                                                                                                                                                                     3684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
3744 GAACCCAGACGACAGTACACCCTAGAAGACTGGCAAGAGATAAAAAAGATAGACCAGTTC 3803
                                                                                                                                                                                                1531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/766,528
                                                       3804 TCTGAGACTCCGGAGGGGACCTGCTATACCTCATATGGGAAAGGAAATCCTGCCCCACAAA 3863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Louis Myers
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                        gaacccagacgacagtacaccctagaagactggcaagagataaaaaagatagaccagttc 1650
                                                                                                                                                                     gccaagcaggcaggcccaggctgttaaccttctgcctataatagaaacgcccaaagcccca 1590
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 Mismatches

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                                        2551 tcagtctatgttagacgccaccgtgcaggaaacctcgagactcggtggaagggaccttat 2610
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                                                                                                   2671 gcatcccacgttaagccggcgccacctcccgattcggggtggaaagccgaaaagactgaa 2730
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TYPE: nucleic acid

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US-09-075-272-1
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                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
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Patent No. 6136598
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                SEQUENCE CHARACTERISTICS:
                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                              FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BOHHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
       LENGTH:
                                                                                            NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5345 AGATTACTTAAAAATAAGTTTCACTGAAAAAAGGAAAAACAAGAAAATA 5391
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                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 08-MAY
                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                          3935 GTGACTGTCGTGGCCCTCATGCCCTGGAGAGTATTGTGCGGCAGCCACCTGATAGATGG 3994
                                                                                                                                    3875 GCTATTGCAGCAGTAGCCCTGCTGATCAAAGATGCTGATAAACTGACAATGGGACAGCAG 3934
919 atgaccaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtcactttc 978
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                                                                                859 ataactgtaatagccccccatgcattggagaacatcgttcggcagcccccagaccgatgg 918
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                                                                                                                                                                                                                                  739 gttgcctacctgtcaaagaagcttgatcctgtagccagtggttggcccgtatgtctgaag 798
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Query Match
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Matches 1251; Conserv

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Score 1131; DB 3; Pred. No. 0; 0; Mismatches 130;

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                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09111085 Patent No. 6100034
                                                                                                           CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                 TITLE OF INVENTION: Detection of retroviral subtypes based TITLE OF INVENTION: Specific sequences EILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
                                                                                                                                                                                                                                                             APPLICANT: Stoye, Jonathan P APPLICANT: Weiss, Robin A
                                     TYPE: DNA
                                                    LENGTH: 3482
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Matches 1761; Conserv
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                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                        LOCATION: 1..8535
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                     NAME/KEY:
                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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            Score 1088;
Pred. No. 0;
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1102 ccg 	Qy 1042 catgat	Qy 982 ccacca Db 4331 CCCCC	Qy 922 accaace Db 4271 ACCAAT	Qy 862 actgta Db 4211 ACTGTG	Qy 802 atcgcag Db 4151 GTTGCAG	Qy 742 gccta Db 4091 GCATA	Qy 682 cgtaa Db 4031 AGAGC	Qy 622 agcgca 	Qy 562 ggattc	Qy 502 tggatco Db 3851 TGGATCO	Oy 442 gcccca Db 3791 GTTCCT	373	Qy 322 agagcctc	Oy 262 aaaca Db 3611 TATGA	Oy 202 caacac Db 3551 CTCAAC	Qy 142 aagaa Db 3491 AAGAA	Qy 82 agaga Db 3431 AAAGA	337
actgg CCCGG	tgcca GCTC	agccgctctcaaccctgccactct	ogcccgcatgacccacta 	atagcccccatgcattggagaacatcg 	igctgtggccatactggtc: GCAGTAGCACTCCTTCTC	acctgtcaaagaagcttg PATCTATCAAAAAAACTGG	agggagtagcccgaggagttttaa 	acctgetetggeeeteee CTGCATTGGCCCTCCC	ctcctgggctcctgag	cccggggtttgcgacctta CCTGGGTTTGCTTCCCTG	accacagccaaa ACGACCCCCAGA(gcgggcagcgat AAGGAAAAAGATO	tgctaagaaggco 3GCTAAGAAGGCO	aggactgcttagaaggt AAGACTGCAAAAAAGGA	ccctcaggtgaccctcct CCCCAGGTGGTGTTACT	ctccccgaccatctttç CTCTCCCACTCTCTTCC	tccaggtacgggaagaa 	CTTTTTCTGCCTCAGGC
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2 ctgcattgtgcatacagaccccaaagctcaggacaggtagaaggatgaatagaaccatt 2241 	Qy 218; Db 5456
2 ccagctttcgttgcccaggtaagtcagggactggccaagatattggggattgatt	Qy 212: Db 5390
2 atactggaggaaatttttccaagatttggaatacctaaggtaatagggtcagacaatggt 2121 	Qy 206: Db 533:
02 tcaggatgggtagaggcttatcctactaagaaaggacttcaaccgtggtggctaagaaa 2061 	Qy 200 Db 527
2 actgaggtaaagccggctaaatacggaaacaaatatctattggtttttgtagacaccttt 2001	194 521
12 atacetecaggaaagagaetaaggggaageeacecaggegeteaetgggaagtggaette 1941 	15
22 gctgacteggtggtcaaacattgtgtgccctgccagctggttaatgctaatccttccaga 1881 	182 509
32 aaacacctgcagcagttggtcagaacatcccottatcatgttctgaggctaccaggagtg 1821	176 503
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2 gaccagttctctgagactccggaggggacctgctatacctcatatgggaaggaa	164
32 aaagccccagaacccagacgacagtacaccctagaagactggcaagagataaaaaagata 1641	158 492
22 gaccgggttgccaagcaggcagccaggctgttaaccttctgcctataatagaaacgccc 1581	152 486
52 atacactgtcctggacatcagaaagccaaagatctcatatctagagggaaccagatggct 1521 	Qy 146 Db 480
02 aacaaagaggaaattotaagcotattagaagcottacatttgocaaaaaggotagctatt 1461 	14 47
42 gtacacggggccatctataaacaaagggggttgcttacctcagcagggaggg	Qy 134 Db 468
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22 ccggaaggaacttcagcgcaaaaggctgagctcatggccctcacgcaagctttgcggctg 1281 	Qy 122 Db 456
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ATTORNUL/:--
NAME: Jacobs, Set::...32,140
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER: 1169/
TELECOMMUNICATION INFORMATION:
""".EPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pinter, Applicant: Kayman, Samuel
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
TOTAL OF SECULATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5756
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                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 45 Rock
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttgctctacgggggacccccccgttggcagaaattgcctttgcacatagtgctgatgtg 2421
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3169 TTCAAAAACAGTCCCACCCTGTTTGATGAAGCCCTGCACAGGGACCTCGCAGACTTCCGG
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STRANDEDNESS: double
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ataactgtaatagccccccatgcattggagaacatcgttcggcagcccccagaccgatgg 918
                                                                gctatogcagctgtggccatactggtcaaggacgctgacaaattgactttgggacagaat 858
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                                             ATGGTAGCAGCCATCGCCGTTCTGACCAAAGACGCTGGCAAGCTCACCATGGGACAGCCA 3888
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Pred. No. 1.2e-273;
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TITLE OF INVENT	Qy 1921 gctcactgggaagtggacttcactgaggtaaagccggctaaatacggaaacaaatatcta 1980	Qy
INFORMATION: ANT: Pinter, Abraham ANT: Kayman, Samuel	Qy 1861 gttaatgctaatccttccagaatacctccaggaaagagactaaggggaagccacccaggc 1920	Ωy
RESULT 8 US-08.86-642-8 ; Sequence 8, Application US/08886642 ; Patent No. 5952474	Qy 1801 gttctgaggctaccaggagtggctgactcggtggtcaaacattgtgtgccctgccagctg 1860	ОУ
5866 GGGCCAGATCCGCAGCAC	Qy 1747 acccacctaggaactaaacacctgcagcagttggtcagaacatccccttatcat 1800	Ωу
Db 5806 AAGATAAGATTGACCGCGGGACCTCCTA Qy 2800 acqccttqtqqacaqccc 2817	OY 108/ 999aa99aaaccctgcccacaagaa999ttagaatatgtccaacagatacatcgccta 1/40	Db 03
5746 ACCAGGATTGAGCCACCATCGGAATCGA	1635 aaagatagaccagttctctgagactccggaggggacctgctatacctcatat 168	of d
5686 GCTCTCAAAGT	Qy 1576 acgcccaaagccccagaaccc-agacgacagtacaccctagaagactggcaagagataaa 1634	Dp Qq
5626 ACTAAAAATCTAGAACCCCGCTGGAAAG	Qy 1516 atggctgaccgggttgccaagcaggcagcccaggctgttaaccttctgcctataatagaa 1575	ДУ
	Qy 1456 gctattatacactgtcctggacatcagaaagccaaagatctcatatctagagggaaccag 1515	QУ
5506 TACCTGGTCCAGCACGAAGTCTGGAC	Qy 1396 ataaagaacaaagaggaaattotaagoctattagaagocttacatttgccaaaaaggcta 1455	Db Qy
5446	Qy 1336 gcacacgtacacggggccatctataaacaaagggggttgcttacctcagcagggaggg	Qy Db
5386	Qy 1276 cggctggccgaagggaaatccataaacatttatacggacagcaggtatgcctttgcgact 1335	ОУ
5326 AGGGACTGGGTGCTCCCCTAG 2341 tttgggctgaccccctatgaattgctct	Qy 1216 agectgeeggaaggaactteagegeaaaaggetgaageteatggeecteaegeaagetttg 1275	Db.
Db 5266 GAAAGAATGGATGGCCATTGCCCTTGCCTGCCTGCCTGCCTGCCCTTGCCTGCCTGCCCTTGCCTGCCTGCCTGCCCTGCCTGCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCTGCCCTGCCCTGCCCTGCCCTGCCTGCCCTGCCTGCCCTGCCTGCCTGCCCCTGCCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCC	Qy 1156 gaaaggtaagaggatggctgggggggggggggggggggg	QУ
5206	Oy 1096 gacataccgctgactggagaagtgctaacctggttcactgacggaagcagctatgtggtg 1155	Фр
5146	Qy 1036 gtgactcatgattgccatcaactattgattgatgaggactggggtccgcaaggaccttaca 1095	Qу
5086	Qy 976 ttcgctccaccagccgctctcaaccctgccactcttctgcctgaagaagactgatgaacca 1035	Оу
5026 2041	Qy 919 atgaccaacgccgcatgacccactatcaaagcctgcttctcacagagagggtcact 975	ДУ
Db 4966 ACCCACTGGGAAATTGATTTCACTGAGGT Qy 1981 ttqqtttttqtaqacaccttttcaggatq	Db 3889 CTAGTCATTCTGGCCCCCATGCAGTAGAGGCACTAGTTAAGCAACCCCCTGATCGCTGG 3948	DЬ

FUSION GLYCOPROTEINS: 25

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                                                                                                                                                                                                                      TACCTGGTCCAGCACGAAGTCTGGAGACCGTTGGCGGCAGCTTACCAAGAACAACTGGAC 5565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gagtgggtgaggcagcgaggggaggcagctccgggaggcctactcaggaggagacttg 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aatgattggatggctctcctgccctttgtgcttttttagggtgaggaacacccctggacag
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                               acgccttgtggacagccc 2817
                                                                                                     aagcttcgcctccatcgcgtggttccttactctgtcaataactcctcaagttaatggtaa 2799
                                                                                                                                                                                                                                                                                                                    GATCCTGACATGGCAAAGGTTACTCATAACCCCTCTCCCAAGCCCATTTACAGGCACTC
                                                                        AAGATAAGATTGACCCGCGGGACCTCCTAATCCCCTTAATTCTCTTCTTCTGTCTCTCAAAG 5865
                                                                                                                                                  ACCAGGATTGAGCCACCATCGGAATCGACATGGCGTGTTCAACGCTCTCAAAATCCCCTA
                                                                                                                                                                                                                                                                                                   ACTAAAAATCTAGAACCCCGCTGGAAAGGACCTTATACCGTCCTACTGACTACCCCCACC
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                                                                                                                                                                  -gccacctcccgattcggggtggaaagccgaaaagactgaaaatcccctt 2739
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APPLICATION NUMBER: US/08/886,642

FILING DATE: 01-JUL-1997

PRIOR APPLICATION NUMBER: 08/110,300

FILING DATE: 20-AUG-1993

APPLICATION NUMBER: 07/938,100

FILING DATE: 28-AUG-1992

ATTORNEY/AGENT INFORMATION:
NAME: HODE, William J.
REGISTRATION NUMBER: 07763/010002

TELEPHONE: 212/765-5070

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/758-2291

INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
I PNOTTH: 8727 PAGE DAILS
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Best Local Similarity
Matches 1702; Conserv
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                                                                                                                                                              379
                                                                                                                                                                                                                                                                                               259 accaaacaggactgcttagaaggtacgaaggcactactgctggaattgtctgacctaggc 318
                                                                                                                                                                                                                                                                                                                                                                                                199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible operATING SYSTEM: Windows95 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C.
STREET: 45 Rockefeller Plaza, Suite 2800
CITY: New York
STATE: NY
                                                                                                                 CTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGGCAG 3468
                                                                                                                                          agtttgcggggcgggcagcgatggctgacggaggcacggaagaaaactgtagtccagata 438
                                                                                                                                                                                                                  tacagagcctctgctaagaaggcccagatttgcaggagagaggtaacatacttggggtac
                                                                                                                                                                                                                                                                     TCTGAGCTTGACTGTCAACAAGGTACGCGGGCCCTGTTACAAACCCTAGGGGACCTCGGA 3348
                                                                                                                                                                                                                                                                                                                                                                         alcomacaccotcaggitgaccotcotccagtacgtggatgacctgcttctggcgggagcc
                                                                                                                                                                                                                                                                                                                                                                                                                            TTCAAAAACAGTCCCACCCTGTTTGATGAAGCCCTGCACAGGGACCTCGCAGACTTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttcaagaactccccgaccatctttgacgaagccctacacaggggacctggccaacttcagg 198
                                     CCTACTCCGAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGACGGCAGGCTTCTGTCGC 3528
                                                               ccggccccaaccaccagccaaacaagtgagagagtttttggggacagctggattttgcaga 498
                                                                                                                                                                                              TATCGGGCCTCGGCCAAGAAAGCCCCAAATTTGCCCAGAAACAGGTCAAGTATCTGGGGTAT 3408
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60.0%;
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Pred. No. 1.2e-273;
0; Mismatches 1094;
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tggcaagagataaa 1634 	acycccaaagccccagaaccc-agacgacagtacaccctagaagac	1576	Qy
AGAC	GGCCGACCAAGCGGCCCGAGAAGTAGCCACTAGAGAAACTCCAG	4546	Db
tgcctata	tggctgaccgggttgccaagcaggcagcccaggctgttaaccttc	1516	Qy
tctagagggaaccag 1515 	gctaltalacactglcctggacatcagaaagccaaagatctcatat 	4486	Db
TGCCCAAAAGACTT 448	TOTAL TARBUST CONTRACT CONTRAC	, t	2 5
tgccaaaaaggcta 145	attotaagootattagaagoottacat		D, 29
TCAGAAGGAAAAGAA 4425	ATATTCACGGAGAAATATATAGAAGGCGCGGGTTGCTCACA	4366	Db
agcagggaggga	cacacgtacacggggccatctataaacaaagggggttgcttacc	1336	Qу
PATGCTTTTGCCACT 4365	AAAATGGCAGAAGGTAAAGAAGCTGAATGTTTACACCGATAGCCGTTAT	4306	Db
gccttgcgac	ggccgaagggaaatccataaacatttatacggacagca	1276	Qy
CTCACCCAAGCCTTA 4305	GCACTGCCAGCCGGGACATCGGCCCAAAGAGCTGAGTTGATAGCGC	4246	Db
tcacgcaagett	tyccygaaggaacttcaycycaaaagyctgayctcatgycc	1216	Qy
	GCCAGCGCAAGGCCGGAGCAGCAGTAACCACCGAGACCGAG	4186	Db
cgatctgggcc	aaggtaagaggatggctggggcggcagtggtggacggggac	1156	Qy
GCAGCTTCCT	TO-	4126	Db
gcagctatg	acataccgctgactggagaagtgctaacctggttcactgacgga	1096	Qy
8=	CTGCCTTGACATCTTGGCTGAAGCCCACGGAACT	4066	Db
caaggacctta	gactcatgattgccatcaactattgattgaggagactggggtc	1036	Qу
CCTGAGGAGGGG	GACCAATAGTGGCCCTAAACCCAGCTACGCTGCTCCCTCTA	4009	Db
agactgatg	tegetecaceageegeteteaaceetgecactettetgeetga	976	Qy
ACGGACCGAGTCCAG 4008	GAC	3949	Db
cagagagg	gaccaacgcccgcatgacccactatcaaagcctgcttctc	919	Qy
GATCGCTG	AGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTTAAGCAA	3889	Db
ccccagaccgat	aatagccccccatgcattggagaacatcgttcggcag	859	Qy
	ATCGCCGTTCTGACCAAAGACGCTGGCAAGCTC	3829	Db
ctttggga	cycagctytygccatactyytcaayyacyctyacaaatty	799	Оу
CTTGCCTACG	GTGGCCTACCTGTCCAAAAAGCTAGACCCAGTGGCAGCTGGGTGG	3769	Db
ccgtatgtc	ttycctacctytcaaagaaycttyatcctytagccagtyyttyy	739	Оу
CCTTGGCGTCGGCCG 3768	GAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGGG	3709	dd
catggaggagac	agcgtaagggagtagcccgaggagttttaacccaaaccctagga	679	Qy
ര് —	CIGGGATIGCCAGACTIGACTAAGCCCTIC	3649	Db
tttatgtgg	gagcgcacctgctctggccctccctgacgtaactaaacccttt	619	Оу
TCAAGCAGGCTCTC 36		3589	Db
aaaaaggccctg 618	gggggattctcctgggctcctgagcaccagaaggcatttgatgo	559	Ωу
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                                                                                                                                                                                                                                                                                                                                                      5506 TACCTGGTCCAGCACGAAGTCTGGAGACCGTTGGCGGCAGCTTACCAAGAACAACTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5446 GATCCTGACATGGCAAAGGTTACTCATAACCCCTCTCTCCAAGCCCCATTTACAGGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5386 CATGGTCTCACCCCATATGAAATCTTATATGGGGCACCCCGCCCCTTGTAAACTTCCCT
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GCTCTCAAAGTGGACGGCATTGCAGCGTGGATCCACGCTGCCCACGTAAAGGCTGCCGAC
                        gctgtgaaagtcgaaggaatcccacctggatccatgcatcccacgttaagccggc----
                                                                                                                                                9caggaaacctcgagactcggtggaagggaccttatctcgtactttttgaccacaccaacc
                                                                                                                                                                                                                                                                   c-----aagttccacatcgcttccaagttggagattcagtctatgttagacgccaccgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trtgcacatagtgctgatgtgctgctttccccagcctttgttctctaggctcaaggcgctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGGACTGGGTGCTCCTGCTTCCCCTAGCCCTGTATCGAGCCCGCAACACGCCGGGCCCC
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PCT-US93-08041-8
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                                                                  Matches 1702;
                                                                                      Best Local Similarity
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application PC/TUS9308041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
HYPOTHETICAL:
                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: FUSION GLYCOPROTEINS NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: The Public Heat APPLICANT: New York, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5866 GGGCCAGATCCGCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2800 acgccttgtggacagccc 2817
                   19 acagatgocttottotgoctgagattacaccoccactagoccaccactttttgccttogaa 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: New York
STATE: New Yor
                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jacobs, Seth H. REGISTRATION NUMBER: 32,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 28-AU
                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US93/08041
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Pred. No. 1.2e-273;
                                                                    Mismatches 1094;
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2100 5145	2041 tcaaccgtggttggctaagaaaatactggaggaaatttttccaagatttggaatacctaag 	Qy Db
2040 5085	cttatcctactaagaaagagact CTTTCCCAACCAAGAAAGAAACT	Qу
1980 5025	1921 gotcactgggaagtggacttcactgaggtaaagccggctaaatacggaaacaaatatcta 	Qу
1920 4965	1861 gttaatgctaatccttccagaatacctccaggaaagagactaaggggaagccacccaggc 	Qy Db
1860 4905	1801 gttctgaggctaccaggagtggctgactcggtggtcaaacattgtgtgccctgccagctg	Оу
1800 4845	1747 acccacctaggaactaaacacctgcagcagttggtcagaacatccccttatcat	Qy Db
1746 4785	687 gggaaggaaatcctgccccacaaagaaggttagaatatgtccaacagatacatcgtcta 	Qy Db
1686 4725	635 aaagatagaccagttctctgagactccggaggggacctgctatacctcatat	Qy Db
1634 4665	576 acgcccaaagccccagaaccc-agacgacagtacaccctagaagactggcaagagataaa	Qу
1575 4605	1516 atggctgaccgggttgccaagcaggcagcccaggctgttaaccttctgcctataatagaa 	Оу
1515 4545	1456 gctattatacactgtcctggacatcagaaagccaaagatctcatatctagagggaaccag 	Qy Db
1455 4485	396 ataaagaacaaagaggaaattctaagcctattagaagccttacatttgccaaaaaggcta 	Qy Db
1395 4425	1336 gcacacgtacacggggccatctataaacaaagggggttgcttacctcagcagggaggg	Оу
1335 4365	1276 cggctggccgaagggaaatccataaacatttatacggacagcaggtatgcctttgcgact	Qу
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pinter, Abraha APPLICANT: Kayman, Samuel TITLE OF INVENTION: FUSIO NUMBER OF SEQUENCES: 25
             REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/110,300A
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                                                                                                    FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H.
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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3767 ATGGTAGCAGCCATCGCCGTTCTGACCAAAGACGCTGGCAAGCTCACCATGGGACAGCCA 3708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3887 GAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGGCCTTGGCGTCGGCCG
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                                                                                                       619 ctgagcgcacctgctctggccctccctgacgtaactaaaccctttaccctttatgtggat 678
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                                                                                  GTGGCCTACCTGTCCAAAAAGCTAGACCCAGTGGCAGCTGGGTGGCCCCCTTGCCTACGG
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; Sequence 9, Application US/08886642; Patent No. 5952474; GENERAL INFORMATION:
APPLICANT: Pinter, Abraham APPLICANT: Kayman, Samuel TITLE OF INVENTION: FUSION GLYCOP NUMBER OF SEQUENCES: 25; CORRESPONDENCE ADDRESS:

GLYCOPROTEINS

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RESULT

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212/258-2291
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/765-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hone, William J.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                               4247 TATCGGGCCTCGGCCAAGAAAGCCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTAT 4188
                                                                                                                                                                                                                                                                                                 4307 TCTGAGCTTGACTGTCAACAAGGTACGCGGGCCCTGTTACAAACCCTAGGGGACCTCGGA 4248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish
STREET: 45 Rocke
CITY: New York
STATE: NY
                                            4127 CCTACTCCGAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGACGGCAGGCTTCTGTCGC 4068
                                                                                                                              4187 CTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAG 4128
                                                                                                                                                                                                                                   319 tacagagcctctgctaagaaggcccagatttgcaggagagaggtaacatacttggggtac 378
                                                                    439 ccggccccaaccacagccaaacaagtgagagagtttttggggacagctggattttgcaga 498
                                                                                                                                                    379 agtttgcggggcgggcagcgatggctgacggaggcacggaagaaaactgtagtccagata 438
                                                                                                                                                                                                                                                                                                                     259 accaaacaggactgcttagaaggtacgaaggcactactgctggaattgtctgacctaggc 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/110,300 FILING DATE: 20-AUG-1993 APPLICATION NUMBER: 07/938,100 FILING DATE: 28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CONTOPERATING SYSTEM:
499 ctgtggatcccggggtttgcgaccttagcagccccactctacccgctaaccaaagaaaaa 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                 ATCCAGCACCCAGACCTGATTCTGCTCCAGTATGTAGATGACTTACTGCTGGCCGCCACT 4308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acagatgocttcttctgcctgagattacaccccactagccaaccactttttgccttcgaa 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAGAGATCCAGAGATGGGAATCTCAGGACAATTAACCTGGACCAGACTCCCGCAGGGT 4428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCAAAAACAGTCCCACCCTGTTTGATGAAGCCCTGCACAGGGACCTCGCAGACTTCCGG 4368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1036 gtgactcatgattgccatcaactattgattgaggagactggggtccgcaaggaccttaca 1095
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                                                              3050 ATGGCCGACCAAGCGGCCCGAGAAGTAGCCACTAGAGAAACTCCAGAGACTTCCACACTT 2991
                                                                                                                                                                                                                                                                    | 1396 ataaagaacaaagaggaaattctaagcctattagaagccttacatttgccaaaaaggcta 1455
                                                                                                                                                                                                                                                                                                                              3230 GCCCATATTCACGGAGAAATATATAGAAGGCGCGGGTTGCTCACATCAGAAGGAAAAGAA
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1576 acgcccaaagccccagaaccc-agacgacagtacaccctagaagactggcaagagataaa 1634
                                                                                                      1516 atggctgaccgggttgccaagcaggcagcccaggctgttaaccttctgcctataatagaa 1579
                                                                                                                                                       3110 AGCATAATTCATTGCCCGGGACATCAGAAGGGAAACCGCGCGGAGGCAAGGGGCAACAGG
                                                                                                                                                                           1456 gctattatacactgtcctggacatcagaaagccaaagatctcatatctagaagggaaccag
                                                                                                                                                                                                                                          3170 ATCAAAATAAGGACGAGATCTTGGCCCTACTGAAGGCTCTCTTCCTGCCCAAAAGACTT 3111
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1910 GCTCTCAAAGTAGACGGCATTGCAGCGTGGATCCACGCTGCCCACGTAAAGGCTGCCGAC
                                                      2635 gctgtgaaagtcgaaggaatccccacctggatccatgcatcccacgttaagccggc----
                                                                                                                                                                                                   2575 gcaggaaacctcgagactcggtggaagggaccttatctcgtacttttgaccacaaccg
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                                                                                                                                                       ACTAAAAATCTAGAACCCCGCTGGAAAGGACCCTATACCGTCCTACTGACTACCCCCACC
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PCT-US93-08041-9/c
; Sequence 9, Application PC/TUS9308041
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: The Public Health Research Institute APPLICANT: New York, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 45 Roci
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Pred. No. 4.3e-273;
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taaa 163 CATA 293	acgoccaaagccccagaaccc-agacgacagtac 	1576 2990	Оу	
agaa 157 ACTT 299	_	1516 3050	Qy Db	
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tacatttgccaaaaaggcta 1455 rcTTCCTGCCCAAAAGACTT 3111	ataaagaacaaagaggaaattotaagcotattagaagcot 	1396 3170	Ωу	
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US-09-011-745-3
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APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
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SEQ ID NO 3
LENGTH: 7308
               Matches 1633; Conservative
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                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: GB9517263.1
                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Portion OTHER INFORMATION: construct
                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1850 ACCAGGATTGAGCCACCAGCAGAATCGACATGGCGTGTTCAACGCTCCCAAAATCCCCTA 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1970 ACTAAAAATCTAGAACCCCGCTGGAAAGGACCCTATACCGTCCTACTGACTACCCCCACC 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2461 gagtgggtgaggcagcgagcgtggaagcagctccgggaggcctactcagg-----agga 2514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2150 GATCCTGACATGGCAAAGGTTACTCATAACCCCTCTCTCCCAAGCTCATTTACAGGCACTC 2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2210 CACGGTCTCACCCCATATGAAATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCT 2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2270 AGGGACTGGGTGCTCCTGCTTGCCCTTGCCCTGTATCGAGCCCGCAACACGCCGGGCCCC 2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2281 aatgattggatggctctcctgccctttgtgctttttagggttgaggaacacccctggacag 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gctgtgaaagtcgaaggaatcccacctggatccatgcatcccacgttaagccggc---- 2690
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                             27.6%;
60.6%;
                      Score 916.2; DB 4;
Pred. No. 2.2e-268;
      0; Mismatches 1033;
                                            Length 7308;
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                        1039 actcatgattgccatcaactattgattgaggagactgggggtccgcaaggaccttacagac 1098
                                                                                4960 ggaccggtggtagccctgaacccggctacgctgctccc---actgcctgaggaagggctg
                                                                                                                                                                   4900 tocaacgcccggatgactcactatcaggccttgcttttggacacggaccgggtccagttc 4959
                                                                                                                                                                                                                                                         4840 gtcattctggcccccatgcagtagaggcactagtcaaaccacccccgaccgctggctt 4899
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                                                                                                       979 gctccaccagccgctctcaaccctgccactcttctgcctgaagagactgatgaaccagtg 1038
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                                                                                                                                                                                                                                                                               802 atcgcagctgtggccatactggtcaaggacgctgacaaattgactttggggacagaatata 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 gcctacctgtcaaagaagcttgatcctgtagccagtggttggcccgtatgtctgaaggct 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4480 tggatccctgggtttgcagaaatggcagccccttgtaccctctcaccaaaacggggact 4539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562 ggattctcctgggctcctgagcaccagaaggcatttgatgctatcaaaaaggccctgctg 621
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                                   atagggtcagacaatggtccagctttcgttgcccaggtaagtcagggactggccaagata 2163
                                                                                                                                                                                       accytyytyyctaayaaaatactyyagyaaatttttccaagattttyyaatacctaagyta 2103
                                                                                                                                                                                                                                                                              gctaccaggagtggctgactcggtggtcaaacattgtgtgccctgccagctggttaatgc 1868
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ttgggaactgacaatgggcctgccttcgtctccaaggtgagtcagacagtggccgatctg
                                                                                                                       aaggtcgtaaccaagaagctactagaggagatcttccccaggttcggcatgcctcaggta
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4059

22

Query Match
Best Local Similarity
Matches 1633; Conserv

Conservative

27.6%;

Score 916.2; DB 4; Pred. No. 2.2e-268; 0; Mismatches 1033;

Length

Gaps

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                                                                                                                                      SEQ ID NO 4
LENGTH: 7308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                             EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
                 OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct
                                                                                       ORGANISM: Artificial Sequence
                                                                                                                  TYPE: DNA
                                                                 FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Portion ; OTHER INFORMATION: construct US-09-011-745-2
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; Sequence 2, Application US/09011745
; Patent No. 6165715
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                                                                                                                                                                                                                               Matches 1633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Expression systems FILE REFERENCE: 09/011,745 CURRENT APPLICATION NUMBER: US/09/011,745 CURRENT FILING DATE: 1998-06-22 EARLIER APPLICATION NUMBER: PCT/GB96/02061 EARLIER APPLICATION NUMBER: GB9517263.1 EARLIER APPLICATION NUMBER: GB9517263.1
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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2163 5317	caatggtccagctttcgttgcccaggtaagtcagggactggccaagata 	2 1
2103 5257	ccgtggtggctaagaaaatactggaggaaatttttccaagattttggaatacctaaggta 	2044 5198
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1923 5077	aatcettecagaatacetecaggaaagagactaaggggaagceacecaggeget 	1869 5018
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	tgaccaggttgccaagcaggcagcccaggctgtta-accttctgcctataatagaaac	1519 4658
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Query Match 76.5%; Best Local Similarity 87.1%; Matches 7165; Conservative

Score 6282.4; Pred. No. 0; 0; Mismatches

0;

931; DB 4.

Indels 134; Gaps Length 8132;

19;

60

	RESULT US-08- Sequ Pates TIT CC	O 9996666666666666666666666666666666666
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0 FILING DATE: 14 DEC-1995 ATTORNEY/AGENT INFORMATION: NAME: LOUIS MYSTS REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER: 35, REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION TELEPAN: (617)227-7400 TELEPAN: (617)227-5941 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 8132 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA	1766-528-3 ance 3, A ance 3, A ant No. 61 int No. 61 int Of I inte of I inter of I in	359.4 331.6 331.6 303.0 303.0 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.4 301.6
IOR APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 14 - DEC-199 FILING DATE: 14 - DEC-199 TORNEY/AGENT IMFORMATION NAME: LOUIS MYETS REGISTRATION NUMBER: 35 REGISTRATION NUMBER: 1617)227-740 TELEPHONE: (617)227-740 TELEFAX: (617)227-5941 TELEFAX: (617)227-5941 TELEFAX: 617)227-5941 TRATION FOR SEQ ID NO: 0UBMCE CHARACTERISTICS: 510 TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	EX. COP S C VER S:	3.7 10 3.7 22 3.3 3.4 6 3.3 3.4 6 3.4 6 3.5 6 3.7 2 3.8 6 3.8 6 3.
DATA: US 08/5 I-DEC-1995 ORMATION: BY BER: US 08/5 FORMATION: GROWNER: MG INFORMATION: 7)227-7400 7)227-941 ID NO: 1D NO: 3: RISTICS: Sse pairs soid single single	US ish MO AN 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0970 3 6028 4 1965 1 1965 1 22499 1 22499 1 2001 3 2001 3 2001 3 2079 4 1911 4 1925 4 1789 1 789 1
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101	aaagtcgagccctcttcctcgtatctaccccgagatcgaggagccgccgacttggccgga	957	Qy
953	CCAAGAAAGCCAGGTCCCCGAATTCTGGCTCTTGGAGAGAAAACAAAC	894	Ъ
956	ccaagaaagccaggtccccgaatcctggctcttggagagaaaaacaacactcggccgaa	897	Qy
893	CTTACGTGGCAAGATTTGGCAGAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATAAG	834	Db
896	cttacgtggcaagatttggcagaagatcctccgccatgggttaaaccatggctaaataaa	837	Qy
833	GTTAAAGCAGTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCCCTATATC	774	Db
836		777	Qy
773	CCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAGATTATCCTGGCT	714	Db
776		717	Qy
713	CATAATTTGTCAGTTCAGGTTAAGAAGGGACCTTGGCAGACTTTCTGTGTCTCTGAA	654	DЪ
716	cataatttgtcagttcaggttaagaagggaccttggcagactttctgtgcctctgaatgg	657	Qy
653	ACGGTGACGACCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAGGGCT	594	Db
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                                                  TCTACCAGTTCTAAGATTAGAACTATTAACAAGAGAAGAAGTGGGGAATGAAAGGATGAA
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US-08-766-528-2

: Sequence 2, Application US/08766528

; Patent No. 6190861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,528
TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                   APPLICATION NUMBER: US 08/572,645 FILING DATE: 14-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MOLECULAR SE
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                                  NAME: Louis Myers
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     STREET: 60 S:
CITY: Boston
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VENTION: MOLECULAR SEQUENCE OF
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Best Local Similarity 83.0%;
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: sing
TOPOLOGY: linear
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                                      AGGCAATCATTTTTCAGACTGGACCCGGCTCTCATCCTGATCAGGAGCCCTATATCCTTA
                                                   aggcaatcatttttcagactggacccggctctcatcctgatcaggagccctatatcctta
                                                                                            CATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAAATTATCCTGGCTGTTA
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1989		1930	Db
1919	gagaaggaacagagaaaagaaaaggagagagagaaggaaggaaggaagacgtgatagacgg	1860	Qy
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1799	gggcagtcggctctggatatcaggaagaaacttcagagactggaagggttacaggaggct	1740	Qy
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1739	ttcacccottttgatcctacctcagaggcccagaaagcctcagtggccctggccttcatt		Qy
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1499	gggcgacccacgcagttgcaaaatgagattgacatgggatttcccttgactcgccccggt	1440	Qy
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1319	aaaactaaccatccccctttctcggaggatccccaacgcctcacggggttggtggagtcc	ν	Qy
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1139	cetggagetecggtggtggagggacetgetgeegggacteggageeggagaggegeeace	1080	Qy
1149		1090	Db
1079	caacctgttcccccacccccttatccagcacagggtgctgtgaggggga-cctctgccct	1021	Qy
1089		1030	Db
1020	togagecetetteetegtatetacecegagategaggageegeettggeeggaacee	961	Qy
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5219	tcaggacaggtagagaggatgaatagaaccattaaagagacccttaccaaattgaccaca	5160	ρb
4421		4362	
5159	ggactggccaagatattggggattgattggaaactgcattgtgcatacagaccccaaagc	5100	Qy
4361		4302	Db
5099	ggaatacctaaggtaatagggtcagacaatggtccagctttcgttgcccaggtaagtcag	5040	Фр
4301		4242	
5039	aagaaagagacttcaaccgtggtggctaagaaaatactggaggaaatttttccaagattt	4980	dd
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4121		4062	
4859	ccctgccagctggttaatgctaatccttccagaatacctccaggaaagagactaagggga	4800	Qy
4061		4002	Db
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4001		3942	Db
4739	caacagatacatcgtctaacccacctaggaactaaacacctgcagcagttggtcagaaca	4680	дд
3941		3882	V9
4679	acctgctatacctcatatgggaaggaaatcctgccccacaaagaagggttagaatatgtc	4620	Фр
3881		3822	
4619	accctagaagactggcaagagataaaaaagatagaccagttctctgagactccggagggg	4560	ОУ
3821		3762	
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4499	aaagatctcatatctagagggaaccagatggctgaccgggttgccaagcaggcag	4440	dg
3701		3642	Vo
4439	gaagcettacatttgccaaaaaggctagctattatacactgtcctggacatcagaaagcc	4380	DP 6A
3641		3582	
4379	gcagggagggaataaagaacaaagaggaaattctaagcctatta	4320	Qy
3581		3522	Db
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3516		3517	Db
4259	cggctggccgaagggaaatccataa	4200	Qy
3516		3517	Дb

7375 6510	7316 tgaacaagcttagaaaaagttagagaggcgtcgaaggggaaagaggggtgaccaggggt 	Db 04
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7195 6330	36 tecgageettaaaggagtetgttageaacetagaagagtecetgaettetttgtetgaag 	Дy
7135 6270	076 caggaccacagcagctagagaaaggacttggtgagctacatgcgggccatgacagaagatc 	Ор
7075 6210	016 ctgtaatgctcggattagggacggccgttggcgtaggaacagggacagctgccctgatca 	Оy
7015 6150	956 ttgatgaatatgactatcggtataaccgaccaaaaagagaacccgtatcccttaccctag 	Qy Db
6955 6090	96 atttctgtgtcatggtccaaatcgtcccccgagtgtactaccatcctgaggaagtggtcc	Db Qy
6895 6030	6836 gggcatgcaatactgggttaaccccctgtgtttccacctcagt	Qy Db
6835 5970	76 ctgtggtttatgagcaggcctcagaaaatcagtatttagtacctggttataac	Оy
6775 5910	6716 ccgggaaggggacatgcataggaaaagctcccccatcccaccaacacctttgc 	рь
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6415 5565	6356 aggggcccc 5542 AAGGACCTC	Db Qy
6355 5541	6296 ggatagagacggggacagaaccccctgtggcaatgc 	Db Db

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; Sequence 1, Application US/08766528
; Patent No. 6190861
; GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENTION: AND METHODS OF
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, L
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STREET: 60
CITY: Bost
       STATE: M
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
}-766-528-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYCE'S
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocies
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acagtgactacccccttagtttgactctcgaccattggactgaagttagatccagggct 656
                               tecgaetettttgeetgettgtggaagaegegggaegggtegegtgtgtetggatetgttg 536
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95.2%;
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                                                                                                                                                                                                                                                            APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
                                                                                                           Matches
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                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Porcine
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99.08;
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                                                                                                                          Score 3376.6;
Pred. No. 0;
                                                                                                             Mismatches
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32 actaccatcctgaggaagtggtccttgatgaatatgactatcggtataaccgaccaaaaa 6991	Qy 693
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72 cctcagtcttcaaccaatccaaagatttctgtgtcatggtccaaatcgtcccccgagtgt 6931	687
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12 tagtacctggttataacaggtggtgggcatgcaatactgggttaaccccctgtgtttcca 6871 	81
52 cccaccaacacctttgctatagtactgtggtttatgagcaggcctcagaaaatcagtatt 6811 	675
92 ataagettaeeeteaetgaagttteegggaaggggaeatgeataggaaaageteeeceat 6751 	86
32 aagaaagaaaattcaatgtgaccaaagagcatagaaatcaatgtacatgggggtcccgaa 6691	663
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72 ccacttcttcttgttggctttgtctatcctcagggcctccttattatgaggggatggcta 6631 	57
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52 ctggattgattcctaccaacacgcctagaaactccccaggtgttcctgttaagacaggac 6511	645
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2 eggtgeceeaattaaeetegetgeggeetgaeataaeaeageegeetageaaeagtaeea 64	63
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2 gacccgataaa 6 gacccgataaa	1 6
72 ggtccactttaaccattcgccttaggatagagacggggacagaaccccctgtggcaatgg 6331	62
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3 aaaagtggataaatggtatgagctggggaatagttttttat-tat 	
5 catcagacttagattatctaaagataagtttcactg-	61
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95 tcaattocggccogggcaagtacaaaatgatgaaacta	60
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35 ccaacgatggagactggaaatggccgatctctctccaggaccgggtaaaattctcctttg 60	60
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                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                          Best Local Similarity Matches 4362; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BONHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS
TITLE OF INVENTION: PACKAGING CELL LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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643 ttagatccagggctcataatttgtcagttcaggttaagaagggaccttggcagactttct
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CITY: San Francisco
STATE: California
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TOPOLOGY: lir
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FILING DATE: 08-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Poor, Brian W. REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                     TAGAAATGGGACAATCTGTCTCCACTCCCCTTTCTCTAACCCTGGAGCATTGGAAGGAGG
                                                                            ttaatatgggacagacagtgactaccccccttagtttgactctcgaccattggactgaag
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Pred. No. 0;
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1705 aggcccagaaagcctcagtggccctggccttcattgggcagtcgg
Qy 1645 tatttettgagaggeteatggaageetteaggeggtteaceeetttt
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3809	0 TGGACGAGAGAGCGGCATAGCCAGAGGGGTGCTGACACAAGCACTAGGACCCTGGAAG	37
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Query Match

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                                                                                                                                                                                                          TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7722 ATGGTATTAAAACAACAATATCAGGTCTTCCAG 7754
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NAME/KEY: misc_feature
LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "Galv SEATO Genome"
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                                                                                                                                STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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SOFTWARE: Patenti
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1286 ggatccccaacgcctcacggggttggtggagtcccttatgttctctcaccagcctacttg 1345
                                                                                                   1226 ttggcccttttcttctgcagatctctataattggaaaactaaccatccccctttctcgga 1285
                                                                                                                                                                                                             1166 attaccgctgcgcacctatggccctcccatgccagggggccaattgcagcccctccagta 1225
                                                                     1642 TIGGCCTTTTTCCTCAGCAGATCTTTATAATTGGAAATCTAATCATCCCTCTTTTTCTGA 1701
                                                                                                                                                                 1582 TTTGCCCCTCCGAGCCATAGGACCCCCGGCCGAGCCCAATGGCCTGGTCCCTCTACAATA 1641
                                                                                                                                                                                                                                                             1522 GACCAGGAGTCGCCGTGCCCGCAGTCCAGCAGACACTCGGGTCCTGACTCCACTGTGAT 1581
                                                                                                                                                                                                                                                                                                         1109 tgccgggactcggag---ccggagagggcgcaccccggagcggacagacgagatcgcgat 1165
                                                                                                                                                                                                                                                                                                                                                           1462 GATCGGACCGCCGTCAGGCCAGATGCCCGATAGTAGCGATCCTGAGGGGGCCAGCCGCTGG 1521
                                                                                                                                                                                                                                                                                                                                                                                                   1050 acagggtgctgtgaggggacctctgcccc-tcctggagctccggtggtggagggacctgc 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1402 CTCTGAACCCACGCCCCCGCCCTATCCGGCGCACTGCCACCCCTCTGGCCCCTCAGGC 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1342 GAGGCCATCAGCTCCTCCCCGACCCCCATCTACCCGGCAACAGACGACTTACTCCTCCT 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1282 ATGGGTGCCAGCCTCCGCCAAGGTCGCTGTTGTCTCTGATACCCGAAGACCAGTTGCGGG 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1222 ACATCCGGACCAAGTTCCATATATCGTGGTATGGCAGGACCTCGCCCAGAATCCCCCACC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1165 TTTTAATCTCTCTGTCATTTTTGCAGTTAAAAAGATTGTCTTTCAG----GAGAACGGGGG 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             992 tcgaggagccgccgacttggccggaac--cccaacctgttcccccacccccttatccagc 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             932 agagaaaaacaaacactcggccgaaaaagtcgagccctcttcctcgtatctaccccgaga 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1045 CTGGAGAGATGTGAGAACAAGGGCTCACAATCTATCCGTGGAAATCAAAAAGGGAAAATG 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            872 atgggttaaaccatggctaaataaaccaagaaagccaggtccccgaatcctggctcttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     812 tcatcctgatcaggagccctatatccttacgtggcaagatttggcaggaagatcctccgcc 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752 ctttaattotgaaattatootggotgttaaggoaatcatttttoagaotggaocoggoto 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      632 ttggactgaagttagatccagggctcataatttgtcagttcaggttaagaagggaccttg 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    985 CTCCCAAATCATCAATATGGGACAAGATAATTCTACCCCTATCTCCCTCACTCTAAATCA 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 tgtctacagttttaatatgggacagacagtgactacccccttagtttgactctcgacca 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                925 CCGCCGTCTCTGGTTTCTTTTTGTTTCGTTTCTGGAAAGCCTCTGTGTCACAGTCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 999tc9c9t9t9tct99atct9tt99tttct9tctc9t9t9tcttt9tcttt9tctt9t9c9tcct 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 gcgaaagcttccccctccgcggccgtccgactcttttgcctgcttgtggaagacgcggac 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 agcagacgtgctaggaggatcacaggctgccaccctgggggacgccccgggaggtgggga 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816 GGACCAGGGACGCCTGGTGGACCCCTCG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GTAACGGGTCGTTGTGACCCG
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acgggtaaccca ACAAGTGACCCA	gacttgggagtgggacgggtaaccca 	2361 2762	Дb
-gecacagggeaacggeagtatecatggactacecgaagaa 	tcctgggtgatgggtgccacagggca; 	30	Дb
CATTCAGTATTGACCCAACCCATGGGAAAAGTAGGGTCCAGACGG 2	gataccggagcggagcattcagtgct	6 2	Db Qy
cagggtaactttgaaggt TAGGGTAACACTGACTGT	agggtaactttg AGGGTAACACTO	2181 2581	DЬ
octagctctagaagaagataaagattaggggagacggggttcgga TAGCCCTAGATAACTAGGGAGTCAGGGTTCGGA	aaaggaccgaaggtcctagctctagaa AGAGAAGCCAAGGTTCTAGCCCTAG-	υ ⊢-	Db Qy
agaaaaaggacactgggcaaggaac AGAGAAGGGCCATTGGGCAAGAGAA	aaagaaaaaggaca AAAGAGAAGGGCCAI	.4. 0	Qy Db
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<pre>ctggaagggttacaggaggctgagttacgtgatctagtgagagaggc 1825 </pre>	gaaacttcagagactggaagggttac -	76 18	ду Ду
cagtggccttggccttcattgggcagtcggc 	ggcccagaaagcctcagtggccctggc 	70	Оу
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aaggtaagagaggtgatgcagggaccg AAGGTAAGAGAGGTCTTGCAGGGACCG	gcccactaatttggctaaggtaagac 	00	Дb
tatcgccaggctcts ACCGCCGACTCT	ggagagettgaaaatetategeeagge	94	Оу
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aatgtt AATGTC	gttagaggctagaaaaaatgttcctgg CCTGGAGGCCCGCAAAAATGTCCTTGG	82	Оу
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TCACGGGGCTCCTTG!	AAACCCAGCAGGTCTCACGGGGCTCC	70	Db

3500 3898	3441 ttttgcagactgtggatcccggggttttgcgaccttagcagccccactctacccgctaacc	Оy
3440 3838	3381 gtocagataccggccccaaccacgccaaacaagtgaqagagttttttggggacagctgga 	Qу
3380 3778	3321 ttggggtacagtttgcggggcgggcagcgatggctgacggaggcacggaagaaaactgta 	Qу
3320 3718	3261 gacctaggctacagagcctctgctaagaaggcccagatttgcaggagagaggtaacatac	Qу Дъ
3260 3658	3201 gcgggagccaccaaacaggactgcttagaaggtacgaaggcactactgctggaattgtct	Qу
3200 3598	3141 aacttcaggatccaacacoctcaggtgaccotcctccagtacgtggatgacctgcttctg	Qy Db
3140 3538	3081 ccccaagggttcaagaactccccgaccatctttgacgaagccctacacagggacctggcc	Qy Db
3080 3478	3021 gccttcgaatggagagatccaggtacgggaagaaccgggcagctcacctggacccgactg	Qу
3020 3418	2961 ttggacttaaaagatgccttcttctgcctgagattacaccccactagccaaccacttttt	Qy Db
2960 3358	2901 glocogaaccottataacctottgagogocotocogoctgaacggaactggtacacagta	Qy Db
2900 3298	2841 tatcgaccagtacaggacttgagagaggtcaataaaagggtgcaggacatacacccaacg	Qy Db
2840 3238	2781 cctgtccaatccccttggaatactcccctgctaccggttaggaagcctgggaccaatgat	Qy Db
2780 3178	2721 gaggetegagaaggaatttggeegeatgtteaaagattaateeaacagggeateetagtt	Qy Db
2720 3118	2661 gttattcaactgaaggccagtgctacaccagtatcagtcag	Qy Db
2660 3058	2601 tttccccaagcctgggcagaaaccgcagggatgggtttggcaaagcaagttcccccacag	Qy Db
2600 2998	2541 tatcgactatattctccccaagtaaagcctgatcaagatatacagtcctggttggagcag	Qу
2941	88	Db
248	totaggtagagacttactgaccaagatgggagctcaaatttcttttgaacaaggaag 	Db Qy

4640	gactccggaggggacctgctatacctcatatggg	0у 458	
4968	CAAAACCTCAAGAGCCAATCGAGCCCGCTCAAGAAAAGACCAGGCCGAG	Db 491	
4580	tagaaacgcccaaagccccagaacccagacgacagtacaccctagaagactggcaagag		
4520 4915	gcaggcagcccaggctgttaaccttctgcctata 	Qy 446 Db 485	
4855	ω—ω	Db 479	
79	GATATCAAAAACAAGAAGAAATTTTGGCCCTGCTAGAGGCCATCCAT	47	
4400	gggaaataaagaacaaagaggaaattctaagcctattagaagccttacatttgccaaaa	Qy 434	
4340 4735	1 gcgactgcacacgtacacggggccatctataaacaaagggggttgcttacctcagcaggg	Qy 428 Db 467	
4280 4675	GCTTACGCCTGGCCGAAGGAAAAACATCAACATCTACACGGACAGCAGGTATGCTTTT	0y 422 Db 461	
	. gccagcagcctgccggaaggaacttcagcgcaaagggctgaggtcatggccctcacgca 	4 4 5 +	
55	6 ATCACGAAGGTAAACGGAAGCAGGGCACCCGATCGTAGATGGCAAGCGGACGGTAT	44	
4160	1 gtggtggaaggtaagaggatggctggggcggcagtggtggacgggacccgcacgatct	Qy 410	
4100 4495	1 cttacagacataccgctgactggagaagtgctaacctggttcactgacggaagcagctat	QY 404 Db 443	
4040 4438	11 gaaccagtgactcatgattgccatcaactattgattgaggagactggggtccgcaaggac	Qy 398 Db 437	
3980 4378	11 gtcactttcgctccaccagccgctctcaaccctgccactcttctgcctgaagagactgat	•	
3920 4318	1 gaccgatggatgaccaacgccogc	38 42	
3860 4258	1 ggacagaatataactgtaatagccccccatgcattggagaacatcgttcggcagcccca 	Qy 380 Db 419	
3800 4 198	1 tytotgaaggotatogoagotgtggooataotggtoaaggaogotgaoaaattgaotttg 	Qy 374 Db 413	
3740 4138	11 aggagacctgttgcctacctgtcaaagaagcttgatcctgtagccagtggttggcccgta 	Qy 368 Db 407	
3680 4078	1 tatgtggatgagcgtaagggagtagcccgaggagttttaacccaaaccctaggaccatgg	Qy 362 Db 401	
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3560 3958	1 aaagaaaaagggggattctcctggggtcctgagcaccagaaggcatttgatgctatcaaa 	Qy 350 Db 389	

5655 tcggggtggagagccgaaaagactgagaatccccttaagcttcgcctccatcgcctggtt 5714	Qγ
5601 ggaatcccacctggatccatgcatcccacgttaagccggcgcacctcccgac 5654 	ДУ
, 5541 actoggtggaagggaccttatctcgtacttttgaccacaccaacggctgtgaaagtcgaa 5600	Qy Db
7 5481 catcgcttccaagttggagattcagtctatgttagacgccaccgtgcaggaaacctcgag 5540 	Db dd
7 5421 aggcagcgagcgtggaagcagctccgggaggcctactcaggaagaacttgcaagttcca 5480	Db Qy
	Db VQ
5301 acccectatgaattgetetaegggggaecececegttggeagaaattgeetttgeacat 53	Qy Db
7 5241 atggctctcctgccctttgtgctttttagggtgaggaacacccctggacagtttgggctg 5300	Db Qy
5181 aatagaaccattaaagagacccttaccaaattgaccacagagactggcattaatgattgg 524 	Db Db
7 5121 attgattggaaactgcattgtgcatacagaccccaaagctcaggacaggtagagaggatg 5180	Db Qy
/ 5061 tcagacaatggtccagctttcgttgcccaggtaagtcagggactggccaagatattgggg 5120 	Qy Db
	Db Qy
/ 4941 gtagacacottttcaggatgggtagaggcottatcctactaagaaagagacottcaaccgtg 5000	Qy Db
/ 4881 gaagtggacttcactgaggtaaagccggctaaatacggaaacaaatatctattggttttt 4940 	Qy Db
4821 aatcettecagaatacetecaggaaagagaetaaggggaagceacecaggegeteactgg 488 11	Db Qy
4761 ctaccaggagtggctgactcggtggtcaaacattgtgtgccctgccagctggttaatgct 482	dd dy
4701 cacctaggaactaaacacctgcagcagttggtcagaacatccccttatcatgttctgagg 47	Qy Db
/ 4641 aaggaaatcctgccccacaaagaagggttagaatatgtccaacagatacatcgtctaacc 4700	Qy Db
4969 GGA 4971	Db

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7062
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                                          agaaatcaatgtacatgggggtcccgaaataagcttaccctcactgaagtttccggggaag 6723
---GACCGGTGCCGCTGGGGGACCCAAGGAAAGCTCACCCTCACTGAGGTCTCAGGACAC
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                                                                                                                                                                                                                999cctccttattatgaggggatggctaaagaaagaaaattcaatgtgaccaaagagcat 6663
                                                                                                                                                                                                                                                                                                 tccccaggtgttcctgttaagacaggacagagactcttcagtctcatccaggggaggtttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ataacacagccgcctagcaacagtaccactggattgattcctaccaacacgcctagaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cccctgtggcaatgggacccgataaagtactggctgaacaggg------gccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTATGTGTCTGGACATCCAGGCGTACAGTTCACCATTCGCTTAAAAATCACCAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCACAGACAAAGGAAAATTATCCAAGGACTGGATAACGGGAAAAAACCTGGGGATTAAGA
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                                                                                                                                              GGCCCCCCTTATTATGAAGCAATAGCCTCATCAGGAGAGGTCGCCTACTCCACCGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAAACACTCCGCCTCCCACCACAGGCGACAGACTTTTTGATCTTGTGCAGGGGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTCCACAGCCCTGGCGACTAGTGCACAAACTCCCCACGGTGAGAAAAACAATTGTTACC
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RESULT 7 US-08-110-300A-8

Sequence 8, Application US/08110300A Patent No. 5443756
GENERAL INFORMATION:
APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel

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TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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CITY: New York
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TTCGTGCACCCTAAACCTCCCCTCTCTCTCCCCCCTTCAGCCCCCTCTCTCCCCACCTGAA 975
                                                                    GAACGGACAGCCCACAACCTGTCGGTAGAGGTTAGAAAAAGGCGCTGGGTTACATTCTGC 735
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                                      gagaagaatttgactaagatcttggccgcagtggttgaagggaagagcagcagcaggagaga 1982
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/ 2627 agggatgggtttggcaaagcaagttcccccacaggttattcaactgaaggccagtgc	pb Qy
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/ 2333 gtatccatggactacccgaagaaccgttgacttgggagtgggacgggtaacccactc	ф
/ 2273 accattaggaaaactaaaagaaaaaaatcctgggtgatgggtgccccagggcaacgg	DP OA
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/ 2102 ctgccccaagaagggaaacaaaggaccgaaggtcctagctctagaag	dd Vy
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4202		4143	Db
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3905		3846	Db
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                  Query Match
Best Local :
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APPLICANT: Pinter,
APPLICANT: Kayman,
TITLE OF INVENTION:
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: Hone, William J.

REGISTRATION NUMBER: 26,739

REFERENCE/DOCKET NUMBER: 0776

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212/765-5070
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8323 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: FastSEC
 Local Similarity
nes 4058; Conserv
                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/938,100 FILING DATE: 28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/886,642 FILING DATE: 01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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STATE: NY
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Score 1747; I
Pred. No. 0;
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                                  DB 2;
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856 GTCCCTTACATCCTGGGAACCTATAGCARTACCCCCTTCCCTT	525 ctggatctgttggtttctgtctcgtgtgtctttgtccttgtcgcgtccttgtctcaagtttt 584
1923 gagagaatttgactaagatcttggccgaftgftgagggaaggaggaggaggaggaggaatttaggcaaggacaccagaftgftgacgaAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Db 1636 GGTCTCCAAAACGCGGGCAGAAGCCCCACCAATTTGGCCAAGGTAAAAGGGATAACCCAG 1695 Qy 1623 ggaccgaacgaacctccctcggtatttcttgagaggctcatggaagccttcaggcggttc 1682 Qy 1623 ggaccgaacgaacctccctcggtatttcttgagaggctcatggaagccttcaggcggttc 1682

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cgacggg 1442 GGACGGA 1515	accyagyagcgagagagaattctyttagaggctagaaaaaatyttcctygggcc 	1383 1456	
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cettate 1045 ACTCACG 1095	ccgagatcgaggagccgccgacttggccggaaccccaacctgttcccccacccc	986 1036	
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taaacca 884 CAGACCC 915	gagccctatatccttacgtggcaagatttggcagaagatcctccgccatgggtt	825 856	
tgatcag 824 GATCAG 855	attatcctggctgttaaggcaatcatttttcagactggacccggctctcatcct	765 796	
ttctgaa 764 CCCAGAC 795	gcctctgaatggccaacattcgatgttggatggccatcagaggggacctttaat 	705 736	
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467 tgcgaccttagcagcccactctacccgctaaccaaagaaaaaagggggattcccctgggc 352 1 1 1 1 1 1 1 1 1	Qy Db
ggattttgcagactgtggatcccggggtt 346	Qy Db
347 gegatggetgaeggaggeaeggaagaaaetgtagteeagataeeggeeecaaecaeage 340 	Qу
287 gaaggcccagatttgcaggagagaggtaacatacttggggtacagtttgcggggcgggc	Qу
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167 gaccotcotcoagtaogtggatgacotgottotggogggagocaccaaacaggactgott 322	Qy Db
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2687 accagtatcagtcagacagtaccccttgagtagagaggctcgagaaaggaatttggccgca 2746	Qy 2 Db 2
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4922	4769 agtggctgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaatccttc	Оу
86	ctaccag CGGGATC	Оу
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68	agttc TAAAC	Qy Db
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38	acacggggc TCACGGAGA	Qy Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application PC/TUS9308041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Public Health Research Institute of the City of APPLICANT: New York, Inc.
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7671
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                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      STREET: 45 Roc
CITY: New York
STATE: New Yor
    APPLICATION NUMBER:
                   CLASSIFICATION:
                                                                      FILING DATE
                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                             COUNTRY: U
                                                                                          APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                           1106 tgctgccgggactc-----
                                                                                                          1096 GAGGACCCTCCGCCTTACCGGGACCCAGGGCCACCCTCTCCTGACGGGAACGGCGATAGC 1155
                                                                                                                                                                             1046 cagcacagggtgctgtgaggggacctctgcccctcctggagctccggtggtggagggacc 1105
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-AUG-1993 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             976 CCCCCACTCTCGACCCCGCCCCCAGTCCTCCCTCTATCCGGCTCTCACTTCTCCTTTAAAC
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                                                                            GAAGCTGAATGTTTACACCGATAGCCGTTATGCTTTTGCCACTGCCCATATTCACGGAGA 4382
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tccaca 5482 	agcgtggaagcagctccgggaggcctactcaggaggagacttgcaagtt	5429	Qy
GCACGA 5522	GGTTACTCATAACCCCTCTCTCCAAGCCCATTTACAGGCACTCTACCTGGTCCAGC	5463	Дb
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ii i GCAAA 5462	AATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGATCCTGACAT	5403	Db
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II II CCATA 540		5343	DЬ
a 530	ccttgtgcttttagggtg	5249	Qy
T 534		28	Db -
ui Ui	ttqacc	5189	Qy
52	CTACATTGTGCTTAC	5223	Db
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ta 616 AC 636	Qу
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6975 7196	6916 atcgtcccccgagtgtactaccatcctgaggaagtggtccttgatgaatatgactatcgg 	ОУ
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6855 7076	6796 toagaaaatoagtatttagtacotggttataacaggtggtgggcatgcaatactgggtta 	Qу
6795 7016	6736 ggaaaagettccccatcccaccaacactttgctatagtactgtggtttatgagcaggcc	Qу
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	6556 tocacogaccotgatgccacttcttcttgttggctttgtctatcctcagggcctccttat	Qy Db
6782	6505acaggacagagactcttcagtctcatccaggagctttccaagccatcaac	Оy
50	451 actggattgattcctaccaacacgcctagaaactccccaggtgttcctgttaag	Qy Db

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US-08-258-420-13
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 3932; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 8202 bases
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nienhuis, Arthur W. APPLICANT: Vanin, Elio F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Olstein, Elliot M.
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APPLICATION NUMBER: US/08/258,420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 14
                                                                                                                                                                                             7089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                          585 aatatgggacagacagtgactaccccccttagtttgactctcgaccattggactgaagtt 644
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OPERATING SYSTEM:
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6015 gagatggagotgogtcacotocaaogatggagactggaaatggoogatotototoca	Db :
5962 ccaggcacagagaaagagaaatactgtgggggttctggggaatccttctgta	
764	Db
842 cgaggfgftfgctcctagaggcacctggtggcctgaactgcatttctgcctccga	•
784 tttatccottacotggctgattattgaccotgatacgggtgtcactgtaaatagca 784 tttatccottacotggctgattattgaccotgatacgggtgtcactgtaaatagca 784 tttatccottacctgctgctgattattgaccoctgatacgggtgtcactgtaaatagca 884 ATGACAGCCCTCACCAGGTCTTCAATGTTACTTGGAGAGTTACCAACTTAATGACAGG	•
724 aaca 944 ACCC	
5664 agagocgaaaagactgagaatocoettaagottogoctocatogoctggttocttactot	Qу
5604 atccccacctggatccatgcatcccacgttaagccggcgccacctcccgactcggggtg	Qу
5544 cggtggaagggacettatetegtaettttgaceaeaecaacggetgtgaaagtegaagga 	Qу Db
5484 cgcttccaagttggagattcagtctatgttagacgccaccgtgcaggaaacctcgagac 	Qу
5430 gcgtggaagcagctccgggaggcctactcaggaggagacttgcaagttccacat	Qу
53/0 grycrycricccagocricgicaegocraaggogocagagryggryaggoagoga 	90
310 g	
5250 ctgccctttgtgctttttagggtgaggaacacccctggacagtttgggctgacccccta	Qy Db
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                                                                             7267 gaagaatgttgcttctatgtagatcactcaggagccatcagagactccatgaacaagctt 7326
                                                                                                                                                                                                                                                                                                                                                                                               aaggagtetgttageaacetagaagagteeetgacttetttgtetgaagtggttetaeag 7206
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aaccggaggggattagatctgctgtttctaagagaaggtgggttatgtgcagccttaaaa 7266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAACCCAGCA---GTTTGAGCAGCTTCATGCCGCTATCCAGACAGACCTCAACGAAGTC 518
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                                                                                                                          Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TELEFAX: (510) 655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 6013517man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Driver, David A. TITLE OF INVENTION: CROSSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                    618 AATATGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTC 677
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                                                                                     585 aatatgggacagacagtgactaccccccttagtttgactctcgaccattggactgaagtt 644
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 05-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box CITY: Emeryville
                                                                                                                        Local Similarity
les 3964; Conserv
                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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agagaacgagtgagtgcagtccagatcatggtacttaggcaacagtacca 7556
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                                                                                                                          Conservative
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                                                                                                                                        Score 1687.4;
Pred. No. 0;
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ag 1622 AA 1697 AC 1682 Jg 1742	638 GGTCTCCAAAACGCGGGCAGAAGCCCACCAATTTGGCCAAGGTAAAAGGAATAACACA [1]
14 CG 11 G	gacccacycagttgcaaaatgagattgacatgggatttcccttgactcgccccggttg
36 CC TT	203 actaaccatcccctttctcggaggatccccaacgcctcacggggttggagtccct
GT GT	106 tgctgccgggactcggagccggagaggcgccacccggagcg
CA CC	926 tettggagagaaaacacteggccgaaaaagtcgagccetettectcgtatctace
ca CC	825 gagccctatatccttacgtggcaagatttggcagaagatcctccgccatgggttaaacca
AG AG	678 GAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAAGATGTTAGGTTACCTTCTGC 705 gcctctgaatggccaacattcgatgttggatggccatcagaggggacctttaattctgaa

DD QY DD QY

thaatocaacagggcatoctagttoctgtccaatccccttggaatactccc 2807	atcc TTGG	2748 2829	Db Qy
gtcagacagtaccccttgagtagagggctcgagaaggaatttggccgcat 2747 	cagac AAAAC	2688 2769	Qy Db
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actacccgaagaaccgttgacttgggagtgggacgggtaacccactcgttt 2393 	taccc CACGG	4 ω	ДУ
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Ltttaggaaaattaggtcaggccctagacagtcagggaacctgggcaatagg 2042 	gagagagattttagga 	1983 2052	ДУ
<pre>tttgactaagatcttggccgcagtggttgaaggggaagagcagcagggagaga 1982 </pre>	gagaagaatttgacta GAGCAGAAAGAGAAAG	1923 1998	ОУ
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agaatataactgtaatagccccc 3827	ggatgagcgtaagggagtagcc 3647				
	4746 GACCAGTTTACTTTTGAATTATTAGACTTTCTTCATCAGCTGACCTCACCTCAGCTTCTCA 4715 acacctgcagtagttggtcagaacatccccttatcatgttctgaggctaccaggagtggc 4715 acacctgcagcagttggtcagaacatccccttatcatgttctgaggctaccaggagtggc 4716 AAAATGAAGGCTCCCTAGAGAGAAGCCACAGTCCCTACTACATGCTGAACCGGGATCGA 4806 AAAATGAAGGCTCCTAGAGAGAAGCCACCAGTCCCTACTACATGCTGAACCGGGATCGA 4775 tgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaatccttccagaat 4775 tgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaatccttccagaat 4775 tgactcggtggtcaaacattgtgtgccctgccagctggttaatgctacctccagaat 4775 tgactcggtggtcaaacattgtgtgccctgccagctggttaatgctaaccGcCaGCAAGTCT 4866 ACACTCAAAAATATCACTGAGACCTGCAAAGCTTGTGCACAAGTCAACGCCAGCAAGTCT 4835 acctccaqqaaaqqactaaqgagagccaccccaggcgctcactgggaagtggac	Qy 4485 aagcagccaggctgtta-accttctgcctataatagaaacgcccaaagcccaga 4543 Db 4566 CGAAAGGCAGCCATCACACAGACACTCCAGACACCTCTACCCTCCTCATAGAAATTCATCA 4625 Qy 4544 acccagacgacagtacaccctagaagactggcaagagataaaaagatagacagttct 4603	Oy 4305 atctataacaaaggggttgcttacctcagcaggggaagaagaagaagaagaagaagaagagaa 4364	4125 ggggcggcagtggtggacggaccgcacgatctgggccagcagcatgccggaaggaa	

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aaaalaciggagaaatttttocaagatttggaataccaaaggraataggacaat 5 aaaalaciggagaaatttttocaagattttggaataccaaaggraataggacaat 5 aaaactgcattggaggaaatttttocaagattttggaataccaaaggacaat 5 aaactgcattagtgccaagtaagtcaggacagacagacag
CCTTCCCAACCAAGANAGAAACCGCCAAGGTCGTAACCAAG tttccaagatttggattagatcagattgtttgttttccaagatttgttgtttgt
ACCAAGAAACCGCCAAGGTCGTAACCAAG
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AAAA TITTAG GAAT TITTAG AAT TITTAG GAAT TITTAG AAT TITTAG AAT TITTAG GAAT TITTAG AAT TIT

7004 cccttaccctagctgtaatgctcggattagggacggccgttggcgtaggaacagggacag 7063	Qy Db
6944 aggaagtggtccttgatgaatatgactatcggtataacccgaccaaaaagagaacccgtat 7003	Qy Db
6884 accaatccaaagatttctgtgtcatggtccaaatcgtcccccgagtgtactaccatcctg 6943	Qy
6824 ataacaggtggtgggcatgcaatactgggttaaccccctgtgtttccacctcagtcttca 6883	Qy Db
6764 tttgctatagtactgtggtttatgagcaggcctcagaaaatcagtatttagtacctggtt 6823	Qу Db
6704 tcactgaagtttccgggaaggggacatgcataggaaaagctcccccatcccaccaccacc 6763 	Qу Дъ
6644 tcaatgtgaccaaagagcatagaaatcaatgtacatgggggtcccgaaataagcttaccc 6703	Qу
6584 gttggctttgtctatcctcagggcctccttattatgaggggatggctaaagaaag	Дy
524 9 723 A	Оу
470 acacgccta 663 GTGGGACTC	Qy Db
6410 cyctycygoctyacataacacagccycctaycaacagtaccactygattyattcctacca 6469	Qy Db
υ w	Qy Db
629	Qy Db
6233 agctggggaatagttttttattatatggcggggggagcagggtccactttaaccattcgcc 6292	Qу Db
6173 taaagataagtttcactgaa. 6363 TAAACAACAATCTCACCTCT	Qy Db
6303 GCTGTGAGACAACCGGTAGAGCTTACTGGAAGCCCTCCTCATCATGGGATTTCATCACAG 6362	Db QY
6084 attotoctttgtcmattccggcccgggcmagtmcmam	Qy Db
/ 6024 ctgcgtcacctccaacgatggagactggaaatggccgatctctctc	ДУ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                           TELEFAX: 212-586-1461 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7544 ggcaacagtacca 7556
                                   SEQUENCE CHARACTERISTICS:
                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              NAME: Jacobs, Seth H. REGISTRATION NUMBER: 32,140
                                                                                                                                                                                                                              FILING DATE: 20-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/110,300A
                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                   LENGTH:
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45 Rockefeller Pl.
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Best Local Similarity
Matches 3161; Conserv
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HYPOTHETICAL: NO
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  1323 atgttctctcaccagcctacttgggatgattgtcaacagctgctgcagacactcttcaca 1382
                                               6260 AATAACAACCCCTCTTTCTCCGAGGACCCAGCTAAATTGACAGCTTTGATCGAGTCCGTT
                                                                       1263 actaaccatcccctttctcggaggatccccaacgcctcacggggttggtggagtccctt 1322
                                                                                                                                       6320 GGAGGGAATGGACAGTATCAATACTGGCCATTTTCCTCCTCTGACCTCTATAACTGGAAA 6261
                                                                                                                                                                                                                             6380 GGAAGAAAAGAACCCCCCGTGGCGGATTCTACTACCTCTCAGGCGTTCCCCCTTCGCCTG 6321
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Pred. No. 0;
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2392 5131	/ 2333 gtatccatggactacccgaagaaccgttgacttgggagtgggacgggtaacccactcgtt	Db Qy
2332 5191	/ 2273 accattaggaaaactaaaagaaaaaaatcctgggtgatgggtgccacagggcaacggca	Qy Db
2272 5251	/ 2213 ggaggggcaaccagttgagttcctggttgataccggagcggagcattcagtgctgctaca	Qу
2212 5311	2153 taaagaltaggggagacggggttcggaccccctccccgagcccagggtaactttgaaggt	Db Oy
2152 5371	2102. ctgccccaagaagggaaacaaaggaccgaaggtcctagctctagaagaaga 	Дb
2101 5431	7 2042 gaccccactcgacaaggaccagtgtgcgtattgtaaagaaaaaggacactgggcaaggaa	Дy
2041 5491	/ 1983 gagagagattttaggaaaattaggtcaggccctagacagtcaggga-acctgggcaatag	DP 64
1982 5551	/ 1923 gagaagaatttgactaagatcttggccgcagtggttgaagggaagagcagcaggagagag	ОУ
1922 5601	7 1863 aaggaacagagaaaagaaaaggagagaaaggaggaaaggcgtgatagacggcaa	ОУ
1862 5661	7 1803 ttacytyatctagtyagayagycagagaagytytattacagaagygagacagaagagygag	Оy
1802 5721	1743 cagtcggctctggatatcaggaagaaacttcagagactggaagggttacaggaggctgag	Qу
1742 5781	/ 1683 acccettttgatcetacetcagaggcecagaaagcetcagtggcectggcettcattggg	Qy Db
1682 5841	/ 1623 ggaccgaacgaacctccctcggtatttcttgagaggctcatggaagccttcaggcggttc 	Db 04
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3334		3393	Db
4123	4 agaagtgctaacctggttcactgacggaagcagctatgtggtggaaggtaagaggatggc	4064	Дb
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3766	7 gaagettgateetgtageeagtggttggeeegtatgtetgaaggetategeagetgtgge	70	Db Qy
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                                                                                                                                                                                                                     Matches 3161;
                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-AUG-1993
APPLICATION NUMBER: 07,938,100
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hone, William J.
REGISTRATION NUMBER: 26,739
REFERENCE/DOCKET NUMBER: 07763/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/765-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212/258-2291
INFORMATION FOR SEQ ID NO: 9:
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APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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SOFTWARE: FastSE(
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COMPUTER: IF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                          Local Similarity
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AACATGGGCCAGGCTGTTACCACCCCCTTAAGTTTGACTTTAGACCACTGGAAGGATGTC 6921
                    aatatgggacagacagtgactaccccccttagtttgactctcgaccattggactgaagtt 644
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5900 GGACCTAATGAGTCTCCCTCAGCCTTTTTAGAGAGACTCAAGGAGGCCTATCGCAGATAC 5841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tggctaaataaa-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGGGAATGGACAGTATCAATACTGGCCATTTTCCTCCTCTGACCTCTATAACTGGAAA
                      ggaccgaacgaacctccctcggtatttcttgagaggctcatggaagccttcaggcggttc 1682
                                                                                                                                                                                                                                                                                                                                                                 accgaggagcgagagagaattctgttagaggctagaaaaaatgttcctggggccgacggg 1442
                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTTACTCATCAGCCCACTTGGGATGACTGCCAACAGCTATTAGGGACCCTGCTGACG 6141
                                                                                                                                                                                                                                                                                                                                                                                                                                                atgttctctcaccagcctacttgggatgattgtcaacagctgctgcagacactcttcaca 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAACAACCCCTCTTTCTCCGAGGACCCAGCTAAATTGACAGCTTTGATCGAGTCCGTT
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                                                                                 GGTCTCCAAAACGCGGGCAGAAGCCCCACCAATTTGGCCAAGGTAAAAGGGATAACCCAG
                                                                                                            ggtctccggggcgcctcaagacggcccactaatttggctaaggtaagagaggtgatgcag 1622
                                                                                                                                                                       GACTACAACACCCAACGAGGTAGGAACCACCTAGTCCACTATCGCCAGTTGCTCCTAGCG
                                                                                                                                                                                                        gactacaacacggctgaaggtagggagagcttgaaaatctatcgccaggctctggtggcg 1562
                                                                                                                                                                                                                                                       CGCCCAACTCAGCTGCCCAATGACATTAATGATGCTTTTCCCTTGGAACGTCCCGACTGG
                                                                                                                                                                                                                                                                             cgacccacgcagttgcaaaatgagattgacatgggatttcccttgactcgccccggttgg 1502
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                                                       4830 CCCCGTGTCCATAAAACAATACCCCCATGTCACAAGAAGCCAGACTGGGGGATCAAGCCCCA 4771
                                                                                              2687 accagtatcagtcagacagtaccccttgagtagagaggctcgagaaggaatttggccgca 2746
                                                                                                                                                                                                                                                                      4950 AGATGTGCCTCTAGGGTCCACATGGCTCTCTGATTTTCCCCAGGCCTGGGCAGAAACCGG 4891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5310 CGGGGGGCAACCCGTCACCTTCCTAGTGGATACTGGGGCCCAACACTCCGTGCTGACCCA 5251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2153 taaagattaggggagacggggttcggaccccctccccggagcccagggtaactttgaaggt 2212
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tgttcaaagattaatccaacagggcatcctagttcctgtccaatccccttggaatactcc 2806
                                                                                                                                                              GGGCATGGGCCGTTCGCCAAGCTCCTCTGATCATACCTCTGAAGGCAACCTCTAC
                                                                                                                                                                                          agggatgggtttggcaaagcaagttcccccacaggttattcaactgaaggccagtgctac 2686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGGCCACTTATGACGATGCAAAGAAGTGTTGGGTTTATCAGGGAAAGCCTGTAATGCC
                                                                                               TGCCGTCAAACAAGGGACTAGAGTTCGAGGGCACCGACCCGGCACCCACTGGGAAATTGA
                                                                                                                         cagaatacctccaggaaagagactaaggggaagccacccaggcgctcactgggaagtgga 4888
                                                                                                                                                                                            AACGCTCAAAGACATCACTGAGACTTGCCAAGCCTGTGCACAGGTCAATGCCAGCAAGTC
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PCT-US93-08041-9/c
; Sequence 9, Application PC/TUS9308041
; GENERAL INFORMATION:
                                          TITLE OF INVENTION: FUSION GLYCOPROTEINS NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                       APPLICANT: The Public Health Research Institute of the City of APPLICANT: New York, Inc.
STREET:
                          ADDRESSEE:
  45 Rockefeller Pl
                       Davis Hoxie Faithfull and Hapgood
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CITY: New York

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Matches 3161;
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TELEPHONE: 212-757-2200
TELEPAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 6800 ATTATTACACAGGTTAAGATCAAGGTCTTCTCACCTGGCCCCACATGGACATCCGGATCAG 6741
                                                                                                                                                                                                                           6860 TCTGCAGAATGGCCAACCTTCAACGTCGGATGGCCACGAGACGGCACTTTTAACCCCAGAC
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FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TYPE: nucleic acid
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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5600 GTGCAGAGAGAGAGGAGGGACCGCAGAAGACATAGAGAAATGAGTA----
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                                                                             TGGGCCTGCCTTCGAAGGTAAGTCAGACAGTAGCCGATTTATTGGGGGTTGATTG
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                                                                                                                                                                                                                                                    TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: Specific sequences FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
BARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER APPLICATION NUMBER: GB 9710154.7
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09111085 Patent No. 6100034
                                                                             Query Match
Best Local Similarity
Matches 2002; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
                                                                                                                                                                                             TYPE: DNA ORGANISM: Porcine retrovirus
                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2013
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                      5603 aatccccacctggatccatgcatcccacgttaagccggc-----gccacc
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tcgagtgggtgaggcagcgagcgtggaagcagctccgggaggcctactcaggaggagact 60
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                                                                               Conservative
                                                                                                   19.18;
79.68;
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                                                                                                   Score 1568.4;
Pred. No. 0;
                                                                                 Mismatches
                                                                                 396;
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                                                                                 Indels
                                                                                                                        Length 2462
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Search time (sec): 134.760000
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-O=/cgn2_1/USPTO_spool/US09171553/runat_22022002_122826_11171/app_query.fasta_1.3312
-O=/cgn2_1/USPTO_spool/US09171553/runat_22022002_122826_rni
-DB=Issued_Patents_NA -OFMT=fastap -SUFFIX=feb22std.rni
-GAPOD=12_000 -GAPEXY1=4_000 -MINMARYCH=0_100 -LOOPCL=0_000
-LOOPEXT=0_000 -GGAPOD=4_500 -GGAPEXT=0_050 -XGAPOD=10_000
-XGAPEXT=0_500 -PGAPOD=6_000 -FGAPOXT=7_000 -YGAPOD=10_000
-XGAPEXT=0_500 -FGAPOD=6_000 -FGAPEXT=7_000 -YGAPOD=10_000
-YGAPEXT=0_500 -DELOP=6_000 -DELEXY=7_000 -START=1
-MATRIX=blosum62 -TRANS=human40_cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=PCt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM-ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=-US09171553_@CGN1_1_158 -NCPU=6 -ICPU=3 -LONGLOG
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                                                                                           /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-793-610-2 +
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-336-13
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-848-760B-1 + 403.00 530.46
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-789-333F-58 + 402.00 531.4
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-133-944-1 - 401.50 522.82
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-182-612B-3 + 399.50 556.18
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                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MOLECULAR SITITLE OF INVENTION: AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08 FILING DATE: 14-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                           598 ATGGGACAGACAGTGACTACCCCCCTTAGTTTGACTCTCGACCATTGGAC
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698 CTTGGCAGACTTTCTGTGCCTCTGAATGGCCAACATTCGATGTTGGATGG
                                      34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/766,528
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milarity: 99.810
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14-DEC-1995
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AND METHODS OF USE
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                                                                                                                                                                      317 ysileTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgArg 333
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                                          GACTCGCCCCGGTTGGGACTACAACACGGCTGAAGGTAGGGAGAGCTTGA 1546
                                                                                                                                                                                                                                            uThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLeuL
                                                                                                                                                                                                                                                                                                         GACGGGCGACCCACGCAGTTGCAAAATGAGATTGACATGGGATTTCCCTT 1496
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seq_documentation_block:
; Sequence 3, Applicatio
; Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08766528 Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997
             FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2147 TAGCTCTAGAAGAAGATAAAGAT 2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2047 AATAGGACCCCACTCGACAAGGACCAGTGTGCGTATTGTAAAGAAAAAGG
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                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SE
TITLE OF INVENTION: AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2097 ACACTGGGCAAGGAACTGCCCCAAGAAGGGAAACAAAGGACCGAAGGTCC
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                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                     FILING DATE:
                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massa
NAME:
                                                                                                      APPLICATION NUMBER: US/08/766,528
                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                      60 State Street
                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR SEQUENCE OF AND METHODS OF USE
                                                  US 08/572,645
                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                            SWINE RETROVIRUS
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US-08-766-528-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 2640.00
Ratio: 5.116
Percent Similarity: 98.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-171-553B-4 x US-08-766-528-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-766-528-3 from: 1 to: 8132
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635 TGAAGTTAAATCCAGGGCTCATAATTTGTCAGTTCAGGTTAAGAAGGGAC 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 ATGGGACAGACGGTGACGACCCTCTTAGTTTGACTCTCGACCATTGGAC 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   885 CTGAATAAGCCAAGAAAGCCAGGTCCCCGAATTCTGGCTCTTGGAGAGAA 934
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                                                                                                                                                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuGlyGluLy 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTGGCAGACTTTCTGTGTCTCTGAATGGCCGACATTCGATGTTGGATGG 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCCTATATCC
                                                                                                                    ProLeuSerSerThrGlyCysCysGluGlyThr.SerAlaProProGlyA 167
                                                                                                                                                                                                                                                                                 GAGATTGAGGAGCCACCGGCTTGGCCGGAACCCCAATCTGTTCCCCCACC 1033
                                                                                                                                                                                                                                                                                                                                                                          AAACAAACACTCGGCTGAAAAAGTCAAGCCCTC.TCCTCATATCTACCCC
ACCCCGGAGCGGACAGACGAGATCGCGACATTACCGCTGCGCACGTACGG
                                            ThrProGluArgThrAspGluIleAlaIleLeuProLeuArgThrTyrGl 200
                                                                                           CTCCGGCGGTGGAGGGACCTGCTGCAGGGACTCGGAGCCGGAGGGGCGCC
                                                                                                                                                                                     CCCTTATCTGGCACAGGGTGCCGCGAGGGGACCCTTTGCCCCTCCTGGAG 1083
                                                                                                                                                                                                                                                                                                                           rgAspArgGlyAlaAlaAspLeuAlaGlyThrProThrCysSerProThr 150
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(617)227-5941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGP-038CP
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1184 CCCTCCCACACCGGGGGCCCAATTGCAGCCCCTCCAGTATTGGCCCCTTTT 1233
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                                                                                                                                                                                                                                                                                                                                                                                1834 ATTACAAAAGGGAGACAGAAGAAGAAAGGGAACAAAGAAAAGAGAGAGAAA 1883
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                                                                                                                                                                                                             1934 TAAGATCTTGGCTGCAGTGGTTGAAGGGAAAAGCAATACGGAAAGAGAGA 1983
                                                                                                                                                                                                                                                                                             1884 AGAGAAGGAAAGGGAAAGACGTAATAAACGGCAAGAAGAATTTGAC 1933
                                                                                                                             1984 GAGATTTTAGGAAAATTAGGTCAGGCCCTAGACAGTCAGGGAACCTGGGC
                                                                                                                                                                                                                                                                                                                      434 ArgGluGluArgGluGluArgArgAspArgArgGlnGluLysAsnLeuTh 450
                                                                                                                                                                                                                                                                                                                                                                                                         417 yrTyrArgArgGluThrGluGluGluLysGluGlnArgLysGluLysGlu 433
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                                            467 rgAspPheArgLysIleArgSerGlyProArgGlnSerGlyAsnLeuGly 483
500 yHisTrpAlaArgAsnCysProLysLysGlyAsnLysGlyProLysVall 517
                                                                   484 AsnArgThrProLeuAspLysAspGlnCysAlaTyrCysLysGluLysGl 500
                                                                                                                                                                                                                                                   450 rLysIleLeuAlaAlaValValGluGlyLysSerSerArgGluArgGluA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLeuL 317
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alignment_block:
US-09-171-553B-4 x US-08-766-528-1
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                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-766-528-1 from: 1 to: 8060
                                                                                                                                                                                                                                                                                                                                  Quality: 2634.00
Ratio: 5.105
Percent Similarity: 98.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/572,645
EILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: LOUIS Myers
NAME: LOUIS Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
CEPOITEMED CARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08766528 Patent No. 6190861
3112 ATGGGACAGACGGTGACGACCCCTCTTAGTTTGACTCTCGACCATTGGAC 3161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8060 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,528
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2134 TAGCTCTAGAAGAAGATAAAGAT 2156
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TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      517 euAlaLeuGluGluAspLysAsp 524
                                                                                                                                                                         1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
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TOPOLOGY: lir
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CITY: Boston
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INFERDATE THE PROPERTY OF THE

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seq_documentation_block:
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075.27^
FILING DATE: 08-MAV-^^^
CLASSTEYTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09075272 Patent No. 6136598 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4611 ACACTGGGCAAGGAACTGCCCCAAGAAGGAACAAAGGACCAAGGATCC 4660
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APPLICANT: BOUNDA, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4461 TAAGATCTTGGCTGCAGTGGTTGAAGGGAAAAGCAATACGGAAAGAGAGA 4510
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                                                                                                                                                                                                                                                                                STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euAlaLeuGluGluAspLysAsp 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-075-272-1
APPLICATION DATA
                                                                                                                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                     Two Embarcadero Center, 8th
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MILLER, A. DUSTY WOLGAMOT, GREG
                                                                                                                                                                                                                                                                                                                              TOWNSEND and TOWNSEND and CREW LLP
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US-09-075-272-1
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                                                                                                                                                                                                           1104 ATCCAGAGATTGACGACCTCCTCTGGATGGACTCCCCAACCTCCCCCTTAC 1153
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132 euProArgAspArgGlyAlaAlaAspLeuAlaGlyThrProThrCysSer 148
                                                                                                                                                                                                                                                                                                                                                           117 sAsnLysHisSerAlaGluLysValGluProSerSer.....SerTyrL 132
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FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                922 TGTTTTTCAGGAA...GAAGGGGGTCACCCTGATCAGATCCCCTACATTG
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TOPOLOGY: lin
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REGISTRATION NUMBER: 32,928
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                           ......ProGlyAlaProValValGluGlyProAlaAlaGlyThrArgS 179
                                                                                                    CCCCTGCCCCAGCAGCCACCTGCAGCAGCCCCACCTGTGGCAGCCCCTCA 1203
                                                                                                                                                     ProThrProLeuSerSerThrGlyCysCysGluGlyThrSerAlaPro.. 164
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Ratio: 3.907
milarity: 79.667
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                                                                                                                          ArgAspArgArgGlnGluLysAsnLeuThrLysIleLeuAlaAlaValVa
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                                                                                                                                                                                                                                                                                               AGATTTAGTGAAGGAAGCAGAGAAGGTTTATCACAAGAGAAAACAGAAG
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                                                                                                                                                                                                                                    luGluLysGluGlnArgLysGluLysGluArgGluGluArgGluGluArg
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                                                                              lGluGlyLysSerSerArgGluArgGluArgAspPheArgLysIleArgS
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alignment_block: us-09-171-553B-4 \times us-08-716-351A-1
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                                                                                                                                                                                                                       alignment_scores:
                                                                        Align seg 1/1 to: US-08-716-351A-1
                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08716351A Patent No. 6033905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 543-50-
INFORMATION FOR SEQ ID NO:
2218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/I
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 ysValLeuAlaLeuGluGluAsp 522
                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "Galv SEATO Genome"
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian,, Kevin REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/716,351A
                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAGGACACTGGGCTAAAGACTGCCCTAAGAAA...AGAAGGCAATTCA 2264
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                                                                                                                                                                                                        Quality:
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                                                                                                                                                                                     Ratio:
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(415) 543-5043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1418 CCGCCCTATCCGGCGCACTGCCACCCCCTCTGGCCCCTCAGGCGATCGG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1324 CCGAAGACCAGTTGCGGGGAGG......CCATCAGCTCCTCCCCGACCCC 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 laGlyThrArgSerArgArgGlyAlaThrPro.......GluArgThr 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 100
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                                                                                                                                                                                                                                                                                                                            GlnLeuGlnAsnGluIleAspMetGlyPheProLeuThrArgProGlyTr 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yrAsnTrpLysThrAsnHisProProPheSerGluAspProGlnArgLeu
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CAGCTCGAGAACCTCATTAATGAGGCCTTCCCCCTCAATCGACCTCACTG
                                                                                                       TTCTCCTGGAGGCCCGCAAAAATGTCCTTGGGGACAATGGGGCCCCTACA 1867
                                                                                                                                       LeLeuLeuGluAlaArgLysAsnValProGlyAlaAspGlyArgProThr
                                                                                                                                                                                                                     TTGCCAACAGCTCCTACAGATTCTTTTCACCACTGAGGAACGGGAAAGAA
                                                                                                                                                                                                                                               pCysGlnGlnLeuLeuGlnThrLeuPheThrThrGluGluArgGluArgI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAATTGGAAATCTAATCATCCCTCTTTTTCTGAAAACCCAGCAGGTCTC
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GAGAAGCCAAGGTTCTAGCCCTAGAT 2557
                                             ysGlyProLysValLeuAlaLeuGlu 520
                                                                                                                                                                                                                                                                                                                                                                                                                    aValValGluGlyLysSerSerArgGluArgGluArgAspPheArgLysI
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                                                                                                                                     sLysGluLysGlyHisTrpAlaArgAsnCysProLysLysGlyAsn...L 512
                                                                                                                                                                                       ACACCTAGGGATGGAAGACCTCCACTAGACAAAGACCAGTGCGCATACTG
                                                                                                                                                                                                                                                                                 ..GGGTCCACAGGTAGGCAGACAGGGAACCTGAGCAACCAGGCAAAGAAG
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                                                                                                                                                                                                                .....ArgThrProLeuAspLysAspGlnCysAlaTyrCy 496
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seq_documentation_block:
sequence 3, Application US/09011745
Patent No. 6165715
Patent No. 6165715
Patent No. 6165715
Patent No. 6165716
PapelICANT: Collins, Mary KL
AppLICANT: Weiss, Robin A
AppLICANT: Takeuchi, Yasushiro
AppLICANT: Takeuchi, Yasushiro
AppLICANT: Cosset, Franccis-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
PARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: BS9517263.1
EARLIER FILING DATE: 1995-08-23
PARLIER FILING DATE: 1995-08-23
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 $p {\tt AspTyrAsnThrAlaGluGlyArgGluSerLeuLysIleTyrArgGlnA}$

NUMBER OF SEQ ID NOS: 29 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3 LENGTH: 7308 TYPE: DNA ORGANISH: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Por OTHER INFORMATION: construct S-09-011-745-3 Length: 578 Length: 578 Gaps: 15 Length: 578 Ratio: 3.440 Percent Similarity: 68.166 Percent Identity: 48.962	rtion of
lignment_block: US-09-171-553B-4 x US-09-011-745-3	
09-011-745-3 fr	
1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTTpTh 17 	.7
17 rGluvalArgSerArgAlaHisAsnLeuServalGlnvalLysLysGlyP 34 ::: :::	.666
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51 ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaII 67	766
67 ellepheGlnThrGlyProGlySerHisProAspGlnGluProTyrlleL 84 ::: ::: :::	84
84 euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 10 :: :::	.866
AlaLeuGlyGluLy 1	L17 L890
isSerAlaGluLysValGluProSerSerSerTyrLeuProA 1 ::: :::	134 1918
	L43 L968
ProThrProLeuSerSerThrGl 1	156 2018
ThrSerAlaProPro 1	165 2059
	165
60 ATAGGGACCCAAGACCACCCCTTCCGACAGGGACGGAAATGGTGGAGAA 2	1 —
100 GUGAROPOTEGEGAGAGAGAGACACCOTECCCAATGGCATCTCGCT 2: 2110 GUGAROPOTEGEGAGAGAGAGACCCTTCCCCAATGGCATCTCGCTT 2: 2110 GUGAROPOTEGAGAGAGAGAGACCCTTCCCCAATGGCATCTGCTT 2: 2110 GUGAROPOTEGAGAGAGAGAGAGACCCTTCCCCAATGGCATCTGCTT 2:	2159

0		2989
466	hrt.vsTlet.eualavalValGluGlvf.vsSerSer&r	ъ.
449 2988	AGGATGAGCAGAAAGAGAAAGAAGAAGATCGTAGGAGACATAGAAGAGAGAG	441 2939
440 2938	UGlnArgLysGluLysGluArgGluGluArgGluGluArg	427 2889
.427 2888	ArgGluAlaGluLysValTyrTyrArgArgGluThrGluGluGluLysGl	411 2839
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394 2788	aSerValAlaLeuAlaPheIleGlyGlnSerAlaLeuAspIleArgLysL:::: ::::::	377 2739
377 2738	AlaPheArgArgPheThrProPheAspProThrSerGluAlaGlnLysAl	361 2689
360 2688	etGlnGlyProAsnGluProProSerValPheLeuGluArgLeuMetGlu 	344 2639
344 2638	UATGGlyAlaSerArgArgProThrAsnLeuAlaLysValArgGluValM ::::: :::	327 2589
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310 2538	leAspMetGlyPheProLeuThrArgProGlyTrpAspTyrAsnThrAla:: :::	294 2489
294 2488	9LysAsnValProGlyAlaAspGlyArgProThrGlnLeuGlnAsnGluI 	277 2439
277 2438	GlnThrLeuPheThrThrGluGluArgGluArgTleLeuLeuGluAlaAr ::: ::::: :::	261 2389
260 2388	erLeuMetPheSerHisGlnProThrTrpAspAspCysGlnGlnLeuLeu :::::::::::::	244 2339
244 2338	nHisProProPheSerGluAspProGlnArgLeuThrGlyLeuValGluS ::: ::: ::: ::: TAACCCTTCTTTTCTGAAGATCCAGGTAAACTGACAGCTCTGATCGAGT	227 2289
227 2288	PheSerSerAl	211 2239
210 2238	roMe	194 2210
194 2209	<pre>rargSerArgArgGlyAlaThrProGluArgThrAspGluIleAlaIleL ::: acgTgggagAcgggagCcccTgTggcCcgacTcCacTAcCTCGCAGGCAT</pre>	177 2160

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CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 7308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-011-745-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Portion of ; OTHER INFORMATION: construct US-09-011-745-4
                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-171-553B-4 x US-09-011-745-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-011-745-4 from: 1 to: 7308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 68.166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Takeuchi, yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3147 AAGACCCCAGACCTCCCTGACCCTAGATGAC 3180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3097 GGGCACTGGGCTAAAGATTGTCCCAAGAAACCACGAGGACCTCGGGGACC 3146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3028 .......GATAGACAGGGAGGAGAA...C 3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 GlyHisTrpAlaArgAsnCysProLysLys......GlyAsnLysGlyPr 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 uArgAspPheArgLysIleArgSerGlyProArgGlnSerGlyAsnLeuG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514 oLys.....valLeuAlaLeuGluGlu 521
                                                                                                                          1617 AGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGAC 1666
                                          1717 CCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAA 1766
                                                                                                                                                                                                                                      17 rGluValArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP 34 :::|||:::
                                                                                 51 ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl 67
67 eIlePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1355.50
Ratio: 3.440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 578
Gaps: 15
Percent Identity: 48.962
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LM 344	327 u
Le 327 CT 2588	311 GluGlyArgGluSerLeuLysIleTyrArgGlnAlaLeuValAlaGlyL :: ::
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II 294 : :G 2488	277 gLysAsnValProGlyAlaAspGlyArgProThrGlnLeuGlnAsnGlu
r 27 G 24	261 GlnThrLeuPheThrThrGluGluArgGluArgIleLeuLeuGluAlaA ::: :::: :::
u 26 G 23	244 erLeuMetPheSerHisGlnProThrTrpAspAspCysGlnGlnLeuLe
· ω +>	227 nHisProProPheSerGluAspProGlnArgLeuThrGlyLeuValGlus
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22	ProM
22	a I Le GGCA
21	AlaAlaGlyT ::: CCCTCCCCAATGGCATCTCGCC
21	CCCTTCCGACAGGGACGGAAATGGTGGAGA
165	19 GGGGCCGCTCATCGACCTACTTACAGAAGACCCCCC
5 0	156 yCysCysGluGlyThrSerAlaProPro
156 2018	144 ThrProThrCysSerProThrProLeuSerSerThrGl
	134 rgAsp
. 'o w	SSerAlaGluLysValGluProSerSerSerTyrLeuPro ::: ::: ::
∞ ⊢	aLeuGlyGluL
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	1767 GGTCTTTTCACCTGGCCCGCATGGACACCCAGGACCAGGTCCCCTACATCG

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seq_documentation_block:
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           SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 7616
                                                                      CURRENT APPLICATION NUMBER: US/09/011,745
COURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09011745
Patent No. 6165715
                                                                                                                                                                                                                                                                           APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
                                                                                                                                                                                                                                TITLE OF INVENTION: Expression systems FILE REFERENCE: 09/011,745
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3147 AAGACCCCAGACCTCCCTCCTGACCCTAGATGAC 3180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3097 GGGCACTGGGCTAAAGATTGTCCCCAAGAAACCACGAGGACCTCGGGGACC 3146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3047 GAAGGAGGTCCCAACTCGATCGCGACCAGTGTGCCTACTGCAAAGAAAAG 3096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3028 .....GATAGACAGGGAGGAGAA...C 3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 oLys........ValLeuAlaLeuGluGlu 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2989 AGCAAGCTATTGGCCACTGTCGTTAGTGGACAGAAACAG...... 3027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 GlyHisTrpAlaArgAsnCysProLysLys......GlyAsnLysGlyPr 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2939 AGGATGAGCAGAAAGAAGAAGAAGAGATCGTAGGAGACATAGAGAGATG 2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483 lyAsnArgThrProLeuAspLysAspGlnCysAlaTyrCysLysGluLys 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 uArgAspPheArgLysIleArgSerGlyProArgGlnSerGlyAsnLeuG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2889 GGAACGTATCAGGAGAGAACAGAGGAAAAAGAAGAACGCCGTAGGACAG 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 ThrLysIleLeuAlaAlaValValGluGlyLysSerSerArgGluArgGl 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 .....ArgAspArgArgGlnGluLysAsnLeu 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2789 AGTTÁGAGAGGTTÁGAAGATTTÁAAAAACAAGACGCTTGGAGATTTGGTT 2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 uGlnArgLysGluLysGluArgGluGluArgGluGluArg...... 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 ArgGluAlaGluLysValTyrTyrArgArgGluThrGluGluGluLysG1 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2739 TAATGTGTCTATGTCTTTCATTTGGCAGTCTGCCCCAGACATTGGGAGAA 2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2689 GCCTATCGCAGGTACACTCCTTATGACCCTGAGGACCCAGGGCAAGAAAC 2738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 ysLeuGlnArgLeuGluGlyLeuGlnGluAlaGluLeuArgAspLeuVal 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 aSerValAlaLeuAlaPheIleGlyGlnSerAlaLeuAspIleArgLysL 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AlaPheArgArgPheThrProPheAspProThrSerGluAlaGlnLysAl 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 etGlnGlyProAsnGluProProSerValPheLeuGluArgLeuMetGlu 360
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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Portion of OTHER INFORMATION: construct US-09-011-745-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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Ratio: 3.440 Gaps: 15
Percent Similarity: 68.166 Percent Identity: 48.962
1321 ACGTGGGAGACGGGAGCCCCCTGTGGCCGACTCCACTACCTCGCAGGCAT 1370
                                                                               1271 GCGACCCCTGCGGGAGAGGCCACCGGACCCCTCCCCAATGGCATCTCGCCT 1320
                                                                                                                                                                 1221 ATAGGGACCCAAGACCACCCCCTTCCGACAGGGACGGAAATGGTGGAGAA 1270
                                                                                                                                                                                                                                                   177 rArgSerArgArgGlyAlaThrProGluArgThrAspGluIleAlaIleL 194
                                                                                                                     166 GlyAlaProValValGluGlyPro.....AlaAlaGlyTh 177
                                                                                                                                                                                                         1080 TTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTC 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1052 .....CTTCCTCCATCCGCCCCGTCTCTCCCCC 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 yCysCysGluGly.......ThrSerAlaProPro.... 165
                                                                                                                                                                                                                                                                                                                                                                           144 ThrProThrCysSerProThrPro.....LeuSerSerThrG1 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 rgAsp.....ArgGlyAlaAlaAspLeuAlaGly 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 sasnLysHisSerAlaGluLysValGluProSerSerTyrLeuProA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuGlyGluLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              928 GGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCG 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878 CCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               828 GITGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGG 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778 AGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGAC 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 eIlePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 ATGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 rGluValArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHiSTrpTh 17
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1500 CTGTTCTCATCACCCATCAGCCCACCTGGGACGACTGTCAGCAGCTGTTG 1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1550 GGGACTCTGCTGACCGGAGAAGAAAAACAACGGGTGCTCTTAGAGGCTAG 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1900 TAATGTGTCTATGTCTTTCATTTGGCAGTCTGCCCCAGACATTGGGAGAA 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1850 GCCTATCGCAGGTACACTCCTTATGACCCTGAGGACCCAGGGCAAGAAAC 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1700 GCAGGTAGGAACCACCTAGTCCACTATCGCCAGTTGCTCCTAGCGGGTCT 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1650 TCGATGCCGCTTTTCCCCTCGAGCGCCCAGACTGGGATTACACCACCCAG 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 euProLeuArgThrTyrGlyProProMetProGlyGlyGlnLeuGlnPro 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1950 AGTTAGAGAGGTTAGAAGATTTAAAAAACAAGACGCTTGGAGATTTGGTT 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 gLysAsnValProGlyAlaAspGlyArgProThrGlnLeuGlnAsnGluI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 GlnThrLeuPheThrThrGluGluArgGluArgIleLeuLeuGluAlaAr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 erLeumetPheSerHisGlnProThrTrpAspAspCysGlnGlnLeuLeu 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 nHisProProPheSerGluAspProGlnArgLeuThrGlyLeuValGluS 244
                                                 361 AlaPheArgArgPheThrProPheAspProThrSerGluAlaGlnLysAl 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 etGlnGlyProAsnGluProProSerValPheLeuGluArgLeuMetGlu 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 GluGlyArgGluSerLeuLysIleTyrArgGlnAlaLeuValAlaGlyLe 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2100 AGGATGAGCAGAAAGAAAGAAAGAAAGATCGTAGGAGACATAGAGAGATG 2149
                                                                                                                                                                                                                                                                                                                                                                                          2050 GGAACGTATCAGGAGAGAAACAGAGGAAAAAGAAGAACGCCGTAGGACAG 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                        427 uGlnArgLysGluLysGluArgGluGluArgGluGluArg...... 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 ArgGluAlaGluLysValTyrTyrArgArgGluThrGluGluGluLysGl 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 ysLeuGlnArgLeuGluGlyLeuGlnGluAlaGluLeuArgAspLeuVal 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 aSerValAlaLeuAlaPheIleGlyGlnSerAlaLeuAspIleArgLysL 394
                                                                                                        466 uArgAspPheArgLysIleArgSerGlyProArgGlnSerGlyAsnLeuG 483
                                                                                                                                                                                                                       450 ThrLysIleLeuAlaAlaValValGluGlyLysSerSerArgGluArgGl 466
483 lyAsnArgThrProLeuAspLysAspGlnCysAlaTyrCysLysGluLys 499
                                                                                                                                                                                                                                                                                                                                .....ArgAspArgArgGlnGluLysAsnLeu 449
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                              alignment_block: us-09-171-553B-4 \times us-08-850-961-1
                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08850961
Patent No. 6013517
                                                                                                                                Align seg 1/1 to: US-08-850-961-1 from: 1 to: 8332
                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (510) 655-354 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2308 AAGACCCCAGACCTCCCTCCTGACCCTAGATGAC 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2208 GAAGGAGGTCCCAACTCGATCGCGACCAGTGTGCTACTGCAAAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 oLys......valLeuAlaLeuGluGlu 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Driver, David A.
TITLE OF INVENTION: CROSSLESS RETROVIRAL VECTORS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, NO. 6013517man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 93004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 8332 base pairs
                                                          621 ATGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
17 rGluvalArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP 34 :::|||:::
                                                                                            1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                     Quality: 1355.50
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Emeryville
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                                                                                                                                                                                                                                                     Ratio:
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De Polo, Nicholas J.
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                                                                                                                                                                                                                                                                                                                                                                    linear
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68.166
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655-3542
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                                                                                                                                                                                                                                     Percent Identity: 48.962
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277 9LysAsnValProGlyAlaAspGlyArgProThrGlnLeuGlnAsnGluI 294
4 6
9 4
11 LeuGlnTyrTrpProPheSerSer
94 euProLeuArgThrTyrGlyProProMet :: ::: 64 TCCCCTCCGCGCAGGAGGA
77 rArgSerArgArgGlyAlaThrProGluA ::: 14 ACGTGGGAGACGGGAGCCCCCTGTGGCCG
.66 GlyAlaProValValG :::::: ::: GCGACCCCTGCGGGAGF
14 ATAGGGACCCAAGACCACCCCTTCCGACAGGGACGGAAATGGTGGAGA
G1y
144 ThrProThrCysSerProThrProLeuSerSerThrGl 156 ::::: 1023 ACTCCTTCTCTAGGCGCCAAACCTAAACCTCAAGTTCTTTCT
73 TTGAACCTCCTCG
17 sAsnLysHisSerAlaGluLysValGluProSerSerSerTyrLeu::: :::
01 LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuc :::::: :: 21 GTACACCCTAAGCCTCCGCCTCCT
84 euThrTrp
7 eIlePhe ::: 1 GGTCTT
51 ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaII 67
34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50
671 AGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGAC 720

<pre>seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-258-420-13 seq_documentation_block: Sequence 13, Application US/08258420 Patent No. 5710037 General Invormation: APPLICANT: Nienhuis, Arthur W. APPLICANT: Vanin, Elio F. TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR and Retroviral NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein</pre>	GGCTAAAGATTGTCCCAAGAAACCACGAGGACCTCGGGGACC 2ValLeuAlaLeuGluGlu 521! ::: :::	82 83 01	93 AGGATGAGCAGAAAGAAAGAAAGAAAGAAAGAGATCGTAGGAGAGAGA		394 ysLeuGlnArgLeuGluGlyLeuGlnGluAlaGluLeuArgAspLeuVal 410	361 AlaPheArgArgPheThrProPheAspProThrSerGluAlaGlnLysAl 377 ::: ::: ::: :::	327 uArgGlyAlaSerArgArgProThrAsnLeuAlaLysValArgGluValM 344 :::::	294 leaspMetGlyPheProLeuThrArgProGlyTrpAspTyrAsnThrAla 310 :: :::
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alignment_block: us-08-258-420-13/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1354.50
Ratio: 3.438
Percent Similarity: 68.166
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 8202 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: genomic DNA
FEATURE:
NATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: US-08-258-420-13 from: 1 to: 8202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOrdPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,420
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ENTIRE CAREE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY_AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 2710
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201994-1700
                                                                                                                                                                                                                                                                                                                                                    7146 ATGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAA 7097
6896 TGACCTGGGAAGCCTTGGCTTTTGACCCCCCCCCCCTGGGTCAAGCCCCTTT 6847
                    101 LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuGlyGluLy 117
    :::::: | | | | ::: | | | |
                                                                                        1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-994-1744
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CITY: Roseland
STATE: New Jers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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ZIP: 07068
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Gaps: 15
Percent Identity: 48.789
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377 597	AlaPheArgArgPheThrProPheAspProThrSerGluAlaGlnLysAl	361 6024
360	etGinGlyProAsnGluProProSerValPheLeuGluArgLeuMetGlu 	344 6074
344 607	UATGGlyAlaSerArgArgProThrAsnLeuAlaLysValArgGluValM :::::: :::	327 6124
32: 61:	GluGlyArgGluSerLeuLysIleTyrArgGlnAlaLeuValAlaGlyLe ::: ::: GAGGTAGGAACCACCTAGTCCACTATCGCCAGTTGCTCCTAGCGGGGTCT	311 6174
31(617	leAspMetGlyPheProLeuThrArgProGlyTrpAspTyrAsnThrAla:: ::	. 294 6224
29 <i>i</i> 623	gLysAsnValProGlyAlaAspGlyArgProThrGlnLeuGlnAsnGluI 	277 6274
27; 62;	GlnThrLeuPheThrThrGluGluArgGluArgTleLeuLeuGluAlaAr ::: ::::: :::	261 6324
260 632	erLeuMetPheSerHisGlnProThrTrpAspAspCysGlnGlnLeuLeu :::::::::	244 6374
244 637	nHisProProPheSerGluAspProGlnArgLeuThrGlyLeuValGluS ::: :: ::: HISPROPHESER	227 6424
227	LeuGlnTyrTrpProPheSerSerAlaAspLeuTyrAsnTrpLysThrAs :::	211 6474
210 647	oProMetProGlyGlyGlnLeuGln ::: AACGGACAG	194 6503
194 650	spGluIleAlaIleL : CTACCTCGCAGGCAT	177 6553
177 655	AlaAlaGlyTh ::: ATGGCATCTCGCCT	166 6603
999	ACCCAAGACCACCCCCTTCCGACAGGGACGGAAATGGTGGAGAA	6653
165		165
165 665	*GG1uG1yThrSeralaProPro	156 6694
156 669	ThrProLeuSerSerThrGl :::::: AAACCTAAACCTCAAGTTCTTTCTGACAGTGG	144 6744
143 674	gGlyAlaAlaAspLeuAlaGly :::::: TCCTCCCTTTATCCAGCCCTC	134 6794
134 679	isSerAlaGluLysValGluProSerSerTyrLeuProA ::: ::: CTTCCTCCATCCGCCCCGTCTCTCCCCC	117 6822

5874

5824

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-110-300A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5774 AGGATGAGCAGAAAGAGAAAGAAGATCGTAGGAGACATAGAGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5924 AGTTAGAGAGGTTAGAAGATTTAAAAAAACAAGACGCTTGGAGATTTGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 uArgAspPheArgLysIleArgSerGlyProArgGlnSerGlyAsnLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyHisTrpAlaArgAsnCysProLysLys.....GlyAsnLysGlyPr 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAAGCTATTGGCCACTGTCGTTAGTGGACAGAAACAG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uGlnArgLysGluLysGluArgGluGluArgGluGluArg.....
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45 Rockefeller Pl.
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US-09-171-553B-4 x US-08-110-300A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 64.856
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                                                                                                                                                                                                                                                                                                            994
                                                                                                                                                                                                                                                                                                                                                                                                         971 CTGAA.....CCCCCACTCTCGACCCCG 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 rgAspArgGlyAlaAlaAspLeuAlaGlyThrProThrCysSerProThr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuGlyGluLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 GGATGTCGAACGGACAGCCCACAACCTGTCGGTAGAGGTTAGAAAAAAGGC 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719 GCTGGGTTACATTCTGCTCTGCAGAATGGCCAACCTTCAACGTCGGATGG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8323 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 rGluValArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                  TTCCTGATAGCGGAGGACCACTCATTGATCTACTCACGGAGGACCCTCCG 1107
                                                                                                                                                                                                    TCCGGCTCTCACTTCTCCT...TTAAACACCAAACCTAGGCCTCAAGTCC 1057
CCTTACCGGGACCCAGGGCCACCCTCTCCTGACGGGAACGGCGATAGCGG 1157
                                             ProLeuArgThrTyrGlyProProMetProGlyGly.....
                                                                                                                                                  hrProGluArgThrAspGluIleAlaIleLeu......
                                                                                                                                                                                                                                                    aProValValGluGlyProAlaAlaGlyThrArgSerArgArgGlyAlaT 184
                                                                                                                                                                                                                                                                                                                                                         ProLeuSerSerThrGlyCysCysGluGlyThrSerAlaProProGlyAl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sAsnLysHisSerAlaGluLysValGluProSerSerSerTyrLeuProA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACCTGGGAAGCTATAGCAGTAGACCCCCCCCCCTGGGTCAGACCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eIlePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84
                                                                                                                                                                                                                                                                                                            CCCCAGTCCTCCCTC....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCAC...CCTAAACCTCCC......CTCTCTCTT..... 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCTTCTCACCTGGCCCACATGGACATCCGGATCAGGTCCCCTACATCG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACGAGACGGCACTTTTAACCCCAGACATTATTACACAGGTTAAGATCAA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1350.50
3.535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....CCCCCTTCAGCCCCTCTCTCCCAC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 47.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
to:
                                                  206
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seq_documentation_block:

514 oLys.....ValLeuAlaLeuGluGlu 521

AAGACCCCAGACCTCCCTCCTGACCCTAGATGAC 5533

Sequence 8, Application US/08110300A Patent No. 5643756

Patent No.

GENERAL INFORMATION:

APPLICANT: Pinter, Abraham
APPLICANT: Rayman, Samuel
APPLICANT: Kayman, Samuel
FUSION GLYCOPROTEINS

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 45 ROC CITY: New York STATE: New Yorl

New York

COUNTRY:

USA

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,
FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H.
REGISTRATION NUMBER: 32,140

COMPUTER READABLE FORM:

10111

MEDIUM TYPE:

Floppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0,

Version

US/08/110,300A

SOFTWARE:

REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-757-2200

11698A50

TELEFAX:

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)7	. 440 .G 200	33 luargGluGluArgGluGluArg	19
57	G 433	16 lTyrTyrArgArgGluThrGluGluGluLysGluGlnArgLySGluLys ::::	19
7	19	00 GlyLeuGlnGluAlaGluLeuArgAspLeuValArgGluAlaGluLysVa :::::: 	18:
7	1 399	.83 heIleGlyGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGlu 	38 180
7	383 180	66 rProbheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlaP :::: 58 TCCTTATGACCCTGAGGACCCAGGGCAAGAACCAATGTGGCCATGTCAT	36 175
7	366 175	50 ProproSerValPheLeuGluArgLeuMetGluAlaPheArgArgPheTh :::	35 170
7	349 170	33 rgProThrAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGlu 	33 165
7	333 1657	16 uLys1leTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgA 	31 160
-	316 1607	00 LeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLe 	30 155
-		33 laAspGlyArgProThrGlnLeuGlnAsnGluIleAspMetGlyPhePro 	28: 150
	283 1507	6 rGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGlyA 	260 1450
	266 1457	0 GlnProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLeuPheThrTh 	250 1408
	249 1407	3 luAspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerHis	233 1358
	ω ω	eSerSerAlaAspLeuTyrAsnTrpLysThrAsnHisProPr ::: TTCCTCCTCTGACCTCTATAACTGGAAAAATAACAACCCCTC	216 1308
	216 1307	8 LeuGlnProLeuGlnTyrTrpProPh	208 1258
	207 1257	GCCTGCGGGGAAGAAAGAACCCCCCGTGGCGGATTCTACTACCTCTCAG	207 1208
	1207	AGAAGTGGCCCCTACAGAAGGAGCCCCTGACCCTTCCCCAATGGTATCCC	Un o
	206		206

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-886-642-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; sequence 8, Application US/08886642; Patent No. 5952474; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: Genomic DNA US-08-886-642-8
alignment_block:
                                                                                                         alignment_scores:
                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/110,300
FILING DATE: 20-AUG-1993
APPLICATION NUMBER: 07/938,100
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hone, William J.
REGISTRATION NUMBER: 26,739
REFERENCE/DOCKET NUMBER: 07763/0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/765-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2166 TTGCCCCAAGAAGCCAAGAGGACCCCGGGGACCACGACCCCAGGCCTCCC 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2081 ATAGACAGGGAGGAGCGA......AGGAGGCCCCAACTC 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2058 TGTCGTTAGCCGGCAG......AGACAGG 2080
                                                                                                                                                                                                                                                                                               TELEPHONE: 212/765-5070
TELEFAX: 212/258-2291
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2216 TCCTGACCTTAGACGAT 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 leArgSerGlyProArgGlnSerGlyAsnLeuGlyAsnArgThrProLeu 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 aValValGluGlyLysSerSerArgGluArgGluArgAspPheArgLysI 472 :||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Composer
COMPUTER: IBM Composer
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 alleuAlaLeuGluGlu 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 45 ...
STREET: New York
CITY: New York
CTATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                             LENGTH:
                                                                     Quality: 1350.50
Ratio: 3.535
                                                                                                                                                                                                                                                         : 8323 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 Rockefeller Plaza, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fish & Richardson P.C
                                                 64.856
                                                                                                                                                                                                                                  single
                                                 Percent Identity: 47.538
                                                                                                                                                                                                                                                                                                                                                                                                                  07763/010002
                                                                                              Length:
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233 luAspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerHis 249
Ö F
58 GCGTTCCCCCTTC
108 GCCTGCGGGGAAGAAAGAACCCCCCGTGGCGGA
GAAGTGGCCCCTACAGAAGGAGCCCCTGACCCTTCCCCAATGGTATCCC 12
206
195 ProLeuArgThrTyrGlyProProMetProGlyGly
Ŭī bo
.67 aProValValGluGlyProAlaAlaGlyThrArgSerArgArgG
ysGluGlyThrSe
.34 rgAspArgGlyAlaAlaAs
.1/ sAsnLysHisSerAlaGluLysValGluPr
.01 LeuAsnLysProArgLysProGlyProArgLysProGlyProArgLysProGlyProArgLysProGlyProArgLysProGlyProArgLysProGlyProArgLysProArgLy
84 euThrTrpGlnAspLeuAlaG1 :: ::: :59 TGACCTGGGAAGCTATAGCAGT
9 GC
Prog
4 roTrpGlnThrPheCysAlaSerGluTrpProTh
17 rGluValArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP 34 ::: :::
1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
Align seg 1/1 to: US-08-886-642-8 from: 1 to: 8323
US-09-171-553B-4 x US-08-886-642-8

516 alLeuAlaLeuGluGlu 521 :: ::: ::::::
505 nCysProLysLysGlyAsnLysGlyProLysV 516 :
489 ASPLYSASPGINCYSALATYTCYSLYSGIULYSGIYHISTTPALAATGAS 505
472 leArgSerGlyProArgGlnSerGlyAsnLeuGlyAsnArgThrProLeu 488 ::: ::::::::::::::::::::::::::
455 aValValGluGlyLysSerSerArgGluArgGluArgAspPheArgLysI 472 : ::: :::
441ArgAspArgArgGlnGluLysAsnLeuThrLysIleLeuAlaAl 455
433 luArgGluGluArgGluGluArg
416 lTyrTyrArgArgGluThrGluGluGluLysGluGlnArgLysGluLysG 433 :::: :: ::: ::::: 1908 CTTTAATAAACGAGAAACCCCCGGAAGAAAGAGAAGGTAATTAGGAGAG 1957
400 GlyLeuGlnGluAlaGluLeuArgAspLeuValArgGluAlaGluLysVa 416
383 heIleGlyGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGlu 399 ::: :::
366 rProPheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlap 383 ::: ::: ::: ::::: 1758 TCCTTATGACCCTGAGGACCCAGGGCAAGAAAACCAATGTGGCCATGTCAT 1807
350 ProProSerValPheLeuGluArgLeuMetGluAlaPheArgArgPheTh 366 :::
333 rgProThrAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGlu 349
316 uLys1leTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgA 333
hrargPr AACGTCC
283 laAspGlyArgProThrGlnLeuGlnAsnGluIleAspMetGlyPhePro 299
266 rGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGlyA 283
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2216 TCCTGACCTTAGACGAT 2232

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alignment_scores:
Quality: 1350.50
Ratio: 3.535
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US-09-171-553B-4 x PCT-US93-08041-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE: PCT-US93-08041-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-08041-8
                                                                                                                                                                                                                                        Align seg 1/1 to: PCT-US93-08041-8 from: 1 to: 8323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1169
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8323 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application PC/TUS9308041 GENERAL INFORMATION:
                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
719 GCTGGGTTACATTCTGCTCTGCAGAATGGCCAACCTTCAACGTCGGATGG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H.
REGISTRATION NUMBER: 32,14(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The Public Health Research Institute of the City of APPLICANT: New York, Inc.
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davis Hoxie-Faithfull and Hapgood
STREET: 45 Rockefeller Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,100
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
                                     34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 45 Rocke
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US93/08041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,140
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Gaps: 14
Percent Identity: 47.538
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249 1407	luAspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerHis ::: ::: ::::::::::	233 .358
233 1357	eSerSerAlaAspLeuTyrAsnTrpLysThrAsnHisProProPheSerG :: TTCCTCCTCTGACCTCTATAACTGGAAAAATAACAACCCCTCTTTCTCCC	216 308
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207 1257	GCCTGCGGGGAAGAAAGAACCCCCCGTGGCGGATTCTACTACCTCTCAG	207 1208
1207	GCCCCTACAGAAGGAGCCCCTGACCCTTCCC	1158
206		206
206 1157	ProLeuArgThrTyrGlyProProMetProGlyGly	195 1108
194 1107	hrProGluArgThrAspGluIleAlaIleLeu	18 4 1058
184 1057	aProValValGluGlyProAlaAlaGlyThrArgSerArgArgGlyAlaT ::::: ::::: rccggcTcTcAcTTCTCCTTTAAACACCAAACCTAGGCCTCAAGTCC	167 1011
1010	CCCCAGTCCTCCTA	994
993	YASPAT YSTYATAATAASPUGUATAGTYYIII FIGIII CYSSEEFIGY	
η 🤄 ω	SASDLYSHISSErAlaGluLySValGluProSerSerSerTyrLeuPr	
117 945	LeuAsnLysProArgLysProGlyProA	101 919
100 918	euThrTrpGlnAspLeuAlaGluAspProProProPrpValLysProTrp :: ::: :	84 869
84 868	ellePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL ::: ::: GGTCTTCTCACCTGGCCCACATGGACATCGGATCAGGTCCCCTACATCG	67 819
67 818	ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl ::: ::: CCACGAGACGCACTTTTAACCCAGACATTATTACACAGGTTAAGATCAA	51 769

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; Sequence 9, Application US/08110300A
; Patent No. 5643756
                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-110-300A-9
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2081 ATAGACAGGGAGGAGGCGA......AGGAGGCCCCAACTC 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1808 TCATCTGGCAGTCCGCCCCGGATATCGGGCGAAAGTTAGAGCGGTTAGAA 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1658 GCCCCACCAATTTGGCCAAGGTAAAAGGGATAACCCAGGGACCTAATGAG 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2216 TCCTGACCTTAGACGAT 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2166 TTGCCCCAAGAAGCCAAGAGGACCCCGGGGACCACGACCCCAGGCCTCCC 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2116 GACCACGACCAGTGTGCCTACTGCAAAGAAAAGGGACATTGGGCTAGAGA 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2058 TGTCGTTAGCGGGCAG......AGACAGG 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2008 AAGGAGAGGGACCGCAGAAGACATAGAGAAATGAGTAAGTTGCTGGCTAC 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1908 CTTTAATAAACGAGAAACCCCGGAAGAAAGAGAGGAACGTATTAGGAGAG 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1708 TCTCCCTCAGCCTTTTTAGAGAGACTCAAGGAGGCCTATCGCAGATACAC 1757
                                                                                                                            APPLICANT: Pinter, Abraham APPLICANT: Kayman, Samuel TITLE OF INVENTION: FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 LeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLe 316
                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 alLeuAlaLeuGluGlu 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 nCysProLysLys.....GlyAsnLysGlyProLys......V 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 leArgSerGlyProArgGlnSerGlyAsnLeuGlyAsnArgThrProLeu 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 aValValGluGlyLysSerSerArgGluArgGluArgAspPheArgLysI 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 GlyLeuGlnGluAlaGluLeuArgAspLeuValArgGluAlaGluLysVa 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 heIleGlyGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGlu 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 rgProThrAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGlu 349
                                                                                           NUMBER OF SEQUENCES:
                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspLysAspGlnCysAlaTyrCysLysGluLysGlyHisTrpAlaArgAs 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTTATGACCCTGAGGACCCAGGGCAAGAAACCAATGTGGCCATGTCAT 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rProPheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlaP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....ArgAspArgArgGlnGluLysAsnLeuThrLysIleLeuAlaAl 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lTyrTyrArgArgGluThrGluGluGluLysGluGlnArgLysGluLysG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGAACGTCCCGACTGGGACTACAACACCCAACGAGGTAGGAACCACCT 1607
E: Davis Hoxie Faithfull and Hapgood 45 Rockefeller Pl.
                                                                                                                            FUSION GLYCOPROTEINS
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alignment_block:
US-09-171-553B-4 x US-08-110-300A-9/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-110-300A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 1350.50
Ratio: 3.535
Percent Similarity: 64.856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-08-110-300A-9 from: 1 to: 10367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                           6777 GGTCTTCTCACCTGGCCCACATGGACATCCGGATCAGGTCCCCTACATCG 6728
                                                                                                                                                                                                                                                                                                                                                                                               6827 CCACGAGACGCACTTTTAACCCCAGACATTATTACACAGGTTAAGATCAA 6778
                                                                                                                                                                                              6727 TGACCTGGGAAGCTATAGCAGTAGACCCCCCCCCCCGGGTCAGACCCCTTC 6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6877 GCTGGGTTACATTCTGCTCTGCAGAATGGCCAACCTTCAACGTCGGATGG 6828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6927 GGATGTCGAACGGACAGCCCACAACCTGTCGGTAGAGGTTAGAAAAAGGC 6878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6977 ATGGGCCAGGCTGTTACCACCCCCTTAAGTTTGACTTTAGACCACTGGAA 6928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 10367 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                           117 sAsnLysHisSerAlaGluLysValGluProSerSerSerTyrLeuProA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,300A
FILING DATE: 20-AUG-1993
                                                                                                                                           101 LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuGlyGluLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 100
                                                                                                                                                                                                                                                                                                                                              67 eIlePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 rGluValArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-757-220
TELEFAX: 212-586-1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
                                                                                       GTGCAC...CCTAAACCTCCC......CTCTCTCTT..... 6651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1011
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 47.538
..CCCCCTTCAGCCCCCTCTCTCCCAC 6626
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383 5789	rProPheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlaP ::: 	366 5838
366 5839	ProProSerValPheLeuGluArgLeuMetGluAlaPheArgArgPheTh	350 5888
349 5889	rgProThrAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGlu 	333 5938
333 5939	uLysIleTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgA	316 5988
316 5989	LeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLe	300 6038
299 6039	laAspGlyArgProThrGlnLeuGlnAsnGluIleAspMetGlyPhePro 	283 6088
283 6089	rGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGlyA :::::: :::	266 6138
266 6139	GlnProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLeuPheThrTh 	250 6188
2 4 9 6189	luAspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerHis 	233 6238
233 6239	yrAsnTrpLysThrAsnHisProProPheSerG ATAACTGGAAAAATAACAACCCTCTTTCTCCG	216 6288
216 6289	GlnTyrTrpProPh GGAATGGACAGTATCAATACTGGCCATT	208 6338
207 6339	Gln AAGAACCCCCCGTGGCGGATTCTACTACCTCTCAG	207 6388
6389	GAAGTGGCCCCTACAGAAGGAGCCCCTGACCCTTCCCCAATGGTATCCC	6438
206		206
206 6439	ProLeuArgThrTyrGlyProProMetProGlyGly	195 6488
194 6489	AGGACCCTCCG	184 6538
18 4 6539	ProAlaAlaGlyThrArgSerArgArgGlyAlaT	167 6585
167 6586	CysCysGluGlyThrSerAlaProProGlyAl	151 6602
150 6603	yAlaAlaAspLeuAlaGlyThrProThrCysSerProThr	134 6625

	NAME: Hone, William J. REGISTRATION NUMBER: 26,739		
	TORNEY/AGENT INFORMATIC	Αĵ	
	ATION NUMBER: 07/		
	ATION NUMBER: DATE: 20-AUG-		
	FILING DATE: 01-JUL-199	; ; PR	
	APPLICATION NU	·. ·.	
	SOFTWARE: FastSEQ for Wind	2	
	ER: IBM		
	OMPUTER READABLE FORM: MEDIUM TYPE: Diskette	C	
	10111		
	TATE: NY		
	15 Rockefeller Plaza, S v York		
	DDRESSEE: Fish & Richardson P.C.	; ;	
	BER OF SEQUENCES: 25	z -	
	LICANT: Kayman, Sam		
	PLIC	GE	
	umentation_block: nce 9, Application US/08886642 t No. 5952474	P S	
	e: /cgn2_6/ptoda	eq.	
	6 alleuAlaLeuGluGlu 521 	51 538	
516 538	5 nCysProLysLysGlyAsnLysGlyProLysV : : ::: ::: 0 TTGCCCCAAGAAGCCAAGAAGCCCCGGGGACCACGACCCCAGGCCTCCC	50 543	
		,	
505 543	9 AspLysAspGlnCysAlaTyrCysLysGluLysGlyHisTrpAlaArgAs 	48 548	
548	CAGGGAGGAGACCAAGGAGGCCCCAAC	551	
488	rgSerGlyProArgGlnSerGlyAsnLeuGlyAsn	47	
5516	GCGG	553	
472	ValValGluGlyLysSerSerArgGluArgGluArgAspPheArgLy	45	
5539		558	
455	rgAspArgArgGlnGluLysAsnLeuThrLysIleI	44	
5589	AGAGGAAAAGGAAGAACG	563	
440	- u - G	43	
5639	AAAGAGAGGAACG	568	
433	TyrTyrArgArgGluThrGluGluGluLysGluGlnArgLys	41	
5689	0 GlyLeuGlnGluAlaGluLeuArgAspLeuVaLArgGluAlaGluLySVa ::::: 8 GATTTGAAGAGTAAGACCTTAGGAGAGATTAGTGAGGGAAGCTGAAAAGAT	400 5738	
, ,	I COLC I GOT COUNTY IN COU		
399 573	3 heIleGlyGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGlu 	383 5788	

100 - SEC NOIL NOIL NOIL NOIL NOIL NOIL NOIL NOIL	REFERENCE/DOCKET NUMBER: 07763/010002 TELECOMMUNICATION INFORMATION: TELEPHONE: 212/765-5070 TELEPHONE: 212/765-5070 TELEPHONE: 212/765-5070 TELEPHONE: 212/765-2291 NFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 10367 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: Genomic DNA 3-886-642-9
lignmen Percent	nt_scores: Quality: 1350.50 Ratio: 3.35 Similarity: 64.856 Percent Identity: 47.538
lignmen US-09-1	t_block: 171-553B-4 x US-08-886-642-9/rev
Align s	eg 1/1 to reverse of: US-08-886-6
1 6977	MetGlyGlnThrValThrThrProLeuSerLeuThrLeuAspHisTrpTh 17
17 6927	rGlu :: GGA1
34 6877	roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50
51 6827	ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaII 67 ::: ::: CCACGAGACGCACTTTTAACCCAGACACTTATTACACAGGTTAAGATCAA 6778
67 6777	ellePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84 ::: ::: :::
84 6727	euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 100 :: :: :::
101 6677	LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeuGlyGluLy 117 :::::: ::: GTGCACCCTAAACCTCCCCTCTCTCTT
117 6650	SASnLysHisSerAlaGluLysValGluProSerSerSerTyrLeuProA 134
13 4 6625	rgAspArgGlyAlaAlaAspLeuAlaGlyThrProThrCysSerProThr 150
151 6602	ProLeuSerSerThrGlyCysCysGluGlyThrSerAlaProProGlyAl 167
167 6585	aProValValGluGlyProAlaAlaGlyThrArgSerArgArgGlyAlaT 184 :::::
184 6538	hrProGluArgThrAspGluIleAlaIleLeu
195	ProMetProGlvGlv 206

155	441ArgAspArgArgGlnGluLysAsnLeuThrLysIleLeuAlaAl 4	
140 5589	433 luArgGluGluArgGluGluArg	
433 5639	416 lTyrTyrArgArgGluThrGluGluGluLysGluGlnArgLysGluLysG 4 :::: :::	
416 5689	400 GlyLeuGlnGluAlaGluLeuArgAspLeuValArgGluAlaGluLysVa .	
399 5739	383 heIleGlyGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGlu :	
383 5789	366 rProPheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlap	
366 5839	350 ProProSerValPheLeuGluArgLeuMetGluAlaPheArgArgPheTh :::	
349 5889	333 rgProThrAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGlu 	
333 5939	316 uLysIleTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgA 	
316 5989	300 LeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLe	
299 6039	283 laAspGlyArgProThrGlnLeuGlnAsnGluIleAspMetGlyPhePro 	
283 6089	266 rGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGlyA 	
266 6139	250 GlnProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLeuPheThrTh	
249 6189	233 luaspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerHis 	
233 6239	216 eSerSerAlaAspLeuTyrAsnTrpLysThrAsnHisProProPheSerG :::	
216 6289	208 LeuGlnProLeuGlnTyrTrpProPh	
207 6339	AAAAGAACCCC	
6389	FIGGCCCCTACAGAAGO	
206	206	
6439	6488 CCTTACCGGGACCCAGGGCCACCCTCTCCTGACGGGAACGGCGATAGCGG	

	5380 TCCTGACCTTAGACGAT 5364	5380
	516 alLeuAlaLeuGluGlu 521	516
5381	5430 TTGCCCCAAGAAGCCAAGAGGACCCCGGGGACCACGACCCCAGGCCTCCC 5381	5430
516		505
5431	5480 GACCACGACCAGTGTGCCTACTGCAAAGAAAAGGGACATTGGGCTAGAGA 5431	5480
505	489 AspLysAspGlnCysAlaTyrCysLysGluLysGlyHisTrpAlaArgAs	489
5481	5515 ATAGACAGGGAGAGCGAAGGAGGCCCCAACTC	5515
488	SerGlyAsnLeuGly	472
5516	5538 TGTCGTTAGCGGGCAGAGACAGG	5538
472	455 aValValGluGlyLysSerSerArgGluArgGluArgAspPheArgLysI 472	455
5539	5588 AAGGAGAGGGACCGCAGAAGACATAGAGAAATGAGTAAGTTGCTGGCTAC 5539	5588

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Sequence
Seq
cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-691-563C-89
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Query length: 1194
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-O-/cgn2_1/USPTO_spoo1/US09171553/runat_22022002_122826_11171/app_query.fasta_1.3312
-OB-ISsued_Patents_NA -QFMT-fastap -SUFFIX=feb22std.rni
-OAPOP=12.000 -GAPEXIT=4.000 -MINARCH=0.100 -LOOPCL=0.000
-LOOPEXIT=0.000 -GAPEXIT=4.000 -GAPEXIT=0.505 -XGAPOP=10.000
-XGAPEXIT=0.000 -GAPOP=6.000 -FGAPEXIT=7.000 -YGAPOP=10.000
-YGAPEXIT=0.500 -FGAPOP=6.000 -FGAPEXIT=7.000 -YGAPOP=10.000
-YGAPEXIT=0.500 -DELOP=6.000 -DELEXIT=7.000 -STARIT=1
-MATRIX=D10sum62 -TRAMS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMIT-pfs -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09171553_@CGN1_11_158 -NCPU=6 -ICPU=3 -LONGIOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*
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Align seg 1/1 to: US-08-766-528-3 from: 1 to: 8132
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                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 98.992
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2260 TGCTACTACAGCCATTAGGAAAACTAAAAAGATAAAAAATCCTGGGTGATG 2309
                                                                                          2210 GGAGGGGCAACCAGTTGAGTTCCTGGTTGATACCGGAGCGAAACATTCAG 2259
                                                                                                                                                                                      2160 GGGAGACGGGGTTCGGACCCCCTCCCCGAGCCCCAGGGTAACTTTGAAGGT 2209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                           34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                       17 lGluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MOLECULAR SEQUENCE TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                 1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 14-DEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/766,528
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Ratio: 5.173
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51 LysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLeuSerAs 36	34 InvalThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGlyAlaThr 35 	17 eAspGluAlaLeuHisArgAspLeuAlaAsnPheArgIleGlnHisProG 33) LeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProThrIlePh 31 	34 roLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThrGlyGln 30 	7 uAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrSerGlnP 28	1 TyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrThrValLe 267 	4 rgGluValAsnLysArgValGlnAspIleHisProThrValProAsnPro 250 	7 uProValArgLysProGlyThrAsnAspTyrArgProValGlnAspLeuA 234 	1 GlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrProLeuLe 217 	4 euSerArgGluAlaArgGluGlyIleTrpProHisValGlnArgLeuIle 200 ::: ::: 0 TGAGTAAAGAAGCTCAAGAAGGAATTCGGCCGCATGTCCAAAGATTAATC 275	7 lileGinLeuLysalaSerAlaThrProValSerValArgGinTyrProL 184 	TrpAlaGluThrAlaGlyMetGlyLeuAlaLySGlnValProProGlnVa 167 	allysproAspGlnAspIleGlnSerTrpLeuGluGlnPheProGlnAla 150 	' rValleuThrleuGlnLeuAspAspGluTyrArgLeuTyrSerProGlnV 134 	SerPheGluGlnGlyArgProGluValSerValAsnAsnLysProIleTh 117 TCTTTTGAACAAGGGAAACCAGAAGTGTCTGCAAATAACAAACCTATCAC 250	roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100 :::	PLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84	GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67 GTGCCACAGGGCAACAACAGTATCCATGGACTACCCGAAGAACAGTTGA 2359
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601 LeuProGluGluThrAspGluProValThrHIsAspCysHisGlnLeuL	AVALLYSASPALAASPLYSLEUTH-LEUGLYGLNASDIL	rLysProi	401 AlaargLysLysThrvalValGlnIleProAlaProThrThrAlaLysG	
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                                                                                                          alGluAlaTyrProThrLysLysGluThrSerThrValValAlaLysLys 950
                                                                                                                                                                                                                                                                                    HisProGlyAlaHisTrpGluValAspPheThrGluValLysProAlaLy 917
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IleLeuGluGluIlePheProArgPheGlyIleProLysValIleGlySe 967
                                                                                      TAGAGGCTTATCCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAAAAAA
                                                                                                                                                                         ATACGGAAACAAATACCTATTGGTTTTTGTAGACACCTTTTCAGGATGGG
                                                                                                                                                                                           sTyrGlyAsnLysTyrLeuLeuValPheValAspThrPheSerGlyTrpV 934
                                                                                                                                                                                                                                                             CACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAA
                                                                                                                                                                                                                                                                                                                                                 TTAATGCTAATCCTTCCAGAATGCCTCCAGGGAAGACTAAGGGGAAGC 4859
                                                                                                                                                                                                                                                                                                                                                                                                                                  uProGlyValAlaAspSerValValLysHisCysValProCysGlnLeuV 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACACCTGCAGCAGTTGGTCAGAACATCCCCTTATCATGTTCTGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGGTTAGAATATGTCCAACAGATACATCGTCTAACCCACCTAGGAACT 4709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAGGGACCTGCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGATGGCTGACCGGGTTGCCAAGCAGGCAGCCCCAGGGTGTTAACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnAlaValAsnLeuL 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAAAGGGGGTTGCTTACCTCAGCAGGGAGGGAAATAAAGAACAAAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCACGCAAGCTTTGCGGCTGGCCGAAGGGAAATCCATAAACATTTATACG
                                                                                                                                                                                                                                                             4909
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seq_documentation_block:
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                                                                                                                                                                                                       Sequence 1, Application US/08766528 Patent No. 6190861
                                                                                                         GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SE
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967
                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
   STATE: Mar
                                 STREET:
CITY: B
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGlnValGluArgMetAsnArgThrIleLysGluThrLeuThrLysLe 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrTrpIleHisAlaSerHisValLysProAlaProProProAspSerGl 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leLeuGlyIleAspTrpLysLeuHisCysAlaTyrArgProGlnSerSer 1000
                                                                                                                                                                                                                                                                                                                                                                                                   yTrpArgAlaGluLysThrGluAsnProLeuLysLeuArgLeuHisArgL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yrLeuValLeuLeuThrThrProThrAlaValLysValGluGlyIlePro 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTTAGACGCCACCGTGCAGGAAACCTCGAGACTCGGTGGAAGGGCCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luTrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSer...
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                                                                                                                                                                                                                                                                                                                       TGGTTCCTTACTCTGTCAATAAC 5732
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                 Massachusetts
                                                       60 State Street
                                                                                                                                                   MOLECULAR SEQUENCE
                                                                                                                                   OF USE
                                                                                                                                                   OF SWINE RETROVIRUS
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-766-528-1 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LOUIS MYDERS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MCP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                             4985
                                                                                                                                                                                                                                                   4935
                                                                                                                                                                                                                                                                                                                                        4885
                                                                                                                                                                                                                                                                                                                                                                                                                              4837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4687 GGGAGACGGGGTTCGGACCCCCTCCCCGAGCCCAGGGTAACTTTGAAGGT 4736
                                                                                                                                                                               101 SerPheGluGlnGlyArgProGluValSerValAsnAsnLysProIleTh 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 8060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
134 alLysProAspGlnAspIleGlnSerTrpLeuGluGlnPheProGlnAla 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                          67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
PILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 1GluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                               rValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProGlnV 134
                                                                                                                                                                                                                                               CAGCACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAAATT 498
                                                                                                                                                                                                                                                                      roValProLeuGeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                                                                   CTTGGGAGTGGGACGGGTAACCCACTCGTTTCTGGTCATACCTGAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGC.ACAGGGCAACAACAGTATCCATGGACTACCCGAAG.ACAGTTGA 4884
                                                                                                                                                        TCTTTTGAACAAGGGAAACCAGAAGTGTCTGCAAATAACAAACCTATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 5637.50
Ratio: 5.061
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151	rpAlaGluThrAlaGlyMetGlyLeuAlaLysGlnValProProGlnVa	167
5135	TGGGCAGAAACCGCAGGGATGGGTTTGGCAAAGCAAGTTCCCCCACAAGT	5184
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184 5235	euSerArgGluAlaArgGluGlyIleTrpProHisValGlnArgLeuIle ::: ::: TGAGTAAAGAAGCTCAAGAAGGAATTCGGCCGCATGTCCAAAGATTAATC	200 5284
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267 5485	uAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrSerGlnP	284 5534
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384 5835	alThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeuThrGlu 4 	100 5884
· 401 5885	AlaArgLysLysThrValValGlnIleProAlaProThrThrAlaLysGl 4	117 5934
417 5935	nValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpIleProG 4 :::	134 5984
434 5985	lyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGluLysGly 4 	150 5034

750	4 GluIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArgLeuAlaII	73
6934		688
733	7 ysGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysAsnLysGlu	71.
688		683
717	0 rAspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAlaIleTyrL	701
6834		678
700 6784	4 LeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsnIleTyrTh	684 6735
683 6734	7 laSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluLeuMetAla CCAGCAGCCTGCCGGGAGGAACTTCAGCACAAAAGGCTGAGCTCATGGCC	667 6685
667) yLysArgMetAlaGlyAlaAlaValValAspGlyThrArgThrIleTrpA	650
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6634		6585
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6584		6535
617	ULeuProGluGluThrAspGluProValThrHisAspCysHisGlnLeuL	600
6534		6485
600 6484	ThrGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrLe	584 6435
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6384		6335
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6334		6285
53 4 6284	UASPPTOVALALASETGLYTTPPTOVALCYSLEULYSALAILEALAALAV	517 6235
517 6234	GlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLysLysLe !	501 6185
500 6184	heThrLeuTyrValAspGluArgLysGlyValAlaArgGlyValLeuThr :	484 6135
484 6134	sAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrLysProP (467 6085
467 6084	GlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaIleLysLy 4	451 6035

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	7784	7734	7684	7634	1584	534	484	434	384	334	284	234	184	134	085	035	985	935
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1066	1050	1033	1016	1000	983	966	950	933	916	900	883	866	850	833	817	800	783	767
	7833	7783	7733	7683	7633	7583	7533	7483	7433	7383	7333	7283	7233	7183	7133	7084	7034	5984

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alignment_block:
US-09-171-553B-5 x US-08-766-528-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-2
   Align seg 1/1
                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08766528 Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7834 AATTACTCTACGGGGGACCCCCCCCTTGGTAGAAATTGCTTCTGTACAT 7883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..GlyGlyAspLeuGlnValProHisArgPheGlnValGlyAspSerVal 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAGGAGACTTGCAGATCCCACATCGTTTCCAAGTGGGAGATTCAGTC 8033
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                                                                                                                                   Quality: 4489.50
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                                                                                                                    Ratio:
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   ţo:
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 US-08-766-528-2
                                                                                                5.033
74.895
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                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                     MGP-038CP
 from: 1
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to: 7333
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2873
3023 CACTTTTTACCTTCGAATGGAGAGCCAGGTACGGGAAGAACCGGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2673 TATTCAACTGAAGGCCAGTGCTACACCAGTATCAGTCAGACAGTACCCCT 2722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2423 CAGTACCCCTTCTAGGTAGAGACTTACTGACCAAGATGGGAGCTCAAATT 2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2373 CTTGGGAGTGGGACGGGTAACCCACTCGTTTCTGGTCATCCCTGAGTGCC 2422
                    284 roLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThrGlyGln 300
                                                                                                                                                                                                                                                                                234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 lIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnTyrProL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SerPheGluGlnGlyArgProGluValSerValAsnAsnLysProIleTh 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2273 TGCTGCTACAACCATTAGGAAAACTAAAAGAAAAAAATCCTGGGTGATG 2322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
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                                                                                                                                                                             TyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrThrValLe 267
                                                                                                                                                                                                                                       GAGAGGTCAATAAAAGGGTGCAGGACATACACCCAACGGTCCCGAACCCCT
                                                                                                                                                                                                                                                       rgGluValAsnLysArgValGlnAspIleHisProThrValProAsnPro 250
                                                                                                                                                                                                                                                                                                                ACCGGTTAGGAAGCCTGGGACCAATGATTATCGACCAGTACAGGACTTGA
                                                                                                                                                                                                                                                                                                                                   uProValArgLysProGlyThrAsnAspTyrArgProValGlnAspLeuA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euSerArgGluAlaArgGluGlyIleTrpProHisValGlnArgLeuIle 200
                                                                             GGACTTAAAAGATGCCTTCTTCTGCCTGAGATTACACCCCACTAGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAGTAGAGAGGCTCGAGAAGGAATTTGGCCGCATGTTCAAAGATTAATC 2772
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901 HisProGlyAlaHisTrpGluValAspPhcThrGluValLysProAlaLy	3527
4015 TTAATGCTAATCCTTCCAGAATACCTCCAGGAAAGAGACTAAGGGGAAGC	584 hrGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrLeu 60
4 alAsnAla	27
867	PArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuLeuLeuT
15 AAACACCT	3527
851 LyshisLeuGlnGlnLeuValArgThrSerProTyrHisValLeuAr	
3865 AAGGGTTAGAATATGTCCAACAGATACATCGTCTAACCCACCTAGGAACT	ThrLeuGlyGlnAsnIle
	3527 3527
817 oGluGlyThrCysTyThrSerTyrGlyLySGlulleLeurroHistySG 	${\tt uAspProValAlaSerGlyTrpProValCysLeuLysAlaIleAlau}$
	3527
801 LeuGluAspTrpGlnGluIleLysLysIleAspGlnPheSerGluThrPr	
3715 TGCCTATAATAGAAACGCCCAAAGCCCCAGAACCCAGACGACAGTACACC	484 heThrLeuTyrValAspGluArgLysGlyValAlaArgGlyValLeuThr 500
4 euProIleI	3527 3527
767 IULIIWECKIGAS PRI Y VALINIALY SOLINIA VALINIALY VILLIMENTA GAS PRI Y VALINIALY SOLINIA VALINIALY VILLIMENTA GAS PRI Y VALINIALY SOLINIA VALINIALY VILLIMENTA GAS PRI Y VALINIALY VILLIMENTA GAS PRI VIL	467 sAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrLysProP 484
ATACACTGT	451 GlyPheSerTrpAlaProGluH18GlnLySAlaPheAspAlalleLySLy 46/ 3523 GGTTG3527
751 IleHisCysProGlyHisGlnLysAlaLysAspLeuIleSerArgGl	GGTTTGCGACCTTAGCAGCCCCACTCTACCCGCTAACCAAAGAAAAAAGGG
39 LULIELEUSEL EULEGG FORDEUTE SEGUE FOLLYSKE YEGENELEUSEL EULEGG FORDEUTE SEGUE FOLLYSKE YEGENELEUSEL EULEGG FORDEUTE SEGUE FOLLYSKE YEGENELEUSEL FOLLYSKE YEGENELEUSEN YEGENEL	434 lyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGluLysGly
28	41/ NVALAFIGGINERGEMENTALAGEMENTE SARGHENTE LEFTOG 434
euThrSerAlaGlyArg	GCACGGAAGAAAACTGTAGTCCAGATACCGGCCCCAACCACAGCCAAACA
	AlaArgLysLysThrValValGlnIleProAlaProThrThrAlaLysGl
${\tt AspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAlaIleTy}$	
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84 enThrGlnalaLeuArgLeuAlaGluGlvLvsSerIleAsnIle	3273 CCTAGGCTACAGAGCCTCTGCTAAGAAGGCCCAGATTTGCAGGAGAGGG 3322
27	367 pLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleCysArgArgGluV 384
acercerTend	3223 AAACAGGACTGCTTAGAAGGTACGAAGGCACTACTGCTGGAATTGTCTGA 3272
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3527	LeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProThrIlePh

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1167 pArgAlaGluLysThrGluAsnProLeuLysLeuArgLeuHisArgLeuV 1184
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                                                 1184 alProTyrSerAsnAsnAsnSer 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017 uThrThrGluThrGlyIleAsnAspTrpMetAlaLeuLeuProPheValL 1034
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TTCCTTACTCTGTCAATAACTCC 4858
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seq_documentation_block:
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/046,140
FILING DATE: 09-MAY-1997
ATTORNEY.AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 14538A-0037
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-075-272-1 from: 1 to: 8655
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-171-553B-5 x US-09-075-272-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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                                                          2391 TACTCACCAGCCCCTGGGCAAACTAGGCTCTAAAAGGACCATAGTGGTT
                                                                                                                                                                                                                                                                                                     2291 GGAAGTCGGGGCTCAGACCCCCTCCCTGAGCCTAGGGTAACTTTGTCTGT 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BONHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO EMBARCAGERO Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8655 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysp:::::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Embard
CITY: San Francisc
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 4339.50
Ratio: 4.201
milarity: 85.940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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384	67 pLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleCysArgArgGluV	36
3437	:	338
367	51 LysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLeuSerAs	33 35
3387	:::	33 35
350	34 InValThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGlyAlaThr	33
3337	::::	328
334	17 eAspGluAlaLeuHisArgAspLeuAlaAsnPheArgIleGlnHisProG	31
3287		323
317	01 LeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProThrIlePh	30
3237		318
300	84 roLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThrGlyGln	28
3187		313
284	67 uAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrSerGlnP 	26 308
267	51 TyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrThrValLe	25
3087		303
250	34 rgGluValasnLysArgValGlnAspIleHisProThrValProAsnPro	23
3037		298
234	17 uProValArgLysProGlyThrAsnAspTyrArgProValGlnAspLeuA	21 ¹
2987		293
217	01 GlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrProLeuLe	20
2937	:::	288
200 2887	84 euSerArgGluAlaArgGluGlyIleTrpProHisValGlnArgLeuIle :: ::: ::: 38 TGAGCAAGGAAGCTAAGGAGGCATCCGACCTCATATTCGGAGGCTGCTA	18 283
184	57 lileGinLeuLysAlaSerAlaThrProValSerValArgGinTyrProL	16
2837	::::: :: ::	278
167	51 TrpAlaGluThrAlaGlyMetGlyLeuAlaLySGlnValProProGlnVa	15
2787		273
150	34 alLysProAspGlnAspIleGlnSerTrpLeuGluGlnPheProGlnAla	13.
2737		269
134 2690	TVALLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProGlnV	11 264
117 2640	1) SerPheGluGlnGlyArgProGluValSerValAsnAsnLysProIleTh ::: ::: :::: :::::: ::::::	10: 259:
100 2590	34 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle :::	254
2540	91 GATAGATAAAAACATGGTGACCCACTCTTTCCTGGTGATACCTGAGTGTC	249:

42 6	2 6	41	6 41	40	40	39	39	38 5	38	5 37	4 37	36	4 36	35	35 4	34	3 4 3
67 a 85 A	51 I	34 1 88 G	17 u 38 G	01 L 88 C	84 h 38 A	67 p 88 T	51 T	34 a - 88 T	17 u 38 G	01 G 88 C	84 h 38 T	67 s : 88 G	51 G 38 C	34 1 88 G	17 n 38 G	01 A 88 G	84 a 38 T
SerSerLeuProGluGlyThrSerAlaGlnLysAlaGluLeuMetAlaL :::	ArgMet CGAAGG	LyGluValLeuThrTrpPheThrAspGlySerSerTyrValValGluGly	IIleGluGluThrGlyValAxgLysAspLeuThrAspIleProLeuThrG ::: 	.euProGluGluThrAspGluProValThrHisAspCysHisGlnLeuLe 	17G1uArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrLeu 	ArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuLeuLeuT 	hrVallleAlaProHisAlaLeuGluAsnIleValArgGlnProProAs ::: \OTGTCGTGGCCCCTCATGCCCTGGAGAGTATTGTGCGGCAGCCACCTGA	alAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGlnAsnIle ::: :::	AspProValAlaSerGlyTrpProValCysLeuLysAlaIleAlaAlaV 	lnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLysLysLe ::: :::	neThrLeuTyrValAspGluArgLySGlyValAlaArgGlyValLeuThr ::: rGTCCTATATGTGGACGAGAGAGCGGGCATAGCCAGAGGGGTGCTGACA	AlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrLysProP :::: ::::	31yPheSerTrpA1aProGluHisGlnLysA1aPheAspA1aTleLysLy ::: CTTTGAATGGAAAGAAGAACCAAAGAGCTTTTGAGGCTATCAAATC	.yPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGluLysGly 	\ValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpIleProG 	\laArgLysLysThrValValGlnIleProAlaProThrThrAlaLysGl ::::: CCCGGAAAAGACTGTCATGATGATTCCACCGCCAACCACACCACGGCA	.lThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeuThrGlu
684 4334	667 4284	650 4234	634 4187	617 4137	600 4087	584 4037	567 3987	550 3937	534 3887	517 3837	500 3787	484 3737	467 3687	450 3637	434 3587	417 3537	400 3487

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734 luIleLeuSerLeuCluAlaLeuHisLeuProLysArgLeuAlaIle 750
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                                                                                                                                                                                        LysIleLeuGluGluIlePheProArgPheGlyIleProLysValIleG1 966
                                                                                                                                                                                                                                                                                                                                                                                                   aLySTyrGlyAsnLySTyrLeuLeuValPheValAspThrPheSerGlyT:
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ys \verb|TleLeuGly| IleAspTrpLysLeuHisCysAlaTyrArgProGlnSer|
                                                                                  ySerAspAsnGlyProAlaPheValAlaGlnValSerGlnGlyLeuAlaL 983
                                                                                                                                                           AAGATTTTTGAAGAAATCCTGCCAAGATATGGAGTACCTAAGGTAATCGG
                                                                                                                                                                                                                                                                   GGGTTGAAGCGTTCCCCACTAAAACTGAGACTGCCCAGATTGTGGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-716-351A-1
                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08716351A Patent No. 6033905
                                                                                                                          TITLE OF INVENTION: Gibbon A
TITLE OF INVENTION: Retrovir
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGGA 5848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTTAAGCTTCGCTTGCGTCGCAGGAGCCCCCTC......CATCAC 5842
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alignment_block:
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LENGTH: 8535 base pair
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              2814 CTGCTCCTCTGTTGGGCAGGGACCTCCTAACCAAACTAAAGGCCCCAGATC 2863
                                          2964 TA...CCCTCCTATCGACCCATCCTGGCTCCAGCTTTTCCCCCACTGTA 3010
                                                                                                                                          2914 GTGCCTGGTCCTAAACCTGGAAGAAGAATACCGACTACATGAAAAGCCAG 2963
                                                                                                                                                                                                                                      2864 CAGTTTTCCGCTGAGGGCCCACAGGTAACATGGGGAGAACGCCCTACTAT 2913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                    117 rValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProGlnV 134
                                                                                                                                                                                                                                                                            101 SerPheGluGlnGlyArgProGluValSerValAsnAsnLysProIleTh 117
                                                                                          134 alLysProAspGlnAspIleGlnSerTrpLeuGluGlnPheProGlnAla 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 1GluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
151 TrpAlaGluThrAlaGlyMetGlyLeuAlaLySGlnValProProGlnVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                                                                                                                                                              84 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1..8535
OTHER INFORMATION: /standard_name= "GalV SEATO Genome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian,, Kevin REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlyArgArgClySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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O
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3011 TGGGCAGAAAGAGCCGGCATGGGACTAGCCAATCAAGTCCCACCAGTGGT 3060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3311 TACAATCTTCTGAGTTCCCCTTCCGCCTAGCTATACTTGGTACTCAGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3511 CGACGAGGCCCTCCACCGAGATTTGGCTCCCTTTAGGGCCCCTCAACCCCC 3560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3461 CTGACCTGGACGCGCTACCACAAGGGTTCAAGAACTCTCCCACTCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3561 AGGTGGTGTTACTCCAATATGTGGACGACCTCTTGGTGGCCGCCCCCACA 3610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrProLeuLe 217
                                                                                                                                                                                                                                                                                           3761 GCCCGAAAGGCTACTGTTATGAAAATCCCTGTTCCTACGACCCCCAGACA 3810
                                                                                                                                                                                                                                                                                                                                                                                                3711 TCACCTATCTGGGGTACCTACTCAAGGAAGGAAAAAGATGGCTAACCCCA 3760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3661 GTTGGGGTACCGGGTATCGGCTAAGAAGGCCCCAGCTCTGCCAGAGAGAAG 3710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3611 TATGAAGACTGCAAAAAAGGAACACAGAAGCTCTTACAGGAGTTAAGTAA 3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 TyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrThrValLe 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 uproValArgLysproGlyThrAsnAspTyrArgProValGlnAspLeuA 234
                                                                           3861 GGTTTGCTTCCCTGGCTGCACCCTTGTACCCCCTAACAAAAGAGAGCATC 3910
                                                                                                                                                                                      3811 GGTCCGTGAATTTCTAGGCACTGCCGGATTCTGCAGGCTCTGGATCCCTG 3860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProThrIlePh 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 roLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThrGlyGln 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 lnValThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGlyAlaThr 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 pLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleCysArgArgGluV 384
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                                                                                                                              434 lyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGluLysGly 450
                                                                                                                                                                                                               417 nValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpIleProG 434
                                                                                                                                                                                                                                                                                                                                           401 AlaArgLysThrValValGlnIleProAlaProThrThrAlaLysG1 417
                                                                                                                                                                                                                                                                                                                                                                                                                                             384 alThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeuThrGlu 400
451 GlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaIleLysLy 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTGTTCGCGTTCGAGTGGAAAGACCCCAGAAAAAGGTAACACAGGTCAG
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	. CCTTTTATTTGGACTGAGGAACATCAGCAGGCTTTTGACCACATAAAAAA 3	960
467 3961	SAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrLysProP 4	84 010
484 4011	GlyValLeuThr 5 GAGTGCTCACT 4	o o
501 4061	LysLe 5	
517 4111	G - V	4 0
534 4161	AsnIle 5	50 210
551 4211	ThrvalileAlaProHisAlaLeuGluAsnIleValArgGlnProProAs 56	57
567 4261	PARGTIPMETTHIASNALAARGMETTHIHISTYTGINSETLEULEULEUT 58	110
584 4311	hrGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrLeu 60::	60
601 4361	LeuProGluGluThrAspGluProValThrHisAspCysHisGlnLeuLe 61	7
617 4411	ulleGluGluThrGlyValArgLysAspLeuThrAspIleProLeuThrG 63	4
634 4461	lyGluValLeuThrTrpPheThrAspGlySerSerTyrValValGluGly 65	07
51	LysArgMetAlaGlyAlaAlaValValAspGlyThrArgThrIleTrpAl 66	7 57
667 4558	aSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluLeuMetAlaL 68 	4 07
4608	eufhrGlnàlaLeuArgLeuAlaGluGlyLysSerIleAsnIleTyrThr 70 	0
701 4658	AspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAlaIleTyrLy 717 	7
717 : 4708 (sGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysAsnLysGluG 734 	7
734 ; 4758 £	luIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArgLeuAlaIle 750	7
751 I 1 4808 A	IleHisCysProGlyHisGlnLysAlaLysAspLeuIleSerArgGlyAs 767 	1

heAlaHi 106 ::: AAACTTT 568	OProLeuAlaGluIleAla ::: CCCCATACTTGAGTCTGGA	
hrProTyr 1049 CTCCTTAT 5632	1033 alLeuPheArgValArgAsnThrProGlyGlnPheGlyLeuT ::: :::	
uProPheV 1033 :::: TCCCTTAG 5582	1016 sLeuThrThrGluThrGlyIleAsnAspTrpMetAlaLeuLe ::: 	
LeuThrLy 1016 TTGACCAA 5532	1000 SerGlyGlnValGluArgMetAsnArgThrIleLysGluThr 	
roGlnSer 999 CCCAGAGC 5482	983 ysIleLeuGlyIleAspTrpLysLeuHisCysAlaTyrArgP ::	
yLeuAlaL 983 ACTGGCCA 5432	966 ySeraspasnGlyProAlaPheValAlaGlnValSerGlnGl 	
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ValAlaLys 949 ::: TCTGTAAA 5332	933 rpValGluAlaTyrProThrLysLysGluThrSerThrValV 	
heSerGlyT 933 TCTCCGGAT 5282	916 aLysTyrGlyAsnLysTyrLeuLeuValPheValAspThrPl ::::	
lLysProAl 916 : :: 'AAAGCCTGG 523;	900 SerHisProGlyAlaHisTrpGluValAspPheThrGluVa :::::: ::::	
LeuArgGly 899 CAACGAGGA 518	883 euValAsnAlaAsnProSerArgIleProProGlyLysArg ::::: 5133 TGACTAATGCGGTCACCACCTACAGAGAGACCGGAAAAAGG	
roCysGlnL 883 : CTTGTGCCA 513	866 9LeuProGlyValAlaAspSerValValLysHisCysValP : ::::::: ::: :::::: 5083 CCTCCAATCTGCAGTTCGCGAAGTCACCAGTCAGTGTCAGG	
.sValLeuAr 866	850 ThrLysHisLeuGlnGlnLeuValArgThrSerProTyrHi ::: ::: 5033 CCAGAAAAGCTTCTCCAACTAGTGAACCGTACCAGCCTCCT	
HisLeuGly 849 CACTTAGGA 503	GluTyrValGlnGlnIleHisArgLeuThr ::::::::::::: ::: GAATTCATTAAGCGGTTACATCAGTTAACT	
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neSerGluTh 816	LysIleAspG	
JArgGlnTyr 799 :::::: CAAGAAAAG 495	84 euProIleIleGluThrProLysA	
/alAsnLeuL 784 :::::::: \CCAGAGTGC 490	'67 nGlnMe ::: 58 CCGGAG	

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1066 sSerAlaAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaL 1083
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                                                                                            TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6033 GGCGG 6037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nienhuis, Arthur W.
APPLICANT: Vanin, Elio F.
TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR and Retroviral Vector NUMBER OF SEQUENCES: 14
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 277
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0: FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                      TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
STRANDEDNESS: single
                       LENGTH: 8202 bases
TYPE: nucleic acid
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: New Jersey
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-258-420-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 3.982
Percent Similarity: 82.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-08-258-420-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-171-553B-5 x US-08-258-420-13/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5429 TGCTGACCCAAAATCCTGGACCCCTAAGTGATAAGTCTGCCTGGGTCCAA 5380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5529 GGAGGTCAGGGTCAGGAGCCCCCCCCTGAACCCAGGATAACCCTCAAAGT 5480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: genomic DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5329 TCTAGCTACCGGTAAGGTCACCCACTCTTTCCTCCATGTACCAGACTGTC 5280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5379 GGGGCTACTGGAGGAAAGCGGTATCGCTGGACCACGGATCGCAAAGTACA 5330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5479 CGGGGGCAACCCGTCACCTTCCTGGTAGATACTGGGGCCCAACACTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5229 CACTTTGAGGGATCAGGAGCTCAGGTTATGGGACCAATGGGGCAGCCCCT 5180
                                                                                                  4929 CTGTTGGACCAGGGCCTACTGGTACCCTGCCAGTCCCCCTGGAACACGCC
                                                                                                                                                                                                  4979 ACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCCACATACAGAGA 4930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5179 GCAAGTGTTGACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCT 5130
                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 GlnAlaTrpAlaGluThrAlaGlyMetGlyLeuAlaLysGlnValProPr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 lnValLysProAspGlnAspIleGlnSer...TrpLeuGluGlnPhePro 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                                                                             199 LeuIleGlnGlyIleLeuValProValGlnSerProTrpAsnThrPr 215
                                        215 oLeuLeuProValArgLysProGlyThrAsnAspTyrArgProValGlnA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 alleuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 1GluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
TCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAAT 4980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProG 133
                                                                                                                                                                                                                                                  yrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArg 198
                                                                                                                                                                                                                                                                                                                                                     oGlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnT 182
                                                                                                                                                                                                                                                                                                                                                                                                           CAGGCCTGGGCGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCC 5030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viral genome
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32 1	515 s 179 A	199 L)29 C		Ğ Ğ	449 I 179 (9 2		29	79	365 429	7 4	332 1529	315 1579	299 4629	282 4679	265 4729	249 4779	232 4829
.aAlaValAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGln 54	ILYSLeuAspProValAlaSerGlyTrpProValCysLeuLysAlaIleA	.euThrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLy 51 	'SProPheThrLeuTyrValAspGluArgLysGlyValAlaA 	eLysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrL 48 ::: :::	IlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaII	laThrLeuAlaAlaProLeuTyrProLeuThrLysGlu 4 :::	aLysGlnValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpI 4 ::: :::	.aArgLysLysThrValValGln1 CAGAAAGAGACTGTGATGGGCC	GluValThrTyrLeuGlyTyrSerLeuAr 	USGTĀSPLEUGlyTYrArgĀlaSGTĀlaLySLYSĀlaGlnīleCySArgĀ 3 :::::	AlaThrLysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLe 3 :::::::: ::	isProGlnValThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGly 3 :::::	rIlePheAspGluAlaLeuHisArgAspLeuAlaAsnPheArgIleGlnH 3 1:::	GlyGlnLeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProTh 	AlaPheGluTrpArgAspProGlyThrGlyArgThr 	rValleuAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrS 	AsnProTyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrTh 	SpLeuArgGluValAsnLySArgValGlnAspIleHisProThrValPro
8	30	.5	30	82 080	65 130	48 180	32 230	15 280	98 330	82 380	430	480	332 4530	315 4580	298 4630	282 4680	265 4730	248 4780

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3059 AGAAATATTGGGTCACTCAAGGAAAGCCTGTTATGCCTGATCAATTCACC 3010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2959 AACAAAGGCTCTCCTAGAGAGAAGCCCCCAGTCCCTACTACATGCTGAACC 2910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1034 LeuPheArgValArgAsnThrProGlyGlnPheGlyLeuThrProTyrGl 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1017 euThrThrGluThrGlyIleAsnAspTrpMetAlaLeuLeuProPheVal 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2559 CTGTTGGGGATTGATTGGAAATTACATTGTGCATACAGACCCCCAAAGCTC 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2659 ACTGCTAGAAGAGATCTTCCCTAGGTTCGGCATGCCGCAGGTATTGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2459 TAACGCTTGCAACTGGCTCTAGAGACTGGGTGCTCCTACTCCCCTTAGCC 2410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 ValAsnAlaAsnProSerArgIleProProGlyLysArgLeuArgGlySe 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       836 LeuGluTyrValGlnGlnIleHisArgLeuThrHisLeuGlyThrLysHi 852
                                                                                                                                                                                                                                                      1084 GluTrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGl 1100
                                                                                                                                                                                                                                                                                                                                                                             1067 erAlaAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeu 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     934 ValGluAlaTyrProThrLysLysGluThrSerThrValValAlaLysLy 950 :::||||||:::|||||
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1115 alTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLysGly 1131
                                                                 2209 CCAGCAAGACCAGCCAGTGATACCACACCCCTTCCGTGTCGGCGACACCG 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       950 sileLeuGluGluIlePheProArgPheGlyIleProLysValIleGlyS 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCAATGCCAGCAAGTCTGCCGTTAAGCAAGGAACTAGGGTCCGCGGGCA 2810
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                                                                                                                                                                                                                                                                                                                     TGACCAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCCCTT 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGTCAGGTAGAAAGAATGAATAGGACCATCAAGGAGACTTTAACTAAAT 2460
                                                                                                                      yGlyAspLeuGln.....ValProHisArgPheGlnValGlyAspSerV 1115
                                                                                                                                                                                              CAAGCAGTACAACGAGGGCTCTGGAAGCCACTGGCTGCGGCCTATCAGGA 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCTGACA 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTACCGAGCCCGCAACACGCCGGGCCCCCATGGCCTCACCCCATATGA 2360
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2159 TGTGGGTACGCCGGCACCAGACTAAGAACTTGGAACCTCGTTGGAAAGGA 2110

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seq_documentation_block:
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                                                                               alignment_block:
US-09-171-553B-5 x US-08-110-300A-8
                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                              US-08-110-300A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08110300A Patent No. 5643756
                                     Align seg 1/1 to: US-08-110-300A-8 from: 1
                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1132 ProTyrLeuValLeuLeuThrThrProThrAlaValLysValGluGlyIl 1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2009 CCGGAACAGCATCAGGACCGACATGGAAGGTCCAGCGTTCTCAAAACCCCC 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pinter, Abraha APPLICANT: Kayman, Samuel
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FUSION GLYCOPROTEINS
                                                                                                                                                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 20-AUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa
                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                            Quality: 3980.00
Ratio: 3.992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacobs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 Rockefeller Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                   N
O
                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                           82.670
                                                                                                                                                                                                                                                                                                                                                              double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,140
                                                                                                                                             Percent Identity: 62.687
                                             to:
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90 49	ASDAlaASDPTOSETATGIleProProGlyLysArgLeuArgGlySerHi ::: ::: ::: :::	885 4909
	roGlyValAlaAspSerValValLysHisCysValProCysGlnLeuVal::::::::::::::::::::::::::::::::::::	868 4859
	UGInGInLeuValArgThrSerProTyrHisValLeuArgLeuP:::	853 4809
	GluTyrValGlnGlnIleHisArgLeuThrHisLeuGlyThrLysHisLe	837 4759
8 4	hrCysTyrThrSerTyrGlyLysGluIleLeuProHisLysGluGlyLeu ::::: :::::: AGTGTTGGGTTTATCAGGGAAAGCCTGTAATGCCTGATCAATTCACCTTT	820 4709
œ 4	pTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluGlyT :::::::::::::::::::::::::::::::::::	803 4662
4 8	AlaProGluProArgArgGlnTyrThrLeuGluAs	792 4612
4	alAsnLeuLeuProIleIleGluThrProLys	781 4582
4 7	rArgGlyAsnGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnAlaV: ::: ::::: :::::	764 4533
4 7	LeuAlaIleIleHisCysProGlyHisGlnLysAlaLysAspLeuIleSe ::: ::::: CTTAGCATAATTCATTGCCCGGGACATCAGAAGGGGAAACCGCGCGCG	748 4483
4 7	SnLysGluGluIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArg ::: ::: ::: ATAAGGACGAGATCTTGGCCCTACTGAAGGCTCTCTTCCTGCCCAAAAGA	731 4433
4 7	alleTyrLysGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysA ::::: ATATATATAGAAGGCGCGGGTTGCTCACATCAGAAGGAAAAGAAATCAAAA	714 4383
4	IleTyrThrAspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAl::::	698 4333
4 6	euMetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsn ::: :::::	681 4283
0 4	rIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluL:::: :::	664 4233
4	ValGluGlyLysArgMetAlaGlyAlaAlaValAspGlyThrArgTh ::: -	648 4183
0 4	roLeuThrGlyGluValLeuThrTrpPheThrAspGlySerSerTyrVal	631 4133
0 4	SGInLeuLeuIleGluGluThrGlyValArgLysAspLeuThrAspTleP	614 4083

	LysLeuArgLeuHisArg 1182 ::: AAGATAAGATTGACCCGC 5823	1177 5806
1176 5805	ProProProAspSerGlyTrpArgAlaGluLysThrGluAsnProLeu ::: :::::::::	1161 5756
1160 5755	eProThrTrpIleHisAlaSerHisValLysProAla	1148 5706
1148 5705	ProTyrLeuValLeuLeuThrThrProThrAlaValLysValGluGlyII 	1132 5656
1131	alTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLySGly ::: :::::	1115 5606
	yAspLeuGlnValProHisArgPheGlnValGlyAspSerV ::: :::	1101 5556
1101 5555	TrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGlyGl ::::::::::: ::: 	1085 5509
1084 5508	laAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeuGlu 	1068 5459
1068 5458	ULeUTyrGlyGlyProProProLeuAlaGluIleAlaPheAlaHisSerA: :::	1051 5409
1051 5408	PheArgValArgAsnThrProGlyGlnPheGlyLeuThrProTyrGluLe:::: :::	1035 5359
103 4 5358	hrThrGluThrGlyIleAsnAspTrpMetAlaLeuLeuProPheValLeu 	1018 5309
1018 5308	yGlnValGluArgMetAsnArgThrIleLysGluThrLeuThrLysLeuT 	1001 5259
1001 5258	LeuGlyIleAspTrpLysLeuHisCysAlaTyrArgProGlnSerSerGl :::	985 5209
984 5208	SPASNG1yProAlaPheValAlaGlnValSerGlnG1yLeuAlaLysIle	968 5159
968 5158	eLeugluGluTlePheProArgPheGlyIleProLysValIleGlySerA:	951 5109
951 5108	GluAlaTyrProThrLysLysGluThrSerThrValValAlaLysLysIl ::: ::: :::	935 5059
934 5058	yrGlyAsnLysTyrLeuLeuValPheValAspThrPheSerGlyTrpVal 	918 5009
918 5008	SPTOGlyAlaHisTrpGluValAspPheThrGluValLysProAlaLysT: :::	901 4959

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-886-642-8

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-886-642-8 from: 1 to: 8323
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-171-553B-5 x US-08-886-642-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08886642 Patent No. 5952474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212/258-2291 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                     2386 GGGGCTACTGGAGGGAAGCGGTATCGCTGGACCACGGATCGCCGAGTGCA 2435
                                                                                                                  2336 TGCTGACCCAAAATCCTGGACCCCTAAGTGACAAGTCTGCCTGGGTCCAA 2385
                                                                                                                                                                                               2286 CGGGGGCAACCCGTCACCTTCCTAGTGGATACTGGGGCCCAACACTCCG 2335
                                                                                                                                                                                                                                                                                2236 GGAGGTCAGGGTCAGGAGCCCCCCCCCTGAACCCCAGGATAACCCCTCAGAGT 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212/765-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/885,0 FILLING DATE: 01-UL-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/110,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 25
                                                            51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 8323 base pair
                                                                                                                                                       34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                    17 lGluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hone, William J.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                       1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/938,100 FILING DATE: 28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 20-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 3980.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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SYSTEM: Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fish & Richardson P.C
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82.670
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3186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2936 ATCTGAGAGAAGTCAACAAGCGGGTGGAAGACATCCACCCCACCGTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2986 AACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2736 TCTGATCATACCTCTGAAGGCAACCTCTACCCCCGTGTCCATAAAACAAT 2785
                    365 uSerAspLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleCysArgA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 GlyGlnLeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProTh 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 erGlnProLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThr 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2886 CCTGCTACCCGTTAAGAAACCGGGGACTAATGATTATAGGCCTGTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2836 CTGCTGGATCAGGGAATTCTGGTACCCTGCCAGTCCCCCTGGAACACGCC 2885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2786 ACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGA 2835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2686 CAGGCCTGGGCAGAAACCGGGGGCATGGGGCTGGCCGTTCGCCAAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2636 CAAAAGGGCCAGATGTGCCTCTAGGGTCCACATGGCTCTCTGATTTTCCC 2685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2586 GCAAGTGCTGACCCTAAACATAGAAGATGAGTATCGGCTACATGAGACCT 2635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 rValLeuAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrs 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 spLeuArgGluValAsnLysArgValGlnAspIleHisProThrValPro 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 OLeuLeuProValArgLysProGlyThrAsnAspTyrArgProValGlnA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 yrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 GlnAlaTrpAlaGluThrAlaGlyMetGlyLeuAlaLysGlnValProPr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 lnValLysProAspGlnAspIleGlnSer...TrpLeuGluGlnPhePro 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                               ACTTCTGAGCTTGACTGTCAACAAGGTACGCGGGCCCTGTTACAAACCCT 3335
                                                                                                                                 AlaThrLysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLe 365
                                                                                                                                                                                                                         isProGlnValThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGly 348
                                                                                                                                                                                                                                                                                                           CCTGTTTGATGAAGCCCTGCACAGGGACCTCGCAGACTTCCGGATCCAGC
                                                                                                                                                                                                                                                                                                                                        rIlePheAspGluAlaLeuHisArgAspLeuAlaAsnPheArgIleGlnH 332
                                                                                                                                                                                                                                                                                                                                                                                                                           GGACAATTAACCTGGACCAGACTCCCGCAGGGTTTCAAAAACAGTCCCAC 3185
                                                                                                                                                                                        ACCCAGACCTGATTCTGCTCCAGTATGTAGATGACTTACTGCTGGCCGCC 3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuIleGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrPr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnProTyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrTh 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oGlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnT 182
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3235
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L 68	664 rIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluL ::: ::::
요:: 글	648 ValGluGlyLysArgMetAlaGlyAlaAlaValValAspGlyThrArg'
ଲ∷ =	631 roLeuThrGlyGluValLeuThrTrpPheThrAspGlySerSerTyrVa 33 CTCTCCCAGACGCTGACCACACCTGGTACACAGATGGGAGCAGCTTCCT
O - O	614 sGlnLeuLeuIleGluGluThrGlyValArgLysAspLeuThrAspIle ::::::
H H.	598 AlaThrLeuLeuProGluGluThrAspGluProValThrHisAspCysH
> − 0	582 euLeuThrGluArgValThrPheAlaProProAlaAlaLeuAsnPro
	565 OPTOASPATGTTPMETThTASNAlaATGMETThTHISTYTGlnSerLeuL
	549 AsnileThrVallleAlaProHisAlaLeuGluAsnIleValArgGlnPr :::::::::::::
	532 laAlaValAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGln ::: ::: ::: 836 CAGCCATCGCCGTTCTGACCAAAGACGCTGGCAAGCTCACCATGGGACAG
	515 SLYSLeuASpProValAlaSerGlyTrpProValCysLeuLysAlaIleA
	499 LeuThrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLy
	482 ysProPheThrLeuTyrValAspGluArgLysGlyValAlaArgGlyVal
	465 eLysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrL
	449 LysGlyGlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaIl 586 GGGACTCTGTTTGAGTGGGCCCAGACCAGCAAAAGGCCTACCAAGAGAT
	432 leproGlyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGlu 536 TCCCTGGGTTTGCAGAAAATGGCAGCCCCCTTGTACCCTCTCACCAAAACG
	15 aLysGlnValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpI::: ::
	99 ThrGluAlaArgLysLysThrValValGlnIleProAlaProThrThrAl
	82 rgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlpArgTrpLeu :::::
	36 AGGGGACCTCGGATATCGGGCCTCGGCCAAGAAAGCCCCAAATTTGCCAGA

951 eLeuG : 5109 ACTAG	935 GluAl 5059 GAAGC	918 yrGly 5009 ATGGG	901 sprog : 4959 ACCCG	885 Asnal 4909 AATGC	868 roGly	853 uGlnG ::: 4809 AAAGG	837 GluTy 4759 GAACT	820 hrCys 4709 AGTGT	803 pTrpG : 4662 CATAA	792 4612 GAAAA	781 alAsnI 4582	764 rArgGl : 4533 AAGGGG	748 LeuAla ::: 4483 CTTAGC	731 snLysG : 4433 ATAAGG	714 alleTy 4383 AATATA	698 IleTyr ::: 4333 GTTTAC	681 euMetA ::: 4283 TGATAG
luGluIlePhePr AAGAAATCTTCCC	aTyrProThrLys ::: TTTCCCAACCAAG	AsnLysTyrLeuL TATAAATATCTTT	lyAlaHisTrpGl ::: GCACCCACTGGGA	aAsnProSerArg ::: CAGCAAGTCTGCC	ValAlaAspSerV ;;; ACGCTCAAAGACA	lnLeuValArgThr ::::: CTCTTCTAGAAAGG	rValGlnGlnIleH :::::: ATTAGATTTTCTTC	TyrThrSerTyrGl :::::: TGGGTTTATCAGGG	lnGluIleLysLys ::::::: AAGATCTGACTAAA	ProGlu	· · · Le	yasnGlnMetAla ::: CAACAGGATGGCC	IleIleHisCysP ATAATTCATTGCC	luGluIleLeuSe :: :: ACGAGATCTTGGC	rLysGlnArgGly :::::: TAGAAGGCGCGGG	ThrAspSerArgT ACCGATAGCCGTT	laLeuThrGlnAl GCTCACCCAAGO
OArgPheGlyIle CAGATTCGGCATG	LysGluThrSerT ::: AAAGAAACTGCCA	euValPheValAs ::: TAGTTTTCATAGA	uValAspPheThr ::: AATTGATTTCACT	IleProProGlyLy ::: GTCAAACAAGGGAC	alvalLysHisCy ::::::: TCACTGAGACTTG	SerPro ::: AACTACTGTCCT	isArgLeuThrH ::: ATCAATTGACCC	yLysGluIleLe AAAGCCTGTAAT		roargarg :::::: CTCaTGAACATTT	eGluThrProLys	AspArgValAlaL :::::: : GACCAAGCGGCCC	roGlyHisGlnLy CGGGACATCAGAA	rLeuLeuGluAla : ::: :CCTACTGAAGGCT	LeuLeuThrSerA TTGCTCACATCAG	yralaPhealaTh aTGCTTTTGCCAC	aLeuArgLeuAla ::::: CTTAAAAATGGCA
ProLysVallleG1 ::: ::: CCACAGGTATTGGG	ThrValValAlaLys	pThrPheSerGlyT CACTTTCTCTGGAT	GluValLysProAli :: GAGGTAAAACCTGG	sArgLeuArgGly ::: TAGAGTTCGAGGG	sValProCysGlnLe 	TyrHisValLeuArg :::::: ::: TATTACATGCTGAAC	isLeuGlyThrLysH ::: ::: ACCTCAGTTTCTCAA	uProHisLysGluGl : GCCTGATCAATTCAC	<pre>%erGluThrProGlu ;;; EATGACGATGCAAAG</pre>	.GlnTyrThrLeu ::: ::: TCACTATACGGTG	ACTTCCACACTTCT	ysGlnAlaAlaGln :::::::: GAGAAGTAGCCACT	sAlaLysAspLeuI ::::: GGGAAACCGCGCGG	LeuHisLeuProLy	laGlyArgGluIle ::: AAGGAAAAGAAATC	rAlaHisValHisG ::: TGCCCATATTCACG	GluGlyLysSerIle ::::: GAAGGTAAGAAGCTG
yserA 968 ::: AACCG 5158	LysIl 951 :: AAGCT 5108	rpVal 934 GGGTA 5058	aLysT 918 : CCTGT 5008	SerHi 901 :: CACCG 4958	euVal 884 AGGTC 4908	LeuP 868 CGGG 4858	HisLe 853 NAAAC 4808	yLeu 836 ::: CTTT 4758	GlyT 820	GluAs 803 ACTGA 4661	791 GATA 4611	AlaV 781 AGA. 4581	leSe 764 :: AGGC 4532	sArg 747 AAGA 4482	Lysa 731 AAAA 4432	lyAl 714 GAGA 4382	eAsn 697 : 3AAT 4332

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seq_documentation_block:
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                                                                                                                                                                                      Sequence 8, Application PC/TUS9308041
GENERAL INFORMATION:
APPLICANT: The Public Health Research Institute of the City of APPLICANT: New York, Inc.
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1177 LysLeuArgLeuHisArg 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5756 AGCCACCATCGGAATCGACATGGCGTGTTCAAACGCTCTCAAAATCCCCCTA 5805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5556 ACAACTGGACCGGCCGGTAGTGCCTCACCCTTTCCGAGTCGGTGACACAG 5605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5509 CTGGTCCAGCACGAAGTCTGGAGACCGTTGGCGGCAGCTTACCAA...GA 5555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5459 CAAAGGTTACTCATAACCCCTCTCTCCAAGCCCATTTACAGGCACTCTAC 5508
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1068 laAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeuGlu 1084
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                                                                                                             ADDRESSEE: Davis ..... Partie Pl. STREET: 45 Rockefeller Pl.
                                                         COUNTRY: USA
                                                                                       STATE:
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                                                                                    New York
                                                                                                                                                                Davis Hoxie Faithfull and Hapgood
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alignment_block:
US-09-171-553B-5 x PCT-US93-08041-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: PCT-US93-08041-8 from: 1 to: 8323
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                               2536 CACTTTGAGGGATCAGGAGCTCAGGTTGTGGGACCAATGGGACAGCCCCT 2585
                                                                                                                                                                                                                                                            2436 CCTAGCCACCGGTAAGGTCACCCATTCTTTCCTCCATGTACCAGATTGCC 2485
                                                                                                                                                                                                                                                                                                                                                       2386 GGGGCTACTGGAGGGAAGCGGTATCGCTGGACCACGGATCGCCGAGTGCA 2435
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                      116 eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2336 TGCTGACCCAAAATCCTGGACCCCTAAGTGACAAGTCTGCCTGGGTCCAA 2385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2286 CGGGGGCAACCCGTCACCTTCCTAGTGGATACTGGGGCCCAACACTCCG
                                                                                                                101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                                                                                                                                          84 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                       67 pLeuGlyValGlyArgValThrHisSerPheLeuValIIeProGluCysp 84
                                                                                                                                                                                                                                                                                                                                                                                  51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 1GluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 20-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jacobs, Seth H. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 8323 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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COMPUTER: IBM PC compati
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Ratio:
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3386 399 3436 3436 415	8 3 6 8	3186 3186 332 3236	282 3086 299 3136	249 2986 265 3036	215 2886 232 2936	182 2786 199 2836	149 2686 165 2736	2586 133 2636
::::: 6 AACAG 9 ThrGl 6 ACTGA 5 ALYSG :::: 6 TCGAC	SerA ::: SerA :::	IleP::: CTGTCTGTCCCA	erGlnP GTCAGT GlyGln GGACAA	AsnPro	oLeuLe CCTGCT spLeuA 	yrProL : ACCCCA LeuIle :::	GlnAla' CAGGCC' oGlnVa ::	GCAAGTG lnValLy :: CAAAAGG
UAL HILL HILL HILL HILL HILL HILL HILL HI	TGAGCT SpLeuG	eAspG TGATG ToVal ::::: ACCTG	roLeu CTCTC CTCTC 	TYTASN TACAAC TGACTT	uProVa ACCCGT rgGluV 	euSerA :: : TGTCAC ::: ::::	TrpAlaG	GCTGACC YSProAs GGCCAGA
TATCTG GLYSLY : AAAAGA rgGluF	 GACTG ATATC	AlaL	PheAlaP TTCGCCT TTrpThr CTGGACC	LeuLeu CTCTTG ULYSAS 	lArgLy ::: TAAGAA alAsnL 	rgGluA::: ::: :AAGAAG GlyIle GGAATT	LuThr AAACC LeuLy 	CCTAAAC apGlnAs ATGTGCC
GGGTAT SThrVa:	CAACA gAlas GGCCT	uHisA GCACA GCACA 	THE SHEET OF THE S	SerAla :::: AGCGGG PAlaPh 	sProG1 ACCGGG ysArgV 	laargG	AlaGlyM ::: GGGGGCA GGGCAACC	CATAGAA SpIleGl ::: CTCTAGG
CTTCTA LValG1 ::: GATGGG LyThrA	Le CC	gAspL	rpArgA 	Leupro	YThrAsı GACTAA' alGlnA ::: TGGAAG	luglyIl TGGGGAT TroValG CCCTGCC	MetGlyL	GATGAG nSer GTCCAC
AAGAG IlePr	::: CGGG SLys rgGl	uAlaA : CGCAG SpAsp ATGAC	AT GG	ProGlu ::: CCGTCC SLeuAr 	nAspTyJ TGATTAJ TGATTAJ SpIleH 	LeTrpPr	Jeualal TGGCCG TPTOVal CCCGTG	TATCGG .TrpLe .
GTCAG Alapr :::: :Alapr CTCCC ACTCC ACTCC ACTCC ACTCC	CTGT CTGT aGln HHHH CCAA	nPheAr: : : : ;euLeuI	lyThrG AGATGG LysAsn AAAAAC	rgAsn ::::: ACCAG LeuHi 	rArgPro	CCTGGA	ysGlnV ::: HTCGCC SerVal :::	CTACAT uGluGl
GATGG 	CAAACC eCysAr : TTGCCA	GATCCA GATCCA cuAlaG [TGGCCG	ArgT : ATCT rPro 	rpTyr GGTAC ProTh CCCAC	ovalGln	lGlnAr : ACAGAG SnThrF 	alProp AAGCTC ArgGln :::	GAGACC' nPhePro
0 - H 0 > H-	 CT 33 GA 38 :: GA 33	nH 33 GC 32 Ily 34 Ily 34 I:: CC 32	31 31 31	α α α α α α α α α α α α α α α α α α α	1A 232 10 293 3G 293 10 248 11 298	9 198 A 283 Y 215 C 288	r 165 C 273 T 182 T 278	T 2635 O 148 I 2685
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714 a 4383 A	698 I 4333 G	681 e 1 4283 T	664 r 4233 A	648 V 4183 C	631 r 4133 C	614 sg : 4083 TG	598 Al 4036 GC	582 eu 3986 TT	565 OP 3936 CC	549 As 3886 CC	532 la 3836 CA	515 sL 3786 AA	499 Le 1 3736 CT	482 ys 11 3686 AG	465 eL 3636 CA	449 Lys 3586 GGG	432 leP 3536 TCC
IleTyrLysG :::: ATATATAGAA	leTyrThrAsp :: TTTACACCGAT	uMetAlaLeuT ::: GATAGCGCTCA	·IleTrpAlaSe ::: :: ;GTCTGGGCCAA	alGluGlyLys ::: AAGAGGGGCAG	oLeuThrGlyG TCTCCCAGACG	lnLeuLeuIl ::::: ACATCTTGGC	aThrLeuLeu TACGCTGCTC	LeuThrG : CTGGACACGG	roAspArgTr CTGATCGCTG	nIleThrValI ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	AlaValAlaIl ::: :: .GCCATCGCCGT	ysLeuAspPro AGCTAGACCCA	uThrGlnThrL AACGCAAAAAC	ProPheThrLe CCCTTCGAACT	ysLysAlaLeu ::: AGCAGGCTCTC	GlyGlyPhes 	roGlyPheAl CTGGGTTTGC
lnArgGlyLeu :: :GGCGCGGGTTG	SerArgTyrA AGCCGTTATG	[hrGlnAlaLe ACCCAAGCCTT	erSerLeuPro ::::: AAGCACTGCCA	ArgMetAlaG CGCAAGGCCG	luValLeuTh CTGACCACAC	eGluGluThr TGAAGCCCAC	ProGluGluT	luargValThr :: accgagTccag	pMetThrAsnA :::::: GCTCTCCAACG	IleAlaProHi ::: TTGGCCCCCCA	leLeuValLys :: ::: rrCTGACCAAA	oValAlaSerG ::: \GTGGCAGCTG	euGlyProTr TGGGGCCTTG	uTyrValAsp ::: TTTTGTTGAC	LeuSerAlaP ::: TTAACTGCCC	erTrpAlaPr :: ::: AGTGGGGCCC	aThrLeuAla. ::: AGAAATGGCA
LeuThrSerA CTCACATCAG	\laPheAlaTh CTTTTGCCAC	uArgLeuAla ::::: AAAAATGGCA	GluGlyThrS GCCGGGACAT	lyAlaAlaVa GAGCAGCAGT	rTrpPheThrA ::: CTGGTACACAG	GlyValArgLy ::: GGAACTAGACC	hrAspGluPro ::: CTGAGGAGGG	PheAlaProf ::: TTCGGACCA/	AlaArgMetTh CCCGAATGAC	SAlaLeuGlu ::: \TGCAGTAGAG	AspAlaAspI GACGCTGGC <i>F</i>	LyTrpProVa GGTGGCCCCC	PArgArgPro	GluArgLysG ::::: GAGAAGCAGG	roAlaLeuAla ::: CTGCCCTGGGA	oGluHisGlnL :::::: AGACCAGCAAA	AlaProLeuTy GCCCCCTTGTA
laGlyArgGl ::: AAGGAAAAGA	rAlaHisVall	GluGlyLysSe :: GAAGGTAAGAA	erAlaGlnLys ::: CGGCCCAAAGA	lValAspGlyT ::: AACCACCGAGI	AspGlySerSe GATGGGAGCAG	/sAspLeuThr CAGATCTTACG	ValThrHisa ::: CTGCAACATG	roAlaAlaLe ::: TAGTGGCCCT	THISTYTGIN	AsnIleVala: ::: : GCACTAGTTA	ysLeuThrLe :: AGCTCACCATo	lCysLeuLysA ::: !TTGCCTACGGA	ValAlaTyrLe GTGGCCTACCT	lyValAlaArg	aLeuProAspV : aTTGCCAGACT	ysAlaPheA :::: AGGCCTACC	/rProLeuThr
uIleLysA AATCAAAA	HisGlyAl CACGGAGA	erIleAsn ::::: AGCTGAAT	SALAGLUL : NGCTGAGT	ThrargTh ::::: ACCGAGGT	rTyrVal ::::: CTTCCTG	AspIleP GACCAGC	SPCYSHI	uAsnPro AAACCCA	SerLeuL 5 ::: GCTCTGC 3	rgGlnPr 5 :: AGCAACC 3	uGlyGln 5 : GGGACAG 3	AlaIleA 5 ::: ATGGTAG 3	euSerLy 5	GlyVal 4 GGTGTC 3	alThrL 4 :: TGACTA 3	SPALAIL 4 :: AAGAGAT 3	LysGlu 4 AAAACG 3
731 4432	714 4382		ν &	664 4232	647 4182	631 4132	614 4082	597 4035	582 3985	65 3935	48 885	32 835	15 785	98 735	82 685	65 635	48 585

1018 hrThrGluThrGlyIleAsnAspTrpMetAlaLeuLeuProPheValLeu 10:	1001 yGlnValGluArgMetAsnArgThrIleLysGluThrLeuThrLysLeuT 10: 	985 LeuGlyIleAspTrpLysLeuHisCysAlaTyrArgProGlnSerSerGl 10 	168 SPASNGlyProAlaPheValAlaGlnValSerGlnGlyLeuAlaLySIle 98 	S1 eLeuGluGluIlePheProArgPheGlyIleProLysValIleGlySerA 96 	35 GluAlaTyrProThrLysLysGluThrSerThrValValAlaLysLysIl 95 ::: ::: 59 GAAGCTTTCCCAACCAAGAAAGAAACTGCCAAAGTTGTAACCAAGAAGCT 51	- 5 H	101 sProGlyAlaHisTrpGluValAspPheThrGluValLysProAlaLysT 9 : :::	ASDALAASNPTOSETATGIleProProGlyLysArgLeuArgGlySerH1 9	168 roGlyValAlaAspSerValValLysHisCysValProCysGlnLeuVal 8 ::::::::::::::::::::::::::::::::::::	153 uGlnGlnLeuValargThrSerProTyrHisValLeuArgLeup 8 :::	37 GluTyrValGInGInIleHisArgLeuThrHisLeuGlyThrLysHisLe 8 :::::::::::::::: ::: ::::::	120 hrCysTyrThrSerTyrGlyLysGluIleLeuProHisLysGluGlyLeu 8	103 pTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluGlyT 8	12 GAAAAT	81 alasnLeuLeuProIleIleGluThrProLys	'64 rArgGlyAsnGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnAlaV :	48 LeualaileileHisCysProGlyHisGlnLysAlaLysAspLeuIleSe :::	31 SHAYSSTAGTILLELENSETLENDEUGLUATALEUHTSLEUPFOLYSARG
034	018	001 258	84 208	68 158			918	901 1958	884 4908	868 4858	853 4808	836 4758	820 4708	803 4661	791 4611	781 4581	764 4532	747 4482

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seq_documentation_block:
; Sequence 9, Applicatio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08110300A Patent No. 5643756 GENERAL INFORMATION:
          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION LOATA:
APPLICATION UNBER: US/08/110,300A
FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H.
REGISTRATION NUMBER: 32,140
REGISTRATION NUMBER: 32,140
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1148 eProThrTrp11eHisAlaSerHisValLysProAla................... 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5756 AGCCACCATCGGAATCGACATGGCGTGTTCAACGCTCTCAAAATCCCCCTA 5805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1161 ..ProProProAspSerGlyTrpArgAlaGluLysThrGluAsnProLeu 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5706 TGCAGCGTGGATCCACGCTGCCCACGTAAAGGCTGCCGACACCAGGATTG 5755
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5806 AAGATAAGATTGACCCGC 5823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5606 TGTGGGTCCGCAGACACCAAACTAAAAATCTAGAACCCCGCTGGAAAGGA 5655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1115 alTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLysGly 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5556 ACAACTGGACCGGCCGGTAGTGCCTCACCCTTTCCGAGTCGGTGACACAG 5605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101 yAspLeuGln......ValProHisArgPheGlnValGlyAspSerV 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5509 CTGGTCCAGCACGAAGTCTGGAGACCGTTGGCGGCAGCTTACCAA...GA 5555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1085 TrpValArgClnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGlyG1 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5459 CAAAGGTTACTCATAACCCCTCTCCCAAGCCCATTTACAGGCACTCTAC 5508
                                                                                                                                                                                                                                                                                                                                                                 STREET: 45 ROCKE
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1068 laAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeuGlu 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1051 uLeuTyrGlyGlyProProProLeuAlaGluIleAlaPheAlaHisSerA 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5309 CGCTTGCAACTGGCTCTAGGGACTGGGTGCTCCCTAGCCCTG 5358
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                            10111
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Davis Hoxie Faithfull and Hapgood
11698A50
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TELEPHONE: 212-757-2200

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alignment_block:
US-09-171-553B-5 x US-08-110-300A-9/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO US-08-110-300A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: US-08-110-300A-9 from: 1 to: 10367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 3.992
Percent Similarity: 82.670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5360 GGAGGTCAGGGTCAGGAGCCCCCCCCTGAACCCCAGGATAACCCCTCAGAGT 5311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5210 GGGGCTACTGGAGGGAAGCGGTATCGCTGGACCACGGATCGCCGAGTGCA 5161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5260 TGCTGACCCAAAATCCTGGACCCCTAAGTGACAAGTCTGCCTGGGTCCAA 5211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5110 CCTATCCTCTGCTAGGAAGAGATTTGCTGACTAAAACTAAAAGCCCAAATT 5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5110 CCTAGCCACCGGTAAGGTCACCCATTCTTTCCTCCATGTACCAGATTGCC 5111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGIA TYPE: DN
                                                                                                                                                                                                                                                                                       4960 CAAAAGGGCCAGATGTGCCTCTAGGGTCCACATGGCTCTCTGATTTTCCC 4911
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                                                                                            4860 TCTGATCATACCTCTGAAGGCAACCTCTACCCCCGTGTCCATAAAACAAT 4811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5060 CACTTTGAGGGATCAGGAGCTCAGGTTGTGGGACCAATGGGACAGCCCCT
4910 CAGGCCTGGGCAGAAACCGGGGGCATGGGGCTGGCCGTTCGCCAAGCTCC 4861
                                                                                                                                                                                                                                                                                                                                                                                           5010 GCAAGTGCTGACCCTAAACATAGAAGATGAGTATCGGCTACATGAGACCT 4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                                                                                                                                                                                      149 GlnAlaTrpAlaGluThrAlaGlyMetGlyLeuAlaLysGlnValProPr 165
                                                                                                                                                                                                                                                                                                                        133 lnValLysProAspGlnAspIleGlnSer...TrpLeuGluGlnPhePro 148
                                                                                                                                                                                                                                                                                                                                                                                                                                    116 eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProG 133
                                                                                                                                          165 oGlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                      182 yrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 roValProLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
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4710 CCTGCTACCCGTTAAGAAACCGGGGACTAATGATTATAGGCCTGTCCAGG 4661
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                                                                                                                                                      3960 CAAGCAGGCTCTCTTAACTGCCCCTGCCCTGGGATTGCCAGACTTGACTA 3911
                                                                                                                                                                                                                                                         4010 GGGACTCTGTTTGAGTGGGGCCCAGACCAGCAAAAGGCCTACCAAGAGAT 3961
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                                                     3910 AGCCCTTCGAACTTTTTGTTGACGAGAAGCAGGCTACGCCAAAGGTGTC 3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 aLysGlnValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpI 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 ThrGluAlaArgLysLysThrValValGlnIleProAlaProThrThrAl 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 rgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeu 398
                                                                                                                                                                                                   465 eLysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrL 482
                                                                                                                                                                                                                                                                                                      449 LysGlyGlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaIl 465
                                                                                             482 ysProPheThrLeuTyrValAspGluArgLysGlyValAlaArgGlyVal 498
499 LeuThrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLy 515
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92AlaProGluProArgArgGlnTy
LeuProllelleGluThrProLys
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731 snLysGluGluIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArg 747 ::: ::: ::: ATAAGGACGAGATCTTGGCCCTACTGAAGGCTCTCTCCTGCCCAAAAGA 3114
12 12
681 euMetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsn 697 ::: :::::
64 rIleTrpAlaSe ::: ::
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614 sGlnLeuLeuIleGluGluThrGlyValArgLysAspLeuThrAspIlep 631 :::::: :::
98 AlaThrLeuLeuProGluGluThr
10 1
9 9
549 AsnIleThrValIleAlaProHisAlaLeuGluAsnIleValArgGlnPr 565 ::::::::::::: ::: ::: :::
532 laAlaValAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGln 548 ::: ::: :
515 SLYSLeuAspProValAlaSerGlyTrpProValCySLeuLySAlaIleA 532
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seq_documentation_block:
; Sequence 9, Application US/08886642
; Patent No. 5952474
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; MOLECULE TYPE: US-08-886-642-9
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                                                                                                  TELEFAX: 212/258-2291
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10367 base pairs
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                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/11
FILING DATE: 20-AUG-1993
APPLICATION NUMBER: 07/93
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-JUL-
PRIOR APPLICATION DATA:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212/765-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 45 ROCI
CITY: New York
STATE: NY
                                                                                                                                                                                                                                        NAME: Hone, William J. REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                         STRANDEDNESS:
TOPOLOGY: lir
                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/886,642
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FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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                                                                                                                                                                                                                                                                                                                             UMBER: 07/938,100
28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997
                       Genomic DNA
                                                                single
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                                                                                                                                                                                                                                                               26,739
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alignment_scores:

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alignment_block:
US-09-171-553B-5 x US-08-886-642-9/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 82.670
                                                                                                                                                                                               4710 CCTGCTACCCGTTAAGAAACCGGGGACTAATGATTATAGGCCTGTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                       4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4760 CTGCTGGATCAGGGAATTCTGGTACCCTGCCAGTCCCCCTGGAACACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4860 TCTGATCATACCTCTGAAGGCAACCTCTACCCCCGTGTCCATAAAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4910 CAGGCCTGGGCAGAAACCGGGGGCCATGGGCCGTTCGCCAAGCTCC 4861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5010 GCAAGTGCTGACCCTAAACATAGAAGATGAGTATCGGCTACATGAGACCT 4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5060 CACTTTGAGGGATCAGGAGCTCAGGTTGTGGGACCAATGGGACAGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5160 CCTAGCCACCGGTAAGGTCACCCATTCTTTCCTCCATGTACCAGATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5210 GGGGCTACTGGAGGGAAGCGGTATCGCTGGACCACGGATCGCCGAGTGCA 5161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5260 TGCTGACCCAAAATCCTGGACCCCTAAGTGACAAGTCTGCCTGGGTCCAA 5211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5360 GGAGGTCAGGGTCAGGAGCCCCCCCCTGAACCCAGGATAACCCTCAGAGT 5311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                                                                              232 spLeuArgGluValAsnLysArgValGlnAspIleHisProThrValPro 248
                                                                                                                                                                                                                                            215 oLeuLeuProValArgLysProGlyThrAsnAspTyrArgProValGlnA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                      yrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnalaTrpalaGluThrAlaGlyMetGlyLeuAlaLySGlnValProPr 165
                                                                                                                                                                                                                                                                                                                                                     LeuIleGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrPr 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oGlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnT 182
                                                                                                      ATCTGAGAGAAGTCAACAAGCGGGTGGAAGACATCCACCCCACCGTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                         ACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCCACATACAGAGA 4761
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Ratio: 3.992
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Gaps: 12
Percent Identity: 62.687
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265 rValleuAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrs 282

868	853 uGlnGlnLeuValArgThrSerProTyrHisValLeuArgLeuP i ::: ::::: ::::	
853 2788	837 GluTyrValGlnGlnIleHisArgLeuThrHisLeuGlyThrLysHisLe (
836 2838	11 :: eu	
820 2888	803 pTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluGlyT (
803 2935	792AlaProGluProArgArgGlnTyrThrLeuGluAs	
791 2985	781 alAsnLeuLeuProIleIleGluThrProLys	
781 3015	764 rArgGlyAsnGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnAlaV :	
764 3064	748 LeuAlaIleIleHisCysProGlyHisGlnLysAlaLysAspLeuIleSe ::	
747 3114	731 snLysGluGluIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArg ::: ::: 3163 ATAAGGACGAGATCTTGGCCCTACTGAAGGCTCTCTTCCTGCCCAAAAGA	
731 3164	714 alleTyrLysGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysA :::::	
714 3214	698 IleTyrThrAspSerargTyralaPheAlaThrAlaHisValHisGlyAl :::	
697 3264	681 euMetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsn ::: :::::	
681 331 4	664 rIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluL :::: ::::: 3363 AGTCTGGGCCAAAGCACTGCCAGGCGGGACATCGGCCCAAAGAGCTGAGT	
664 3364	648 ValGluGlyLysArgMetAlaGlyAlaAlaValValAspGlyThrArgTh ::: ::: 3413 CAAGAGGGCAGCGCAAGGCCGGAGCAGCAGCAGCAGCAGC	
647 3414	631 roLeuThrGlyGluValLeuThrTrpPheThrAspGlySerSerTyrVal	
631 3464	614 sGlnLeuLeuIleGluGluThrGlyValArgLysAspLeuThrAspIleP ::::::	
614 3514	598 AlaThrLeuLeuProGluGluThrAspGluProValThrHisAspCysHi ::: :::	
597 3561	582 euLeuThrGluArgValThrPheAlaProProAlaAlaLeuAsnPro	
3611	3660 CCCTGATCGCTGGCTCTCCAACGCCCGAATGACCCACTACCAGGCTCTGC	

3810

3860

3910 AGCCCTTCGAACTTTTTGTTGACGAGAAGCAGGGCTACGCCAAAGGTGTC

3861

482 ysProPheThrLeuTyrValAspGluArgLysGlyValAlaArgGlyVal 498

499 LeuThrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLy 515

CTAACGCAAAAACTGGGGCCTTGGCGTCGGCCGGTGGCCTACCTGTCCAA

3811

3960 CAAGCAGGCTCTCTTAACTGCCCCTGCCCTGGGATTGCCAGACTTGACTA

3911

3961

465 eLysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrL 482

3760

532 laAlaValAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGln 548

CAGCCATCGCCGTTCTGACCAAAGACGCTGGCAAGCTCACCATGGGACAG 3711

SLYSLeuAspProValAlaSerGlyTrpProValCysLeuLysAlaIleA 532

AAAGCTAGACCCAGTGGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAG 3761

549

3710 CCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTTAAGCAACC

3661

AsnIleThrVallleAlaProHisAlaLeuGluAsnIleValArgGlnPr 565

565 oProAspArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuL 582

853 2788	GluTyrValGlnGlnIleHisArgLeuThrHisLeuGlyThrLysHisLe	837 2837	
836 2838	hrCysTyrThrSerTyrGlyLysGluIleLeuProHisLysGluGlyLeu	820 2887	
820 2888	<pre>PTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluGlyT </pre>	803 2934	
803 2935		792 2984	
791 2985	alAsnLeuLeuProIleIleGluThrProLys	781 3014	
781 3015	rArgGlyAsnGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnAlaV: ::: : :::: :	764 3063	
764 3064	LeuAlaIleIleHisCysProGlyHisGlnLysAlaLysAspLeuIleSe :::	748 3113	
747 3114	snLysGluGluTleLeuSerLeuLeuGluAlaLeuHisLeuProLysArg :::	731 3163	
731 3164	alleTyrLysGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysA :::::: ATATATAGAAGGCGCGGGTTGCTCACATCAGAAGGAAAAGAAATCAAAA	714 3213	
714 3214	IleTyrThrAspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAl:::	698 3263	
697 3264	euMetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsn ::: :::::	681 3313	
681 3314	rIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluL:::: ::::	664 3363	
664 3364	ValGluGlyLysArgMetAlaGlyAlaAlaValValAspGlyThrArgTh :::	648 3413	
647 3414	roLeuThrGlyGluValLeuThrTrpPheThrAspGlySerSerTyrVal	631 3463	
631 3464	SGlnLeuLeuIleGluGluThrGlyValArgLySAspLeuThrAspIleP::::::	614 3513	
614 3514	AlaThrLeuLeuProGluGluThrAspGluProValThrHisAspCysHi 	. 3560	
597 3561	euLeuThrGluArgValThrPheAlaProProAlaAlaLeuAsnPro	582 3610	
3611		3660	

4160

4210 AACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTG

4161

rgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeu 398

399 ThrGluAlaArgLystysThrValValGlnIleProAlaProThrThrAl 415

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382

365

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4261

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4510 GTCAGTCTCTCTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCA 4461

282 erGlnProLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThr 298

TCCCTGGGTTTGCAGAAATGGCAGCCCCTTGTACCCTCTCACCAAAACG leProGlyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGlu 448

4011

4060

432

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901 sproglyAlaHisTrpGluValAspPheThrGluValLysProAlaLysT 918 :||||||:::||||||||||:::||
2637 ACCCGGCACCCACTGGGAAATTGATTTCACTGAGGTAAAACCTGGCCTGT 2588
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                                                                                                                                                                                                                                                                                  1115 alTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLysGly 1131
                                                                                                                                                                                                                                                                                                                                                                                                                              1101 yAspLeuGln......ValProHisArgPheGlnValGlyAspSerV 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1085 TrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGlyGl 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1068 laAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeuGlu 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1051 uLeuTyrGlyGlyProProProLeuAlaGluIleAlaPheAlaHisSerA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2237 TATCGAGCCCGCAACACGCCGGGCCCCCACGGTCTCACCCCATATGAAAT 2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    951 eLeuGluGluIlePheProArgPheGlyIleProLysValIleGlySerA 968
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                                                                                                                     2040 GCAACTAGACCGGCCGGTAGTACCTCACCCTTTCCGGGTCGGTGACACAG
1890 TGCAGCGTGGATCCACGCTGCCCACGTAAAGGCTGCCGACACCAGGATTG 1841
                                                       1148 eProThrTrpIleHisAlaSerHisValLysProAla............ 1160
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seq_documentation_block:
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                                                                                                                                                                                                                 alignment_scores:
                                                                                                                           alignment_block:
                                                                     Align seg 1/1 to reverse of: PCT-US93-08041-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application PC/TUS9308041
GENERAL INFORMATION:
                                                                                                          US-09-171-553B-5 x PCT-US93-08041-9/rev
                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1790 AAGATAAGATTGACCCGC 1773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1161 ..ProProProAspSerGlyTrpArgAlaGluLysThrGluAsnProLeu 1176
APPLICATION NUMBER: US 08 FILING DATE: 20-AGG-1993 ATTORNEY/AGENT INFORMATION: NAME: Jacobs, Seth H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: FUSION GLYCOPROTEINS NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Public Health Research Institute APPLICANT: New York, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-AUG-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212 / TELEPHONE: 212 - 586 - 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jacobs, Seth H. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/938,100
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                              Quality: 3980.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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45 Rockefeller Pl.
                                                                                                                                                                                                                                                                                                                                                                                             10367 base pairs
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82.670
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                                                                            to: 10367
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614 sGlnI ::::	598 AlaThr 3560 GCTACG	582 euLeu 3610 TTCTG	565 oproa 3660 cccTG	549 AsnIl :: 3710 CCACT	532 laAla 3760 CAGCC	515 sLysI 3810 aaa gc	499 LeuT 3860 CTAA	482 ysPr 3910 AGCC	465 eLys 3960 CAAG	449 Lysgl 4010 GGGAC	432 lePr 4060 TCCC	415 aLysg ::: 4110 TCGAC	399 ThrG 4160 ACTG	382 rgG1 :::: 4210 AACA	365 user 4260 AGGG	349 Alar :::: 4310 ACTT	332 isPr 4360 ACCC	::: 4410 CCTG
euLeuIleGluGluTh ::	LeuLeuProGlu CTGCTCCCT	ThrGluArgValT ::: GACACGGACCGAGTCC	spArgTrpMetTh: ATCGCTGGCTCTCC	eThrValIleAlaPı :::::::: AGTCATTCTGGCCCC	ValAlaIleLeuVa ::: ::: : ATCGCCGTTCTGAC	.euAspProValAlaS TAGACCCAGTGGCAG	hrGlnThrLeuGlyPr cGCAAAAACTGGGGCC	oPheThrLeuTyrValAs 	LysalaLeuLeuSerA ::: ::: CAGGCTCTCTTAACTG	yGlyPheSerTrpAl ::: :: CTGTTTGAGTGGGG	OGlyPheAlaThrLeu TGGGTTTGCAGAAATG	lnValArgGluPhe ::: AACTAAGGGAGTTC	luAlaArgLysLysT AGGCCAGAAAAGAGA	.uValThrTyrLeuGlyTy 	AspLeuGlyTyrArgA GACCTCGGATATCGGG	hrLysGlnAspCys ::::: CTGAGCTTGACTGT	OGlnValThrLeuLe :::::: AGACCTGATTCTGCT	
hrGlyValArgLysAsp	GluThrAspGluProValT ::: CTACCTGAGGAGGGGCTGC	hrPheAlaProPro ::: AGTTCGGACCAATA	:AsnAlaArgMetThrHisTyrGln :	COHİSALALEUGLUASN CCATGCAGTAGAGGCA	alLysaspalaaspLysL :: CAAAGACGCTGGCAAGC	erGlyTrpProValCysLeul :: CTGGGTGGCCCCTTGCCTAC	oTrpArgArgProValAla TTGGCGTCGGCCGGTGGCC	AspGluArgLysGlyVal GACGAGAAGCAGGGCTAC	laProAlaLeuAlaLeuP CCCCTGCCCTGGGATTGC	aProGluHisGlnLys	AlaAlaProLeuTyrp 	LeuGlyThrAlaGlyP CTAGGGACGGCAGGCT	rValValGlnIlePr ::: TGTGATGGGGCAGCC	/rSerLeuArgGly ::: ATCTTCTAAAAGAG	laSerAlaLysLys CCTCGGCCAAGAAA	LeuGluGlyThrLysAl ::: ::: CAACAAGGTACGCGGGC	lnTyrValAspA AGTATGTAGATG	
<pre>spLeuThrAspIleP 6 </pre>	ThrHisAspCysHi 6	laLeuAsnPro CCTAAACCCA	SerLeuL ::: GCTCTGC	AsnIleValArgGlnPr ::: ::: GCACTAGTTAAGCAACC	pLysLeuThrLeuGlyGln AAGCTCACCATGGGACAG	SLeuLySAlaIleA ::: ::! CCTACGGATGGTAG	AlaTyrLeuSerLy GCCTACCTGTCCAA	'alAlaArgGlyVal ::: ACGCCAAAGGTGTC	uProAspValThrL ::: GCCAGACTTGACTA	RAlaPheAspAlaIl :::::: GCCTACCAAGAGAT	ProLeuThrLysGlu	heCysArgLeuTrpI TCTGTCGCCTCTGGA	oAlaProThrThrAl ::: TACTCCGAAGACCCC	GlyGlnArgTrpLeu 	AlaGlnIleCysArgA GCCCAAATTTGCCAGA	aLeuLeuGluLe CCTGTTACAAACCCT	spLeuLeuAlaGly ACTTACTGCTGGCCGCC	::
531	514 8514	597 3561	582 3611	565 3661	548 3711	532 3761	515 3811	498 3861	482 3911	465 3961	448 4011	432 4061	415 4111	398 4161	382 4211	365 4261	348 4311	4361

2687 901 2637	868 2737 885	853 2787	837 2837	820 2887	803 2934	792 2984	781 3014	764 3063	748 : 3113 :	731 s 1 3163 A	714 a 3213 i	698 I 3263 G	681 e 3313 T	664 r 3363 A	648 V 3413 C	631 r 3463 c	3513 T
AATGCC. sProGl:: acccgg	GlyV : CGAA	uGlnGln ;;; AAAGGCT	GLUTYTV : GAACTAT	hrCysTy :: AGTGTTG	pTrpGln ::: CATAAAA	GAAAATT	: F	rArgGly : AAGGGGC	LeuAlaI ::: CTTAGCA	nLysGl :: TAAGGA	alleTyr AATATAT	leTyrTh :: TTTACAC	uMetAla ::: GATAGCG	IleTrpA ::: GTCTGGG	alGluGl AAGAGGG	oLeuThr TCTCCCA	GACATCT
aGCAAGT AGCAAGT yAlaHis	lalaas : :GCTCAA	LeuVal ::: CTTCTA	alGlnG ::::: TAGATT	Thrse::: :::: GGTTTA	GluIle :::::: GATCTG	ica la	· · ·	AsnGlnM ::: AACAGGA	leileHi TAATTCA	uGluIle : .CGAGATC	LysGlnA ::::: AGAAGGC	nrAspSe CGATAG	LeuThr CTCACC	lasers :::: CCAAAG	yLysAr ::: GCAGCG	GlyGlu GACGCT	TGGCTG
CTGCCGT CTGCCGT	SerVa ::::: GACAT	ArgThrS ;;; ;GAAAGGA	lnIleHi ::: TTCTTCA	TyrGly CAGGG	ysLysI : CTAAAC	oGlu CTAT	IleIle	etAlaA TGGCCG	sCysPr TTGCCC	LeuSerl	rgGlyLe GCGGGTT	rArgTyr CCGTTAT	GlnAlaL CAAGCCT	erLeuPr :: CACTGCC	gMetAla CAAGGCC	alLeuT ACCACA	AAGCCCAC
: CAAAC alasp :: TTGAI	ValLy ::::: ACTGA	er :: ACTACT	isArgLeu ::: ATCAATTG	LysGluI : AAGCCTG	leAspGl :: TAGGGGC	oArgArg :::::: TCATGAA	GluThrP GAAACTC	spArgVa ::::: ACCAAGC	oGlyHis GGGACAT	LeuLeuG : CTACTGA	uLeuTh GCTCAC	AlaPhe GCTTTT	euArgI :::: TAAAAA	oglugly Agccggg	GlyAlaA GGAGCAG	hrTrpPh :: CCTGGTA	CGGAACT
GACT	ECYSV TGCC	ProTy GTCCTTA	ThrHis	leLeuP :::: TAATGC	nPheSe CACTTA	CATTTTC	roLys ::: CAGAGAC	lAlaLys : ::: GGCCCGA	GlnLysA : CAGAAGG	lualaLe :: AGGCTCT	rSerAlaG ATCAGAAG	AlaThrA GCCACTG	euAlaGl :: TGGCAGA	ThrSer	lavalv : CAGTAA	eThrAs : CACAGA	AGACCAG
AGAGTTC AGAGTTC UValLys	alProC ArgLeu	YrHisVal :::::: ATTACATG	LeuGlyT	roHisLy :: CTGATCA	rGluThrP ;;; TGACGATG	lnTyrT :: ACTATA	TTCCAC	GlnAla :::::: GAAGTA	laLysA ::::: GAAACC	uHisLeu CTTCCTG	GlyArgG ::: GGAAAAG	LaHisVa :: CCCATAT	uGlyLys AGGTAAG	AlaGlnL : GCCCAAA	alAspGl ;; CCACCGA	pGlyser TGGGAGC	SATCTTAC
GAGGGC ProAla	sGlnLe TGCACA	LeuArg ::: CTGAAC	hrLy ICTC	ysGluGly :: AATTCACC	ProGluG ::: GCAAAG.	hrLeuGl ::: CGGTGAC	ACTTCTG	AlaGlnA GCCACTA	pLeuIl CGCGGA	ProLys CCCAAA	luIleI AAATC <i>I</i>	lHisGl : TCACGG	SerIle ::::: AAGCTG	ysalag :: gagcTg	lyThrArg ::: agaccgag	SerTyrV ::::	CGGACCA
ACCG Lyst CTGT	uVal GGTC	LeuP	SHISLE	Leu ::: TTT	lyT	UAS -	ATA	lav GA.	3.5 3.5 3.5	Arg AGA	ysa AAA	yAl AGA	Asn (luL 6	JTh 6	7al 6	iGC 3
2638 918 2588	884 2688 901		853 2788	836 2838	820 2888	803 2935	791 2985	781 3015	764 3064	747 3114	731 3164	714 3214	697 3264	581 3314	564 8364	547 8414	3464

11; 17;	80 1- 0	n i	113 194	111 199	110 204	108 208	106 213	105 218	103 223	101 ₁ 228	100: 233:	985 2387	968 2437	951 2487	935 2537	918 2587
	161ProProProAspSerGlyTrpArgAlaGluLysThrGluAsnProLeu	148 eProThrTrpIleHisAlaSerHisValLysProAla		15 alTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLySGly 1	01 yAspLeuGlnValProHisArgPheGlnValGlyAspSerV 1 ::: :::	85 TrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGlyGl 1 ::::::::::: ::: :::							68 SpAsnGlyProAlaPheValAlaGlnValSerGlnGlyLeuAlaLySIle 98	51 eLeuGluGluIlePheProArgPheGlyIleProLysValIleGlySerA 96 :		
	9 7	160 841	148 891	.131	115 991	101)84)88)68 38	.88	34	18	01 38	88	38	1 88	4 38

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-011-745-3

seq_documentation_block:
; Sequence 3, Application US/09011745

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alignment_scores:
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APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: DCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-011-745-3 from: 1 to: 7308
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                                                      3584 CAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCT 3633
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GENERAL INFORMATION:
                                                                                                                                                                 3534 GCAAGTGTTGACCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCT 3583
                                                                                                                                                                                                                                                                            3484 CACTTTGAGGGATCAGGAGCTCAGGTTATGGGACCAATGGGGCAGCCCCT 3533
                                                                                                                                                                                                                                                                                                                                                                                       3434 CCTATCCTCTGTTAGGAAGAGATTTGCTGACTAAAACTAAAAGCCCAAATC 3483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3384 TCTAGCTACCGGTAAGGTCACCCACTCTTTCCTCCATGTACCAGACTGTC 3433
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NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3284 TGCTGACCCAAAATCCTGGACCCCTAAGTGATAAGTCTGCCTGGGTCCAA 3333
149 GlnAlaTrpAlaGluThrAlaGlyMetGlyLeuAlaLysGlnValProPr 165
                                                                                                     133 lnValLysProAspGlnAspIleGlnSer...TrpLeuGluGlnPhePro 148
                                                                                                                                                                                                                     116 eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3234 CGGGGGCAACCCGTCACCTTCCTGGTAGATACTGGGGCCCAACACTCCG 328:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Portion OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                       84 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 7308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 lGluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                                                                                                                                                                   SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
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4484 TCCCTGGGTTTGCAGAAATGGCAGCCCCCTTGTACCCTCTCACCAAAACG 4533
                                                                                                                                                   4384 ACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCGAAGACCCC 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         4284 AGGGAACCTCGGGTATCGGGCCTCGGCCAAGGAAAGCCCCAAATTTGCCAGA 4333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4234 ACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4184 ACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCC 4233
449 LysGlyGlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaIl 465
                                                                                              432 leProGlyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGlu 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4134 CCTGTTTGATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGC 4183
                                                                                                                                                                                                                                                                                      399 ThrGluAlaArgLysLysThrValValGlnIleProAlaProThrThrAl 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 AlaThrLysGlnAspCysLeuGluGlyThrLysAlaLeuLeuGluLe 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 spLeuArgGluValAsnLysArgValGlnAspIleHisProThrValPro 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 oLeuLeuProValArgLysProGlyThrAsnAspTyrArgProValGlnA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 LeuIleGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrPr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 yrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 oGlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnT 182
                                                                                                                                                                                                                                                                                                                                                                                       rgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeu 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4283
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731 snL 5381 ATA 748 Leu	::: 5281 GTT 714 aIl 5331 AAT	ਦਿ ਉ: E	664 rIl : 5181 AAT	648 Val 5131 CAA	631 roL 5081 ccc	614 sGln ::: 5031 TGAT	598 Alar 1984 GCTA	582 euLe 4934 TTTT	565 oPro 4884 CCCC	549 AsnI : 4834 CCAC	532 laAl 4784 CAGC	515 sLys 4734 AAAG	499 LeuT 4684 CTAA	482 ysPr 4634 AGCC	465 eLys 4584 CAAG	4534 GGGAC
veGluGluT	TATACTGAT TATACTGAT eTyrLysG1 :::::	etAlaLeuT :: TAGCACTCA	eTrpAlaSe: :: CTGGGCTAA	GluGlyLys ::: GAGGGACAG	euThrGlyGl TCCCAGACGC	nLeuLeuIleG :::: TATCCTGGCCG	FhrLeuLeuP ACGCTGCTCC	uThre	AspargTrp GACCGCTGC	leThrValI :::::::: TAGTCATTC	aValAlaIl ::: :: CATTGCCGT	LeuAspPro CTAGACCCA	hrGlnThrLeu cgcaaaaactg	OPheThrLeuT	LysalaLeuL ::: CaagCTCTTC	TCTGTTI
leLeuSerL	AGCCGTTATG AGCCGTTATG AATGG1yLeu :	rGlnAlaL CCAGGCCC	rSerLeuPro :::: AGCCCTGCCA	ArgMetAlaG CGTAAGGCGG	luValLeuThr:	luGluThr AAGCCCAC	roGluGluT CACTGC	luArgValThr :: ;ACCGGGTCCAG	MetThrAsn ::::: CTTTCCAAC	leAlaProH :: TGGCCCCCC	eLeuValLy: : ::: ACTGACAAA	ValAlaSer(::: GTAGCAGCT(GlyProT GGACCTT	uTyrValAsp ::: CTTTGTCGAC	LeuSerAlaP ::: CTAACTGCCC	AATTGGGGCCC
euLeuGluAl	CTTTTGCT LeuThrSe	uArgLeu¤ :::::: AAAGATGG	oGluGlyThr \GCCGGGACA	lyAlaAla GAGCTGCG	rTrpPheThr :::: CTGGTACACG	GlyValArg ::: GGAACCCGA	hrAspGluP ::: CTGAGGAAG	PheAlaPr ::: TTCGGACC	AlaargMet GCCCGGATG	isAlaLeuG ::: ATGCAGTAG	SASPAlaAS GGATGCAGG	GlyTrpProV GGGTGGCCCC	rpArgArgPr gGCGTCGGCC	oGluArgLys :::::: GAGAAGCAG	ProAlaLeuA : CAGCCCTGG	AGACCAAC
laLeuHisLe	CTGCCCAT CTGCCCAT AlaGlyAr	GluGlyL SAAGGTA	SerAlaGln \TCCGCTCAG	ValValAspG ::: GTGACCACCG	rAspGlySe GGATGGAAG	LysaspLeuT CCCGACCTAA	oValThrH ;;; GCTGCAAC	oProAlaAl ::: GGTGGTAGC	ThrHisTyr ACTCACTAT	luAsnIleV ::: AGGCACTAG	pLysLeuTh: CAAGCTAAC	ValCysLeuL : CTTGCCTAC	COVALALATY GGTGGCCTA	3GlyValAla 3GGCTACGCC	\laLeuProA ::: :::GGTTGCCAG	AAAAGGCCT
euProLysAr 	::: TCCATGGA GluIleLy 	SerIleAs ::::: AAGCTAAA	LysAlaGlu ::: CGGGCTGA&	lyThrArgT :::: AGACCGAGG	rSerTyrVa CAGTCTCTT	hraspīle :GGACCAG	isAspCysH ::: ACAACTGCC	aLeuAsnPro CCTGAACCCG	GlnSerLeuL ::: CAGGCCTTGC	alArgGlnPr ::: TCAAACAACC	rLeuGlyGln ::: CATGGGACAG	LysAlaIleA ::: :: :: CGGATGGTAG	rLeuSerLy ACCTGTCCAA	AArgGlyVal ::: CAAAGGTGTC	\spValThrL ::: }ATTTGACTA	ATCAAGAAAT
g 747	GA 5330 SA 731 AA 5380	n 697 5280 714	L 681 C 5230	h 664 : T 5180	1 647 : A 5130	P 631 C 5080	1 614 T 5030	597 1 3 4983	582	4883	548	532	515 4733	498 4683	482	4583

1034 LeuP : 6304 CTGT	1017 euTh 6254 TAAC	1000 rGly 6204 AGGC	984 IleI ::: 6154 CTGT	967 erAs :: 6104 CTGA	950 sile ::: 6054 GCTA	934 Valg ::: 6004 ATAG	917 ysTyr 5954 TGTAT	900 rHis ::: 5904 TCGG	884 ValA 5854 GTCA	867 euPro 5804 GGGAT	852 sLeuG :::: 5754 AATGA	836 LeuGlu ::: 5704 TTTGAA	819 lyThr 5660 ATTGG	803 pTrpG : 5610 TATAA	793 5560 GAAAA	781 alAsn 5524	764 rargG : 5481 Tagag
heargValarga :: ::: accgagcccgca	rThrGluThrGl GCTTGCAACTGG	GlnValGluArg CAGGTAGAAAGA	LeuGlyIleAspT TTGGGGATTGATT	pasnGlyProal CaargggCCTGC	LeuGluGluIle CTAGAGGAGATC	luAlaTyrProT] ::: AAGCCTTCCCAA	GlyAsnLysTy GGCTATAAATA	ProGlyAlaHisT ::: CCCGGCACTCATT	snālaāsnProSe ::: ACGCCāGCāāGTC	Gly\	GlnGlnLeuValA ::: :::: AAGGCTCTCCTAG	luTyrValGlnGl ::::: AATTATTAGACTT	rCysTyrThrSer GGTCTAC	lnGluIleLysL ::::::: AGGACCTAACCA	TTCATCACCCTAC	LeuLeuProIle	lyAsnGlnMetA ::: GCAACCGGATGG
.snThrProGlyG ACACGCCGGGCC	YIleAsnAspTr ::: CTCTAGAGACTG	MetAsnArgThr ATGAATAGAACC	rpLysLeuHisC GGAAATTACATT	apheValAlaGl ::::: CTTCGTCTCCAA	PheProArgPhe TTCCCCAGGTTC	hrLysLysGluT CCAAGAAAGAAA	rLeuLeuValPh TCTTCTAGTTTT	rpGluValAsp ::: GGGAGATCGAT	rArgIleProP ::: TGCCGTTAAAC	erValValLy ::::::::: ATATCACTGA	rgThrs :: ;AGAGAAGCCACA	nIleHisArgLe ::: ::: TCTTCATCAGCT	TyrGlyLysGlu CAAGGAAAACCT	ysIleAspGln. ::: AGTTGGGGGGCCA	.ProGluProAr ;;; CACCTCAGAACA	IleGluThrPro	laAspArgValA ::::: CTGACCAAGCGG
lnPheGlyLeu CCCATGGCCTC	pMetAlaLeuI ::: GGTGCTCCTAC	IleLysGluTh ATCAAGGAGAC	ysalaTyrArg GTGCATACAGA	nValSerGlnG : :GGTGAGTCAGA	:GlyIleProLys ::: ::: :GGCATGCCTCAG	hrserThrValV ::: CCGCCAAGGTCG	eValAspThrPh ::: TATAGATACCTT	PheThrGluVal ::: TTCACCGAGATA	roGlyLysArgL : AGGGAACTAGGG	SHisCysValPr : GACCTGCAAAGC	erProTyrHis ::: GTCCCTACTAC	uThrHisLeuG GACTCACCTCA	IleLeuProHi :::::: GTGATGCCTGA	PheSerGlu :::::::: TTTATGATAA	gArgGlnTyrT : :: .TTTTCATTACA	Lysala ::: GACACCTCTAC	\laLysGlnAlaA :::::: CCCGAAAGGCAG
ThrProTyrGl ACCCCATATGA	.euProPheVal ::::: !TCCCCTTAGCC	rLeuThrLysL TTTAACTAAAT	ProGlnSerSe	lyLeuAlaLys ::: CAGTGGCCGAT	SValIleGlyS : ::: : GGTATTGGGAA	ValAlaLysLy ::: STAACCAAGAA	heserGlyTrp TTTCTGGCTGG	LysProAlaL ::: \AAGCCCGGAT	JeuArgGlySe ::: TCCGCGGGCA	coCysGlnLeu !TTGTGCACAA	ValLeuArgL ::: ::: :ATGCTGAACC	LyThrLysHi :: :: GCTTCTCAAA	SLYSGLUGLY ::: CCAGTTTACT	ThrProGluG ::: ACAAAGAAGT	hrLeuGluAs ::: CAGTGACTGA	CCTCCTCATA	laGlnAlaV CC
1050 6353	1033 6303	1017 6253	1000 6203	983 6153		950 6053	933 6003	917 5953	900 5903	883 5853	867 5803	852 5753	835 5703	819 5659	803 5609	792 5559	781 5523

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TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER APPLICATION NUMBER: GB9517263.1
UNMBER: OF SEQ ID NOS: 29
SOFTWARE: PATENTIA VOR: 29
SOFTWARE: PATENTIA VOR: 2.0
SEQ ID NO 4
LENGTH: 7308
                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                          US-09-011-745-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-011-745-4
                                                US-09-171-553B-5 x US-09-011-745-4
                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Portion of OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6751 TTAAAAATAAGGTTAACCCGCGAGGCCCCC 6780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6701 GTGGACCATCCTCTAGACTGACATGGCGCGTTCAACGCTCTCAAAACCCC 6750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1163 .....ProAspSer......GlyTrpArgAlaGluLysThrGluAsnPro 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1176 LeuLysLeuArgLeuHisArgLeuValPro 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6651 CATCGCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGG 6700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1147 yIleProThrTrpIleHisAlaSerHisValLysProAlaProPro.... 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1131 GlyProTyrLeuValLeuLeuThrThrProThrAlaValLysValGluGl 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1114 erValTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLys 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6551 CAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGGAAA 6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6502 GAACAACTGGACCGACCGGTGGTACCTCACCCTTACCGAGTCGGCGACA 6550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1100 yGlyAspLeuGln......ValProHisArgPheGlnValGlyAspS 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6454 TACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAA.. 6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1084 GluTrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGl 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6404 TGACAAGAGTTACTAACAGCCCCTCTCTCCCAAGCTCACTTACAGGCTCTC 6453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6354 GATCTTATATGGGGCACCCCCCCCCCTTGTAAACTTCCCTGACCCTGACA 6403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1067 erAlaAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeu 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1050 uLeuLeuTyrGlyGlyProProProLeuAlaGluIleAlaPheAlaHisS 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACCTTACACAGTCCTGCTGACCACCCCCCACCGCCCTCAAAGTAGACGG 6650
                                                                                                                                 Quality: 3967.00
Ratio: 3.959
milarity: 82.810
                                                                                                                           Percent Identity: 62.479
                                                                                                                                                                                     Length:
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Align seg 1/1 to: US-09-011-745-4 from: 1 to: 7308
                                                                                3984 TGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCA 4033
                                                                                                                                                                                                                                                                                               3884 ATCTGAGAGAAGTCAACAAGCGGGTGGAAGACATCCACCCCACCGTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                3834 CCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3784 CTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCC 3833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3734 ACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGA
282 erGlnProLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThr 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3684 TCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAAT 3733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3634 CAGGCCTGGGCGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                  215 oLeuLeuProValArgLysProGlyThrAsnAspTyrArgProValGlnA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 LeuIleGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrPr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 yrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArg 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3584 CAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCT 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3534 GCAAGTGTTGACCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCT 3583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3484 CACTTTGAGGGATCAGGAGCTCAGGTTATGGGACCAATGGGGGCAGCCCCT 3533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3384 TCTAGCTACCGGTAAGGTCACCCACTCTTTCCTCCATGTACCAGACTGTC 3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3334 GGGGCTACTGGAGGAAAGCGGTATCGCTGGACCACGGATCGCAAAGTACA 3383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 GlnAlaTrpAlaGluThrAlaGlyMetGlyLeuAlaLySGlnValProPr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3284 TGCTGACCCAAAATCCTGGACCCCTAAGTGATAAGTCTGCCTGGGTCCAA 3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3184 GGAGGTCAGGGTCAGGAGCCCCCCCCTGAACCCAGGATAACCCTCAAAGT 3233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 lnValLysProAspGlnAspIleGlnSer...TrpLeuGluGlnPhePro 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 pLeuGlyValGlyArgValThrHisSerPheLeuValI1eProGluCysP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                      AACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACAC
                                                                                                           rValLeuAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrS 282
                                                                                                                                                                                                                                        AsnProTyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrTh 265
                                                                                                                                                                                                                                                                                                                                   spLeuArgGluValAsnLysArgValGlnAspIleHisProThrValPro 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oGlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnT 182
                                                                                                                                                                                            3983
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582 eu 4934 TT	565 OP 1 4884 CC	549 As 4834 CC	532 la 4784 CA	515 sL 4734 AA	499 Le 4684 CT	482 ys 4634 AG	465 eL 4584 CA	449 Ly 4534 GG	432 le 11 4484 TC	415 aLy :: 4434 TCG	399 Thr 4384 ACT	382 rg :: 4334 AA	365 us : 4284 AG	349 Al :: 4234 AC	332 is 4184 AC	315 rI : 4134 CC	299 Gly 4084 GGA	4034 GTC
LeuThr	roaspargT CCGACCGCT	nIleThrVa ::::::: ACTAGTCAT	aAlaValAla :::: !AGCCATTGCC	ysLeuAspP AGCTAGACC	uThrGlnThrLe: AACGCAAAAACT	ProPheThr CCCTTTGAA	ysLysAlaL ::: AGCAAGCTC	sGlyGlyPhe GACTCTGTTT	ProGlyPhe CCTGGGTTT	SGlnValA : ::: ACAACTAA	GluAlaAr GAGGCCAC	GluValThr' ::: CAGGTCAAG	erAspLeuG: :::: GGAACCTCG	aThrLysGli ::::::: TTCTGAGCT	ProGlnValT ::::: CCAGACTTGA	lePheAspGl :: TGTTTGATGA	GlnLeuThr	AGCCTCTCT
GluArgVal ::: GACCGGGTC	rpMetThrA ::::: GGCTTTCCA	llleAlaPr :::: TCTGGCCCC	IleLeuVal ::: ::: GTACTGAC <i>F</i>	roValAlaSe :: CAGTAGCAGC	rLeuGlyPro ACTGGGACCT	hrLeuTyrValA ::: ;AACTCTTTGTCG	leuLeuSerAl ::: CTTCTAACTGC	eSerTrpAla ::: ::: TAATTGGGGC	AlaThrLeuA ::: GCAGAAATGG	rgGluPheLe GGGAGTTCCT	gLysLysThr ::: ;AAAAGAGACT	TyrLeuGlyT TATCTGGGGT	lyTyrArgAl GTATCGGGC	.nAspCysLeuG : AGACTGCCAAC	hrLeuLeuG rccrgcrac	uAlaLeuHi GGCACTGCA	TrpThrArg TGGACCAG <i>P</i>	TCGCCTTTG
ThrPheAlaP ::: CAGTTCGGAC	snAlaArgMe ACGCCCGGAT	OHISALALEU ::: CCATGCAGTA	Lysaspālaā \AAGGATGCAG	rGlyTrpPr : TGGGTGGCC	TrpArgArg rescerces	spGluArgI :::: ACGAGAAGC	aProAlaLe CCCAGCCCI	ProGluHis	laAlaProLe CAGCCCCCTT	uGlyThrAl AGGGACGGC	ValValGln ::: GTGATGGGG	yrSerLeu? : ATCTTCTA?	aSerAlaLy:	GluGlyThrI ::: : ::AAGGTACTC	lnTyrValAs AGTACGTGGA	sArgAspLeu CAGAGACCT1	LeuProGlnG	AGTGGAGAGI
roProAlaA ::: CGGTGGTAG	tThrHisTy GACTCACTA	GluAsnIleV ::: GAGGCACTAG	SPLYSLeuTh GCAAGCTAAC	OValCysLeuL : CCCTTGCCTAC	ProValAlaT	ysGlyValAla :: !AGGGCTACGCC	uAlaLeuPro ::: GGGGTTGCCA	GlnLysAlaP : CAAAAGGCCT	euTyrProLe TGTACCCTCT	aGlyPheCys AGGCTTCTGT		rgGlyGlyGl ::: raagagggTC#	SLYSAlaGln GAAAGCCCAA	ysAlaLeuI :: :GGGCCCTGT	PASPLeuLe TGACTTACT	uAlaAsnPhe ::: 'AGCAGACTTC	lyPheLysA GTTTCAAAA	ATCCAGAGATG
laLeuAsnPr CCCTGAACCC	rGlnSerLeui ::: NTCAGGCCTTG	alArgGlnP ::: CAAACAAC	nrLeuGlyGln ::: CATGGGACAG	ıLysAlaIleA ::: \CGGATGGTAG	TyrLeuSerLy ACCTGTCCAA	laArgGlyVal ::: CAAAGGTGTC	DASPValThrL ::: \GATTTGACTA	heAspAlaIl ::::: CATCAAGAAAT	euThrLysGlu CACCAAAACG	ArgLeuTrpI CGCCTCTGGA	roThrThrAl	lnArgTrpLeu AGAGATGGCTG	IleCysArgA :::: ATTTGCCAGA	euLeuGluLe TACAAACCCT	uLeuAlaGly	ArgIleGlnH CGGATCCAGC	snSerProTh ACAGTCCCAC	GGGAATCTCA
o 597 G 4983	E 582 C 4933	r 565 4883	n 548 4833	A 532 4783	y 515 h A 4733	1 498 1 4683	482 4 4633	L 465 L 4583	448	432	415	1 398	4333	4283	348	332 4183	315 4133	4083

588	867 euProGlyValAlaAspSerValValLysHiSCYsValProCysGlnLeu ::::::::::::::::::::::::::::::::::::	л
	852 SLeuGlnGlnLeuValArgThrSerProTyrHisValLe ::::::	5
857 57	836 LeuGluTyrValGinGinIleHisArgLeuThrHisLeuGlyThrLysHi::: ::: ::: :::	ران د
570	819 lyThrCysTyrThrSerTyrGlyLysGluIleLeuProHisLysGluGly	Uī
819 565	803 pTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluG :::::::: ::: :::::::	u
560	793	رب ر
555	euLeuProIleIleGluThrProLysAla	UTI
ப் ∞	AlaGlnAlaV GCC	ر. د
764 548	748 LeualaIleIleHisCysProGlyHisGlnLysAlaLysAspLeuIleSe :::	ъ
747 543	731 snLysGluGluIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArg	υı
731 538	714 alleTyrLysGlnArgGlyLeuLeuThrSeralaGlyArgGluIleLysA	ن. ن
714 533	698 IleTyrThraspSerargTyralaPhealaThralaHisValHisGlyAl :::	បា
697 528	681 eumetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsn (u
681 523	664 rIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluL (υī
664 518	648 ValGluGlyLysArgMetAlaGlyAlaAlaValValAspGlyThrArgTh (5
647 513	631 roLeuThrGlyGluValLeuThrTrpPheThrAspGlySerSerTyrVal (ربا ن
631 508	614 sGlnieuLeuIleGluGluThrGlyValArgLysAspLeuThrAspIleP (ر ن
614 503	598 AlaThrLeuLeuProGluGluThrAspGluProValThrHisAspCysHi (4.

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6701 GTGGACCATCCTCTAGACTGACATGGCGCGTTCAACGCTCTCAAAACCCC
                                                                                                                                                                       6651 CATCGCAGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGG 6700
                                                                                                                                                                                                                                                                                              6601 GGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGG 6650
1176 LeuLysLeuArgLeuHisArgLeuValPro 1185
                                                                                                                                                                                                             1147 yIleProThrTrpIleHisAlaSerHisValLysProAlaProPro.... 1162
                                                                                                                                                                                                                                                                                                                                                         1131 GlyProTyrLeuValLeuLeuThrThrProThrAlaValLysValGluGl 1147
                                                                                                                                                                                                                                                                                                                                                                                                                    6551 CAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGGAAA 6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1114 erValTyrValArgArgHisArgAlaGlyAsnLeuGluThrArgTrpLys 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6454 TACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAA.. 6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 GluTrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGl 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1034 LeuPheArgValArgAsnThrProGlyGlnPheGlyLeuThrProTyrGl 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6254 TAACGCTTGCAACTGGCTCTAGAGACTGGGTGCTCCTACTCCCCTTAGCC 6303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6104 CTGACAATGGGCCTGCCTTCGTCTCCAAGGTGAGTCAGACAGTGGCCGAT 6153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6004 ATAGAAGCCTTCCCAACCAAGAAAGAAACCGCCAAGGTCGTAACCAAGAA 6053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 984 IleLeuGlyIleAspTrpLysLeuHisCysAlaTyrArgProGlnSerSe 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900 rHisProGlyAlaHisTrpGluValAspPheThrGluValLysProAlaL 917
:::||||||:::|||||||:::||
5904 TCGGCCCGGCACTCATTGGGAGATCGATTTCACCGAGATAAAGCCCGGAT 5953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 ValAsnAlaAsnProSerArgIleProProGlyLysArgLeuArgGlySe 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erAlaAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeu 1083
                                                                                                            .....ProAspSer.....GlyTrpArgAlaGluLysThrGluAsnPro 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACAACTGGACCGACCGGTGGTACCTCACCCTTACCGAGTCGGCGACA 6550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yGlyAspLeuGln......valProHisArgPheGlnValGlyAspS 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCTGACA 6403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uLeuLeuTyrGlyGlyProProProLeuAlaGluIleAlaPheAlaHisS 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTACCGAGCCCGCAACACGCCGGGCCCCCATGGCCTCACCCCCATATGA 6353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euThrThrGluThrGlyIleAsnAspTrpMetAlaLeuLeuProPheVal 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rGlyGlnValGluArgMetAsnArgThr[leLysGluThrLeuThrLysL 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysTyrGlyAsnLysTyrLeuLeuValPheValAspThrPheSerGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGTTGGGGATTGATTGGAAATTACATTGTGCATACAGACCCCAAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erAspAsnGlyProAlaPheValAlaGlnValSerGlnGlyLeuAlaLys 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTACTAGAGGAGATCTTCCCCAGGTTCGGCATGCCTCAGGTATTGGGAA 6103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGluAlaTyrProThrLysLysGluThrSerThrValValAlaLysLy 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCCAGGTAGAAAGAATGAATAGAACCATCAAGGAGACTTTAACTAAAT 6253
                                                           6750
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CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 7616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-171-553B-5 x US-09-011-745-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Portion of ; OTHER INFORMATION: construct US-09-011-745-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-011-745-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-011-745-2 from: 1 to: 7616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 82.810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                     2495
                                                                                   2645 CACTTTGAGGGATCAGGAGCTCAGGTTATGGGACCAATGGGGCAGCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2395 CGGGGGGCAACCCGTCACCTTCCTGGTAGATACTGGGGGCCCAACACTCCG 2444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2345 GGAGGTCAGGGTCAGGAGCCCCCCCCTGAACCCCAGGATAACCCCTCAAAGT 2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
116 eThrValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6751 TTAAAAATAAGGTTAACCCGCGAGGCCCCC
                                                                                                                                       101 SerPheGlu...GlnGlyArgProGluValSerValAsnAsnLysProIl 116
                                                                                                                                                                                                                              84 roValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnIle 100
                                                                                                                                                                                                                                                                                                                                                               67 pLeuGlyValGlyArgValThrHisSerPheLeuValIleProGluCysP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 alLeuLeuGlnProLeuGlyLysLeuLysGluLysLysSerTrpValMet 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysVa 17
                                                                                                                                                                                              CCTATCCTCTGTTAGGAAGAGATTTGCTGACTAAAACTAAAAGCCCAAATC 2644
                                                                                                                                                                                                                                                                                                           TCTAGCTACCGGTAAGGTCACCCACTCTTTCCTCCATGTACCAGACTGTC 2594
                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGCTACTGGAGGAAAGCGGTATCGCTGGACCACGGATCGCAAAGTACA 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyAlaThrGlyGlnArgGlnTyrProTrpThrThrArgArgThrValAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTGACCCAAAATCCTGGACCCCTAAGTGATAAGTCTGCCTGGGTCCAA 2494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lGluGlyGlnProValGluPheLeuValAspThrGlyAlaGluHisSerV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 3967.00
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432 3644	aLysGinValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpI::: :::	415 3595
415 3594	ThrGluAlaArgLysLysThrValValGlnIleProAlaProThrThrAl	399 3545
398 3544	rgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlyGlnArgTrpLeu:::::	382 3495
382 3494	USERASpLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleCysArgA	365 3445
365 3444	AlaThrLysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuCluLe ::::::::	349 3395
348 3394	isProGlnValThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGly	332 3345
332 3344	rIlePheAspGluAlaLeuHisArgAspLeuAlaAsnPheArgIleGlnH 	315 3295
315 3294	GlyGlnLeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProTh	299 3245
298 3244	erGlnProLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThr	282 3195
282 3194	rValLeuAspLeuLysAspAlaPhePheCysLeuArgLeuHisProThrS	265 3145
265 3144	ASnProTyrAsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrTh	249 3095
248 3094	SpLeuArgGluValAsnLysArgValGlnAspIleHisProThrValPro	232 3045
232 3044	OLEULEUPTOVAlArgLysProGlyThrAsnAspTyrArgProValGlnA	215 2995
215 2994	LeuIleGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrPr :::::: CTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCC	199 2945
198 2944	yrProLeuSerArgGluAlaArgGluGlyTleTrpProHisValGlnArg	182 2895
182 2894	OGINVAlIleGInLeuLysAlaSerAlaThrProValSerValArgGInT :::	165 2845
165 2844	GlnalaTrpAlaGluThrAlaGlyMetGlyLeuAlaLySGlnValProPr 	149 2795
148 2794	InValLysProAspGlnAspIleGlnSerTrpLeuGluGlnPhePro :: ::: ::::: CAAAAGAGCCAGAIGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCT	133 2745
2744	GCAAGTGTTGACCCTAAATATAGAAGATGAGCATCGGCTACATGAGACCT	2695

714 aI 4492 AA	698 I : 4442 G	681 e 1 4392 T	664 r : 4342 A	648 V 4292 C	631 r 1 4242 C	614 sg ; 4192 TG	598 A 4145 G	582 e 4095 T	565 o 4045 C	549 A 3995 C	532 1 3945 C	515 s 3895 A	499 Le 3845 CT	482 ys 3795 AG	465 e 3745 C	449 Ly 3695 GG	432 1 3645 T	
leTyrLysGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysA :::::	leTyrThrAspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAl :: : TTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGA	<pre>uMetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsn ::: </pre>	rIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluL:	alGluGlyLysArgMetAlaGlyAlaAlaValValAspGlyThrArgTh :::	oLeuThrGlyGluValLeuThrTrpPheThrAspGlySerSerTyrVal 	GlnLeuLeuIleGluGluThrGlyValArgLysAspLeuThrAspIleP ::::::	.laThrLeuLeuProGluGluThrAspGluProValThrHisAspCysHi 	uLeuThrGluArgValThrPheAlaProProAlaAlaLeuAsnPro ::: ::: :::	ProAspArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuL :::::	snIleThrYallleAlaProHisAlaLeuGluAsnIleYalArgGlnPr ::::::::::::::::::::::::::::::::::::	aAlaValAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGln ::: ::: ::: AGCCATTGCCGTACTGACAAAGGATGCAAGCAAGCTAACCATGGGACAG	LysLeuAspProValAlaSerGlyTrpProValCysLeuLysAlaIleA :::	euThrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLy	SPTOPheThrLeuTyrValAspGluArgLysGlyValAlaArgGlyVal ::: ::::: :::	LysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrL ::: ::: ::: AGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTA	ysGlyGlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaII ::: ::: :::	eProGlyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGlu CCTGGGTTTGCAGAAATGGCAGCCCCTTGTACCCTCTCACCAAAACG	
731 4541	714 4491	697 4441	681 4391	664 4341	647 4291	631 4241	614 4191	597 4144	582 4094	565 4044	548 3994	532 3944	515 3894	498 3844	482 3794	465 3744	448 3694	

1033	$\verb euThrThrGluThrGlyIleAsnAspTrpMetAlaLeuLeuProPheVal $	1017
1017 5414	TG1yG10Va1G1uArgMetAsnArgThrTleLysG1uThrLeuThrLysL 	5365
ω	TGTTGGGGATTGATTGGAAATTACATTGTGCATACAGACCCCAAAGCTC	5315
1000	eLeuGlyIleAspTrpLysLeuHisCysAlaTyrArgProGlnSerSe :	æ
983 5314	erAspAsnGlyProAlaPheValAlaGlnValSerGlnGlyLeuAlaLys ::: CTGACAATGGGCCTGCCTTCGTCTCCCAAGGTGACTCAGACAGTGGCCGAT	967 5265
967 5264	SIleLeuGluGluIlePheProArgPheGlyIleProLysValIleGlyS :::	950 5215
950 5214	ValGluAlaTyrProThrLysLysGluThrSerThrValValAlaLysLy::: :::	934 5165
933 5164	ysTyrGlyAsnLysTyrLeuLeuValPheValAspThrPheSerGlyTrp :::	917 5115
917 5114	rHisProGlyAlaHisTrpGluValAspPheThrGluValLysProAlaL::: ::: ::: ::: :::	900 5065
900 5064	ValasnalaasnProSerargIleProProGlyLysargLeuArgGlySe ::: 	884 5015
883 5014	euProGlyValAlaAspSerValValLysHisCysValProCysGlnLeu :::::::::::	867 4965
867 4964	SLEUGINGINLEUVAIAIGThrSerProTyrHisValLeuArgL	852 4915
852 4914	LeuGluTyrValGlnGlnIleHisArgLeuThrHisLeuGlyThrLysHi ::: ::: ::: :: ::: TTTGAATTATTAGACTTTCTTCATCAGCTGACTCACCTCAGCTTCTCAAA	836 4865
835 4864	TyThrCysTyrThrSerTyrGlyLysGluIleLeuProHisLysGluGly	819 4821
819 4820	PTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluG ::::::: ::: :::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::	803 4771
803 4770	GAAAATTCATCACCCTACACCTCAGAACATTTTCATTACACAGTGACTGA	793 4721
792 4720	alAsnLe	781 4685
781 4684	rArgGlyAsnGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnAlaV: ::::	764 4642
764 4641	LeualaileTleHisCysProGlyHisGlnLysAlaLysAspLeuIleSe :::	748 4592
747 4591	SnLySGluGluIleLeuSerLeuLeuGluAlaLeuHisLeuProLySArg	731 4542

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1176 5912	1163 5862	1147 5812	1131 5762	1114 5712	1100 5663	1084 5615	1067 5565	1050 5515	1034 5465	5415
LeuLysLeuArgLeuHisArgLeuValPro 1185 :::	ProAspSerGlyTrpArgAlaGluLysThrGluAsnPro 1175	ylleProThrTrpIleHisAlaSerHisValLysProAlaProPro 1162 ::: :::	GlyProTyrLeuValLeuLeuThrThrProThrAlaValLysValGluGl 1147	ervalTyrValArgArgHisArgAlaGlyAsnLeuGluThrargTrpLys 1130 :: :: cAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGGAAA 5761	yGlyAspLeuGlnValProHisArgPheGlnValGlyAspS 1114 ::: :: :::::: :: GAACAACTGGACCGGACCGGTGGTACCTCACCCTTACCGAGTCGGCGACA 5711	GluTrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerGl 1100 ::::::::::: ::: Activation	erAlaAspValLeuLeuSerGlnProLeuPheSerArgLeuLysAlaLeu 1083 :::	uLeuLeuTyrClyGlyProProProLeuAlaGluIleAlaPheAlaHisS 1067 ::: :::	LeuPheArgValArgAsnThrProGlyGlnPheGlyLeuThrProTyrGl 1050	TAACGCTTGCAACTGGCTCTAGAGACTGGGTGCTCCTACTCCCCTTAGCC 5464
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Query length: 656
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Database length: 113238999
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-USER-US09171552_@CGN1_1_158 -NCPU=6 -ICPU=3 -LONGLOG
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         134 rpSerCysValThrSerAsnAspGlyAspTrpLysTrpProIleSerLeu 150
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; TYPE: DNA ; ORGANISM: Porcine retrovirus US-09-111-085-3
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-007-282B-1 + 423.00
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-716-351A-3 + 420.50
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-691-563C-58 + 295.50
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Percent Similarity: 99.240
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APPLICANT: Weiss, Robin A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1011 CTCTAACAATAACTCCCCAGGCCAGTAGTAAACGCCTTATAGACAGCTCG
                                                                                                            1211 ACACCTCCCAACCTAGTCCGTAGTTATGGGTTCTATTGCTGCCCCAGGCAC
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                                                                                                                                                                                                                                                                                                                                                                        67 rGlyValThrValAsnSerThrArgGlyValAlaProArgGlyThrTrpT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AsnProHisArgProLeuSerLeuThrTrpLeuIleIleAspProAspTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 hrLeuThrIleThrProGlnAlaSerSerLysArgLeuIleAspSerSer 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 oLysArgLeuArgIleProLeuSerPheAlaSerIleAlaTrpPheLeuT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetHisProThrLeuSerArgArgHisLeuProThrArgGlyGlyGluPr 17
                                                                                                                                                                                                                                                      rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLysSer 100
                              rGluLysGluLysTyrCysGlyGlySerGlyGluSerPheCysArgArgT 134
                                                                                                                                                                                                                           GGCCTGAACTGCATTTCTGCCTCCGATTGATTAACCCCCGCTGTTAAAAAGC
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AGAGAAAGAGAAATACTGTGGGGGTTCTGGGGGAATCCTTCTGTAGGAGAT 1310
                                                                                                                                                               ThrProProAsnLeuValArgSerTyrGlyPheTyrCysCysProGlyTh 117
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433 leValProArgValTyrTyrHisProGluGluValValLeuAspGluTyr
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                                                    TTCCACCTCAGTCTTCAACCAATCCAAAGATTTCTGTGTCATGGTCCAAA
                                                                                                                                       ProGlyTyrAsnArgTrpTrpAlaCysAsnThrGlyLeuThrProCysVa 416
                                                                    lSerThrSerValPheAsnGlnSerLysAspPheCysValMetValGlnI 433
                                                                                                                       CCTGGTTATAACAGGTGGTGGGCATGCAATACTGGGTTAACCCCCTGTGT
                                                                                                                                                                                                           ysTyrSerThrValValTyrGluGlnAlaSerGluAsnGlnTyrLeuVal
                                                                                                                                                                                                                                                                                                                                               AsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeuThrGluValSe 366
                                                                                                                                                                                                                                                                                                                                                                                                   ATGAGGGGATGGCTAAAGAAGGAAAATTCAATGTGACCAAAGAGCATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                     yrGluGlyMetAlaLysGluArgLysPheAsnValThrLysGluHisArg 349
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                                                                                                                                                                                           GCTATAGTACTGTGGTTTATGAGCAGGCCTCAGAAAATCAGTATTTAGTA
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                                                           Sequence 1, Application US/09111085
Patent No. 610034
GENERAL INFORMATION:
APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral TITLE OF INVENTION: specific sequences FILE REFERENCE: 4238/75168
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                                                                                                                                                                                                                                                                                                                                                              633 alSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeuLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2211 TCGTCCCCGAGTGTACTACCATCCTGAGGAAGTGGTCCTTGATGAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 lyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 uGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnArgArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rValGlyProCysLeuIleAsnArgPheValAlaPheValArgGluArgV 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAGGGGTGGTTTGAAGGATGGTTCAACAGGTCTCCTTGGATGACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluGluCysCysPheTyrValAspHisSerGlyAlaIleArgAspSerMe
                                                                                                                                                                                                                                                                                               SerGlnGlyGluThrAspLeu 656
                                                                                                                                                                                                                                                                                                                                      TGAGTGCAGTCCAGATCATGGTACTTAGGCAACAGTACCAAGGCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCAAGCTTAGAGAAAGGTTAGAGAGGCGTCGAAGGGAAAGAGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTGGGCCTTGCTTAATTAATAGGTTTGTTTGCCTTTGTTAGAGAACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spGlnGlyTrpPheGluGlyTrpPheAsnArgSerProTrpMetThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArgGluAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValSerAsnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laLeuILeThrGlyProGlnGlnLeuGluLySGlyLeuGlyGluLeuHis 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTAATGCTCGGATTAGGGACGGCCGTTGGCGTAGGAACAGGGACAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrGlyThrAlaA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAGAGTCCCTGACTTCTTTGTCTGAAGTGGTTCTACAGAACCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTGATCACAGGACCACAGCAGCTAGAGAAAGGACTTGGTGAGCTACAT
                                       subtypes based upon
                                                                                                                                                                                                                                                                                                                                        2860
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CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION UNMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1

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; TYPE: DNA; ORGANISM: Porcine retrovirus US-09-111-085-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
us-09-171-553B-6 x us-09-111-085-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 2594.50
Ratio: 4.420
Percent Similarity: 86.324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-111-085-1 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 ATGCATCCCACGTTAAGCCGGCGCCCCCCCCGATTCGGGGTGGAAAGCC
                                                                                                                                                                                                                                                                                                                   561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 oGly...ThrGluLysGluLysTyrCysGlyGlySerGlyGluSerPheC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 CAGGCCACACCCCCGGATGTACTCCGTGCTTACGGGTTTTACGTTTGCCC 560
                                                                                                                                                                                                                       170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 GGCCTGAATTATATGTCTGCCTTCGATCAGTAATCCCTGGTCTCAATGAC 510
                                                                                                                                    182 LeuAspTyrLeuLysIleSerPheThrGlu..ArgLysThrGlyLysTyr 197
                                                                                                                                                                                                                                                      711 TTATAATCAATTTAATTATGGCCATGGGAGATGGAAAGATTGGCAACAGC 760
214 lyGlyGlyAla.......GlySerThrLeuThrIleArgLeuArgIle 227
                                                                                                                    811 CTAGATTACTTAAAAATAAGTTTCACTGAAAAAGGAAAACAAGAAAATAT 860
                                                                                                                                                                                    761 GGGTACAAAAAGATGTACGAAATAAGCAAATAAGCTGTCATTCGTTAGAC 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 LysSerThrProProAsnLeuValArgSerTyrGlyPheTyrCysCysPr 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetHisProThrLeuSerArgArgHisLeuProThrArgGlyGlyGluPr 17
                                                                                                                                                                                                         ysLeuTyrLysAspLys......SerCysSerProSerAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaVal..... 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGACCCCCAAATAATGAAGAATATTGTGGAAATCCTCAGGATTTCTTTT 610
                                                                                                                                                                                                                                                                          TCAAAAGTGGGTAAATGGTATATCTTGGGGAATAGTGTAC.....TATG 904
                                                                       SerLysValAspLysTrpTyrGluLeuGlyAsnSer.PheLeuLeuTyrG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 680
Gaps: 11
Percent Identity: 73.088
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905	GAGGCTCTGGGAGAAAGAAAGGATCTGTTCTGACTATTCGCCTCAGAATA 9	54
Ñ	1 yThrGluProProValAlaMetGlyProAspLysValLeuAl 2	-4
Ū	AAACTCAGATGGAACCTCCGGTTGCTATAGAGCCAAATAAGGGTTAGC 2	61
2 44 1005	OHISASHLEUFIOVALFIOS 2	
261	hrSerLeuArgProAspIleThrGlnProProSerAsnSerThr 2	7
1033	AGGCCATCTCCTAACCCCTCTGATTACAATACAA	890
278	hrGlyLeuIleProThrAsnThrProArgAsnSerProGlyValProVa 2 :: ::: :::: :: cmgCamcAcmcAcTAcT	94 103
0	rvsThrGlvGlnArdIeuDheSerTeuTleGlnGlvAlaPheGlnAlaI 3	
1104	AGCCTCATCCAGGGAGCTTTTCAAGCTC 1	
311 1154	leAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSer 3 :: TTAACTCCACGACTCCAGAGGCTACCTCTTGTTGGCTTTGCTTGC	27 203
328 1204	SerglyProProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnVa 3	44 253
344 1254	ThrLysGluHisargAsnGlnCysThrTrpGlySerArgAsnLysLeuT 3	61 303
361 1304	hrLeuThrGluValSerGlyLysGlyThrCysIleGlyLysAlaProPro 3	77 353
378 1354	SerHisGlnHisLeuCysTyrSerThrValValTyrGluGlnAlaSerGl 3	94 403
394 1404	uAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCysAsnThrG 4 :::	11 453
411 1454	lyLeuThrProCysValSerThrSerValPheAsnGlnSerLysAspPhe 4	503
428 1504	CysvalMetValGinIleValProArgValTyrTyrHisProGluGluVa 4	U1 42
444 1554	1ValleuAspGluTyrAspTyrArgTyrAsnArgProLysArgGluProV 4 :	6 6
461 1604	alSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyVal 4 ::	177 L653
478 1654	GlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLySGl	494 1703
494 1704	yLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysG	511 1753
511	luSerValSerAsnLeuGluGluSerLeuThrSerLeuSerGluValVal:::	527 1803

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seq_documentation_block:
    Sequence 2, Application US/08766528
    Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-2
                                                                                  TELEFAX: (617)227-594: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
              SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2154 GTACCAAGGCCTTCTGAGCCAAGGAGAAACTGACCTC 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2104 TTTGTTAGAGAACGAGTGAGTGCAGTCCAGATCATGGTACTTAGGCAACA 2153
                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
FORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2054 TGCTCCTGTTACTTACAGTTGGGCCTTGCTTAATTAATAGGTTTGTTGCC 2103
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                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611 euLeuLeuLeuThrValGlyProCysLeuIleAsnArgPheValAla 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 rProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLeuValValL 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 laIleArgAspSerMetAsnLysLeuArgLysLysLeuGluArgArgArg 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 uCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHisSerGlyA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
CITY: I
STRANDEDNESS:
                                                                                                                                                                            REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheValArgGluArgValSerAlaValGlnIleMetValLeuArgGlnGl 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPheAsnArgSe 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACAGAACAGAAGGGGGTTAGATCTGTTATTTCTAAAAGAAGGAGGGTT 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTTGGATGACCACCCTGCTTTCTGCTCTGACGGGGCCCCTAGTAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                          US/08/766,528
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alignment_block:
US-09-171-553B-6 x US-08-766-528-2
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US-08-766-528-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-766-528-2 from: 1 to: 7333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 85.103
                                                               5401 GGGTAAATGGTATATCTTGGGGAATAGTGTAC....TATGGAGGCTCT 5444
                                                                                                                                                                                                                                                          5301 AAAGATGTACGAAATAAGCAAATAAGCTGTCATTCGTTAGACCTAGATTA 5350
                                                                                                                                                                                                                                                                                                                                                     5251 AATTTAATTATGGCCATGGGAGATGGAAAGATTGGCAACAGCGGGTACAA 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 rLeuLysIleSerPheThrGlu..ArgLysThrGlyLysTyrSerLysVa 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4951 ATATTAACAGCACTCAAGGGGAGGCTCCCTTGGGGACCTGGTGGCCTGAA 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4901 TAAACCCTTATCTCTCACCTGGTTACTTACTGACTCCGGTACAGGTATTA 4950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 lAspLysTrpTyrGluLeuGlyAsnSer.PheLeuLeuTyrGlyGlyGly 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 uGlnAspArgValLysPheSerPheValAsnSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 TrpSerCysValThrSerAsnAspGlyAspTrpLysTrpProIleSerLe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4757 ACCTTATCTCGTACTTTTGACCACACCAACGGCTGTGAAAGTCGA..... 4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 hrValAsnSerThrArgGlyValAlaProArgGlyThrTrpTrpProGlu 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 sArgProLeuSerLeuThrTrpLeuIleIleAspProAspThrGlyValT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ThrLeuSerArgArgHisLeuProThrArgGlyGlyGluProLysArgLe
                                                                                                                                                                   CTTAAAAATAAGTTTCACTGAAAAAGGAAAACAAGAAAATATTCAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAGACAGAGTAAGTTACTCTTTTGTTAACAATCCTACCAGTTATAATC 5250
                                                                                                                                                                                                                                                                                                                                                                                            TGGAGCTGCATAACTTCTAATGATGGGAATTGGAAATGGCCAGTCTCTCA 5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrGluLysGluLysTyrCysGlyGlySerGlyGluSerPheCysArgArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCCCGATGTACTCCGTGCTTACGGGTTTTACGTTTGCCCCAGGACCCC 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rProProAsnLeuValArgSerTyrGlyPheTyrCysCysProGly...T 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATATGTCTGCCTTCGATCAGTAATCCCTGGTCTCAATGACCAGGCCAC 5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuHisPheCysLeuArgLeuIleAsnProAlaVal.....LysSerTh 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 2497.50
Ratio: 4.328
                        .GlySerThrLeuThrIleArgLeuArgIleGluThrGl 230
Percent Identity: 71.829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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5994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           447
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ThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrG1 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCCAAATTGTCCCCCGGGTGTACTACTATCCCGAAAAAGCAGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tValGlnTleValProArgValTyrTyrHisProGluGluValValLeuA 447
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                                                                                                    ACCTACATCGAATTGTAACGGAAGATCTCCAAGCCCTAGAAAAATCTGTC
                                                                                                                                                   luLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerVal
                                                                                                                                                                                                      AACGGCTGCCCTAATCACAGGACCGCAACAGCTGGAGAAAGGACTTAGTA
                                                                                                                                                                                                                                yThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyG
                                                                                                                                                                                                                                                                                                          ACACTAGCTGTAATGCTCGGATTGGGAGTGGCTGCAGGCGTGGGAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCGAAACTTTTTAGCCTCATCCAGGGAGCTTTTCAAGCTCTTAACTCC
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08766528 Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8060 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6694 GCCTTCTGAGCCAAGGAGAACTGACCTC
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                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 LeuLeuThrValGlyProCysLeuIleAsnArgPheValAlaPheValAr 630
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                                                                                                                         REGISTRATION NÜMBER: 35,965
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 021
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STREET: 60 State Str
CITY: Boston
STATE: Massachusetts
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    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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nucleic acid
DEDNESS: single
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60 State Street
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                                                                                                                                                                                                                   Myers
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14-DEC-1995
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; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-766-528-1
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US-09-171-553B-6 x US-08-766-528-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 2360.00
Ratio: 4.252
Percent Similarity: 84.604
225 euArgIleGluThrGlyThrGluProProValAlaMetGlyProAspLys 241
                                                                                                                                                                                                                                                                  683 GAAAATATCCTAAAATGGGTAAATGGTATGTCTTGGGGAATGGTATAT.. 730
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                                                                                                                                                                                                              ACAATTTAATTACCTGACCTGGATTAGAACTGGAAGCCCCAAGTGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLysSer 100
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                                          ....TATGGAGGCTCGGGTAAACAACCAGGCTCCATTCTAACTATTCGCC
                                                                                                                                                        CTTCAGACCTAGATTACCTAAAAATAAGTTTCACTGAGAAAGGAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCTGATCTATACGTTTGCCTCAGATCAGTTATTCCTAGTCTGACCTCA
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Gaps: 11
Percent Identity: 68.445
                                           776
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777	TCAAAATAAACCAGCTGGAGCCTCCAATGGCTATAGGACCAAATACG	823
		U
824	TTGACGGGTCAAAGACCCCCAACCCAAGGACCA	859
258	\lProGlnLeuThrSerLeuArgProAspIleThrGlnProProSer	275
860	- I I I I I I I I I I I I I I I I I I I	872
275	nSerThrThrGlyLeuIleProThrAsnThrProArgAsnSerProGl ::: :::	وتد
٥ -	ATAACTTCTGGATCAGACCCCCACTGAGTCTAGCAGCACGACT	Ď
292 917	VallysThrGlyGlnArgLeuPheSerLeuTleGlnGlyAlaPh 	308 957
0	GlnAlaIleAsnSerThrAspProAspAlaThrSerSerCvsTrpLeuC	
ÚI (CTCCAGAGGCTACCTCTTCTTGTTGGCTAT	0 1
325	SLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluArgLys	41
1008	AAA	1057
342 1058	PheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySerArgAs	358 1107
UT.	nLysLeuThrLeuThrGluValSerGlyLysGlyThrCysIleGlyLysA 	375
375	aProProSerHisGlnHisIeurovatttotogaaanagevattovalValTeralagaaaaaga	
Ui.		
392 1208	AlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCy :::: :::	408 1257
1250	sAsnThrGlyLeuThrProCysValSerThrSerValPheAsnGlnSerL 4	, N
425	AspPheCysValMetValGlnIleValProArgValTyrTyrHisPro	41
ROFT	GATTTTTGCATTATGGTCCAAATTGTTCCCCGAGTGTATTACTATCC	ω
442 1358	GluGluValValLeuAspGluTyrAspTyrArgTyrAsnArgProLysAr 4	58
458 1408	9GluProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaV 4	4 7
475 1458	alGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeu 4 ::	91
492 1508	GluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAl 5	557
508 1558	aLeuLysGluSerValSerAsnLeuGluGluSerLeuThrSerLeuSerG 5	607
525 1608	LuValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGlu	41 657

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08766528
Patent No. 6190861
GENERAL INFORMATION:
APPLICANT: JAY A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                             TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 GlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHi 558
                                                                                                                                                                  NAME: LOUIS MYETS
REGISTATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              558 sSerGlyAlaIleArgAspSerMetAsnLysLeuArgLysLysLeuGluA 575
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 rgArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPhe 591
MOLECULE TYPE:
                                                                                                                                                                                                                                                                             FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/572,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
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alignment_block:
US-09-171-553B-6 x US-08-766-528-3
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Ratio: 4.232
Percent Similarity: 84.756
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                                                                               6311 TCAAAATAAACCAG...CTGGAGCCTCCAATGGCTATAGGACCAAATACG 6357
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                         242 ValLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeuPr 258
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                                                                                                                                                                                                                                                                                                  GAAAATATCCTAAAATGGGTAAATGGTATGTCTTGGGGAATGGTATAT.. 6264
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Percent Identity:
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7092 CCTAGAAAATCTGTCAGTAACCTGGAGGAATCCCTAACCTCCTTATCTG
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               542 GlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHi 558
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GGAGGATTATGTGTAGCCTTGAAGGAGGAATGCTGTTTTTATGTGGATCA
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                                                                                                                                                                                                                                                                                                                                  AGAACCCATATCTCTGACACTTGCTGTGATGCTCGGACTTGGAGTGGCAG
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; OTHER INFORMATION: Description of Artificial Sequence:Contiguous; OTHER INFORMATION: compilation of SEQ ID NOs: 18, 22, and 24. US-09-376-781-25
                                                                                                                                                                                                                                       alignment_block:
US-09-171-553B-6 x US-09-376-781-25
                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Banerjee, Papia T.
APPLICANT: Patience, Clive
APPLICANT: Anderson, Goran K.
TITLE OF INVENTION: Molecular Sequence
Patent No. 626.1806
TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/09376781 Patent No. 6261806 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2000
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                     642 ArgGlnGlnTyrGln 646
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hrLeuThrIleThrProGlnAlaSerSerLysArgLeuIleAspSerSer 50
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Ratio: 3.963
milarity: 82.416
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Gaps:
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344	8 erGlyProProTyrTyrGluGlyMetAlaLysGluArgLysPheAsr	32
328 955	1 eAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSer 	31: 90
311 905	rgLeuPheSerLeuIleGlnGlyAlaPheGlnAla :: ACTTTTTAGTCTCATCCAGGGAGCTTTTCAAGCT	295 856
5		ū
294	GlyLeuIleProThrAsnThrProArgAsnSerProGlyValP	
278 853	hrSerLeuArgProAspIleThrGlnProProSerAsnSerThr ::: :::	<u>⊢</u> 6
	GGTCAAAGAACCCCAACCCCAGGACCATCCTCTGATATA	7
	INTITION OF THE STATE OF THE ST	730
729		
∞ ⊢	yrSerLysValAspLysTrpTyrGluLeuGlyAsnSerPheLeuLeuTyr	ωω
197 633	SpLeuAspTyrLeuLysIleSerPheThrGluArgLysThrGlyLysT 	8 8
181 583	rLysMetMetLysLeuTyrLysAspLysSerCysSerProSerA::::	ωσ
166 533	LeuGlnAspArgValLysPheSerPheValAsnSerGlyProGlyLysTy ::: ::: CTGCAGGATAGGGTAAGCTTTTCTTATGTCAACCCCAATAACCA	9 5
149 489	rgTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpProIleSer::	133
133 439	rGluLysGluLysTyrCysGlyGlySerGlyGluSerPheCysArgA ::::: ::: ::: ::: aCCAAATAATGGAAACACTATGGAAATCCTAGAGATTTCTTTTACAAAC	L17 890
117 389	ThrProProAsnLeuValArgSerTyrGlyPheTyrCysCysProGlyTh	L01 343
100	rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLys	84 93
84 292	rGlyValThrValAsnSerThrArgGlyValAlaProArgGlyThrT ::::::::: ::: 	67 243
57 242	AsnProHisArgProLeuSerLeuThTTrpLeuIleIleAspProAs :::	51 93
192	ATGCACATAG	3

628 PheValArgG ::: : 1856 TTCATTAGAA	611 euLeuLeuLe 	594 rProTrpMet ::: 1756 TCCTTGGTTG	578 rgGluArgGl ::: 1706 GGGAAAAGGA	561 alleArgAsp 1656 CATCAGAGAC	545 CysAlaAlaL ::: 1606 TGTGTAGCCT	528 euGlnAsnAr :: 1556 TACAGAATAA	511 uSerValSer : 1506 ATCTGTCAGT	495 LeuGlyGluLe :::::: 1456 CTTAGTAACCT	478 lyThrGlyTh 1406 GAACAGGAAC	461 lSerLeuThrL : 1356 ATCCCTGACAC	445 ValLeuAspGl ::: 1306 ATTCTCGATGA	428 ysValMetVal ::: 1256 ACATTATGGTC	411 yLeuThrProC 1206 ATTAACCCCTT	395 AsnGlnTyrLe ::: 1156 AGTCAATATCT	378 erHisGlnHis 	361 rLeuThrGluV 1056 CCTTACTGAGG	345 ThrLysGluHi ::: 1006 ACAAAAAAAACA	956 CGGGCCCACCTT
	uLeuThrValGlyProCysLeuIleAsnArgE CTCACAGTTGGGCCATGTATTATTAACAAGT	ThrThrLeuLeuSerAlaLeuThrGlyProLeuV :::: :GCTACCCTACTTTCTACTTTAACAGGACCCTTAA	.uAla.AspGlnGlyTrpPheGluGlyTrpPheA ::: ::	SerMetAsnLysLeuArgLysLysLeuGluArg TCCATGAACAAGCTTAAAAAAAGGTTGGAGAAA	.euLysGluGluCysCysPheTyrValAspHisS maaGGaGaAaTGCTGTTTTATGTAGATCATT	gArgGlyLeuAspLeuLeuPheLeuArgGluGl :::: :AAAGGGTTAGATTTATTTCTAAAAAAAAA	AsnLeuGluGluSerLeuThrSerLeuSerGlu AACCTGGAAAAATCCCTAACCTCCTTATCTGAA	uHisalaalaMetThrGluAspLeuArgAlaI :: :: :: 	ralaalaLeuIleThYGlyProGlnGlnLeuGl TGCAGCTTTAGTTACAGGACCTCAGCAGCTAGA	euAlaValMetLeuGlyLeuGlyThrAlaVa 	luTyrAspTyrArgTyrAsnArgProLysArgGlu ATATGATTACAGGAACCATCGACAAAAGAAAAAA	GlnIleValProArgValTyrTyrHisProGl CAAATTGTTCCCCGAGTATATTACTATCCCA	ysValSerThrSerValPheAsnGlnSerLysAsp GTGTTTCCACCTTGGTTTTCAACCAAACTAAAGAC	uValProGlyTyrAsnArgTrpTrpAlaCysAs GTACCTGGTTATGACAGGTGGTGGGCATGTAA	LeuCysTyrSerThrValValTyrGluGlnAl ::::::: :: ::::::: ::	alSerGlyLysGlyThrCysIleGlyLysAla TTTCTGGAAAGGACACCTGCATAAAAAAGGTT	.sArgAsnGlnCysThrTrpGlySerArgAsnLys ::: ragagaccaargtacarggggatcccaaaataag	TACTATAAGAAAATGGCTAAAAGAGAAAAATTC
ArgGlnGl AGACAACA	hevalAla ::::: TAATTGCC	uValValL ::: AATAGTCC	AsnArgSe AACAGGTC	yArgArgA : ACGTCGAA	SerGlyAl CAGGGGC	LyGlyLeu }AAGATTA	Walvall AGTAGTTC	euLysGl :: TAAAAAA	luLysGly BAAACAGGA	GlyValG GGTGTGA	ProVa	GluVal :::::: AAAACA	PheC	nThrG1 TACTGG	aSerGlu: : :CTCTGAG	ProProS	LeuTh CTTAC	CAATGTG 1
644 1905	627 1855	611 1805	594 1755	578 1705	561 1655	544 1605	528 1555	511 1505	494 1455	478 1405	461 1355	444 1305	428 1255	411 1205	394 1155	378 1105	361 1055	1005

644 nTyrGln 646

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alignment_block:
US-09-171-553B-6 x US-09-376-781-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
; OTHER INFORMATION: consensus sequence of PERV-D.
US-09-376-781-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
    Sequence 30, Application US/09376781
    Patent No. 6261806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-376-781-30 from: 1 to: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-376-781-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Banerjee, Papia T.
APPLICANT: Banerjee, Clive
APPLICANT: Patience, Clive
APPLICANT: Andersoon, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of
Patent No. 6261806
TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
CURRENT FILING NUMBER: US/09/376,781
CURRENT APPLICATION NUMBER: 05/097,015
EARLIER APPLICATION NUMBER: 60797,015
EARLIER APPLICATION NUMBER: 60797,015
EARLIER FILING DATE: 1998-08-18
NUMBER: FILING DATE: 1998-08-18
NUMBER: FILING DATE: 1998-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 30
LENGTH: 2000
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
117 rGluLysGlu...LysTyrCysGlyGlySerGlyGluSerPheCysArgA 133
                                                      343 ACC...CCAGATATCCTCCGTGCTTACGGATTTTATGTTTGCCCCAGGACC 389
                                                                                     101 ThrProProAsnLeuValArgSerTyrGlyPheTyrCysCysProGlyTh 117
                                                                                                                                                         243 AGGTATTAATATCCACAGCGCTCGAGGGGAGGCTCCTTTAGAAACCTGGT 292
                                                                                                                                                                                                                                                                                                                                                                        193 AACTCCCATAAACCCTTATCTCTGACCTGGTTAATTACTGACTCTGACAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 CTCTGTCAATAACCTCTCAGACTAATGGTATGCACATAGGAGACAGCCTG 192
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                                                                                                                                                                                          84 rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLysSer 100
                                                                                                                                                                                                                                                                                                                 67 rGlyValThrValAsnSerThrArgGlyValAlaProArgGlyThrTrpT 84
                                                                                                                                                                                                                                                                                                                                                                                                      51 AsnProHisArgProLeuSerLeuThrTrpLeuIleIleAspProAspTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 hrLeuThrIleThrProGlnAlaSerSerLysArgLeuIleAspSerSer 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetHisProThrLeuSerArgArgHisLeuProThrArgGlyGlyGlyGluPr 17 :::||| | :::|| :::|| :::|| :::|| :::|| 43 ATACATCCCACGTTAAGCCGGCGCCCCCCTCCTGATTCAGGGTGAAAAGCC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 2136.00
Ratio: 3.963
milarity: 82.416
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Percent Identity: 64.526
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428	411 yLeuThrProCysValSerThrSerValPheAsnGlnSerLysAspPheC
411 1205	95 AsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCysAsnThrG1 :::
394 1155	78 erHisGlnHisLeuCysTyrSerThrValValTyrGluGlnAlaSerGlu
378 1105	361 rLeuThrGluValSerGlyLysGlyThrCysIleGlyLysAlaProProS
361 1055	
344 1005	
328 955	311 eAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerS
311 905	lnArgLeuPheSerLeuIleGinGlyAlaPheGinAlaI
855	54 CT
5 7	euThrSerLeuArgProAsplleThrGlpProProSerAsnSerThr
261 816	45 GluGlnGlyProProAlaLeuGluProProHisAsnLeuProValPro
244 777	30 .
228 729	214 .GlyGlyGlyAlaGlySerThrLeuThrIleArgLeuArgIleG
213	LysTrpTyrGluLeuGlyAsnSe AAATGGTATGTCCTGGGGAATAA
197	181 spleuAspTyrLeuLysIleSerPheThrGluArgLysThrGlyLysT
181	166 rlysMetMetLysLeuTyrLysAspLysSerCysSerProSerA ::::
166 1533	150 LeuGlnAspArgValLysPheSerPheValAsnSerGlyProGlyLysTy
. <u>.</u>	133 rgTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpProIleSer ::
: C 439	390 ACCAAATAATGGAAAACACTATGGAAATCCTAGAGATTTCTTTTACAAAC

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-376-781-24
APPLICANT: Banerjee, Papia T.
APPLICANT: Pattence, Clive
APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Sequence 24, Application US/09376781 Patent No. 6261806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1306 ATTCTCGATGAATATGATTACAGGAACCATCGACAAAAGAAAAAACCCAT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1206 ATTAACCCCTTGTGTTTCCACCTTGGTTTTCAACCAAACTAAAGACTTTT 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1356 ATCCCTGACACTCGCAGTAATGCTCGGACTCGGAGTGATAACAGGTGTGA 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1256 ACATTATGGTCCAAATTGTTCCCCGAGTATATTACTATCCCAAGAAAACA 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1406 GAACAGGAACTGCAGCTTTAGTTACAGGACCTCAGCAGCTAGAAACAGGA 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 ValLeuAspGluTyrAspTyrAsgTyrAsgArgProLysArgGluProVa 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 ysValMetValGlnIleValProArgValTyrTyrHisProGluGluVal 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 lSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyValG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 euLeuLeuLeuThrValGlyProCysLeuIleAsnArgPheValAla 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 nTyrGln 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aIleArgAspSerMetAsnLysLeuArgLysLysLeuGluArgArgArgA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeu 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCAGAGACTCCATGAACAAGCTTAAAAAAAGGTTGGAGAAACGTCGAA 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGTAGCCTTAAAGGAGAAATGCTGTTTTTATGTAGATCATTCAGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysAlaAlaLeuLysGluGluCysCysPheTyrValAspHisSerGlyAl 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTAGTAACCTACATCAAATTGTAACAGGAAATCTCCAAGCCCTAAAAAA 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLySGly 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLeuValValL 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTTGGTTGGCTACCCTACTTTCTACTTTAACAGGACCCTTAATAGTCC 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAAAGGAAACTTACTCAAAGATGGTTTAAAAGATGGTTCAACAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgGluArgGluAla.AspGlnGlyTrpPheGluGlyTrpPheAsnArgSe 594
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; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide; OTHER INFORMATION: sequence of the 3' end of the PERV-D env region. US-09-376-781-24
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US-09-171-553B-6 x US-09-376-781-24
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LENGTH: 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 ...ATATTATACAGGTTGGGACAGACAACCAGGCTCCATTCTAACCATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 heLeuLeuTyr.GlyGlyGly.....AlaGlySerThrLeuThrIleAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 sThrGlyLysTyrSerLysVallAspLysTrpTyrGluLeuGlyAsnSerP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 ProGlyLysTyrLysMetMetLysLeu...TyrLysAspLysSer...Cy 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ysValLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeu 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 gLeuArgIleGluThrGlyThrGluProProValAlaMetGlyProAspL
                                                                    341 yspheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySerArg 357
                                                                                                                                     308 PheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTrpLe
                                                                                                                                                                                                                                                                                                                                              291 lyValProValLySThrGlyGlnArgLeuPheSerLeuIleGlnGlyAla 307
                                                                                                                                                                                                                                                                                                                                                                                                                      324 TAACAGCACGACT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                           274 rAsnSerThrThrGlyLeuIleProThrAsnThrProArgAsnSerProG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 CGGTCTTAACGGGTCAAAGAACCCCCAACCCCAGGACCATCCTCTGATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CCCAATAACCACCGGACCTGGAAAACGTCATACAGGTACCATTCTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sSerProSerAspLeuAspTyrLeuLysIleSerPheThrGlu..ArgLy 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTTAAAATA...AGCCAGCTAGAGCCTCCAATGGCTATAGGACCGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......ACTTCTAAATTAGACCCCACTGAG.....TC
AsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysIleGlyLy 374
                                                 AATTCAATGTGACAAAAAAACATAGAGACCAATGTACATGGGGATCCCAA 525
                                                                                                                                                                                                                                 .....AAAACGGGGACAAAACTTTTTAGTCTCATCCAGGGAGCT
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Gaps: 11
Percent Identity: 66.395
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seq_documentation_block:

Sequence 7, Application US/09011745 Patent No. 6165715

GENERAL INFORMATION:

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1376 CTTAGACAACAGTACCAA 1393
                                                                                                                                                                                              1326 AGTTAATTGCCTTCATTAGAAAACGAATAAGTGCAGTCCAGATCATGGTA 1375
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                                                                                                    LeuArgGlnGlnTyrGln 646
                                                                                                                                                                                                                                                            rgPheValAlaPheValArgGluArgValSerAlaValGlnIleMetVal 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oLeuValValLeuLeuLeuLeuThrValGlyProCysLeuIleAsnA 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAACAGGTCTCCTTGGTTGGCTACCCTACTTTCTACTTTAACAGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                         CTTAATAGTCCTCCTCCTGTTACTCACAGTTGGGCCATGTATTATTAACA
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-011-745-7
                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: n is any nucleotide US-09-011-745-7
                                                                                     Align seg 1/1
                                                                                                                          US-09-171-553B-6 x US-09-011-745-7
                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
1428 CACCCGTTCCAGGTCGGGGATCAAGTGCTTGTCAGACGCCATCGACCCAG 1477
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (4249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4247)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (4248)
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (4246)
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OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                       2 HisPro......ThrLeuSerArgArgHisLeuProTh 12
                                                                                                                                                                                      Quality: 1508.50
Ratio: 3.060
milarity: 66.086
                                                                                 to: US-09-011-745-7 from:
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to:

6312

746 24 44.102

235 2332	ySerThrLeuThrIleArgLeuArgIleGluThrGlyThrGluProProV ::: ::: CGTACAGTTCACCATTCGCTTAAAAATCACCAACATGCCAGCTG	218 2289
218 2288	GluLeuGlyAsnSerPheLeuLeuTyrGlyGlyGlyAlaGl ::::::: ::::: 	205 22 4 2
204 2241	erPheThrGluArgLysThrGlyLysTyrSerLysValAspLysTrpTyr::	188 2204
188 2203	uTyrLysAspLysSerCysSerProSerAspLeuAspTyrLeuLysIleS :::::: ::: TCACCAGACCGGCTGGTGTAACCCC	171 2169
171 2168	LysPheSerPheValAsnSerGlyProGlyLysTyrLysMetMetLysLe ::::: ACTGTAAAATGGGACCAAAATAGCGAATGGACTCAAAAATTTCAACAGTG	155 2119
154 2118	hrSerAsnAspGlyAspTrpLysTrpProIleSerLeuGlnAspArgVal :::::	138 2072
138 2071	STYRCYSG1YG1YSerG1YG1uSerPheCysArgArgTrpSerCysValT:	121 2022
121 2021	TyrGlyPheTyrCysCysPro	109 1972
108 1971	LeuValArgSer ::: GGGGAGCCATAGGGTGCAGCCTACCCTCGGGCTAGGACTAGAATGGCAAGC	105 1922
104 1921	SSETThrProProAsn	99 1872
99 1871	AGTCTTGAGTCCTGGGATATCCCGGGGAACCGATGTCTCGTCCTCTAAACG	94 1822
93 1821	rgGlyThrTrpTrpProGluLeuHisPheCysLeuArgLeu	80 1772
80 1771	eAspProAspThrGlyValThrValAsnSerThrArgGlyValAlaProA :::: :: :: :: GTCCCAAACTGGAGACGTTGTCTGGGATACAAAGGCAGTCCAGCCCC	63 1725
63 1724	AspSerSerAsnProHisArgProLeuSerLeuThrTrpLeuIleIl :::::: ::: :::: CTGCAAAATAAGAACCCCCACCAGCCCATGACCTCACTTGGCAGGTACT	48 1675
47 1674	ysargLeuIle	44 1625
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23 1527	rArgGlyGlyGlyFroLysArgLeuArgIleP: :::	12 1478

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, - 0	lyProGlnGlnLeuGluLySGlyLeuGlyGluLeuHisAlaAlaMetT :: :::: ::: ::: GACCTATAGACCTCCAGCAAGGCCTGCAGATCGCCATAG GACCTATAGACCTCCAGCAAGGCCTGCAGATCGCCATAG	യ്യ	
0 00	rGlyThrAlaAlaLeuIleTh ::::: TGGTTCAACTGCCTTAATTAA	470 3047	
470 304	rAsnArgProLysArgGluProValSerLeuThrLeuAlaValMetLeuG:	453 2997	
453 299	ValTyrTyrHisProGluGluValValLeuAspGluTyrAspTyrArgTy::: :: :: :: ::	437 2947	
436 294	alPheAsnGlnSerLysAspPheCysValMetValGlnIleValProArg ::::: ::::: 	420 2897	
42C 289	nArgTrpTrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerV:	403 2847	
403 284	ValValTyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAs ::: ::::::::::::::::::::::::::::::::	387 2797	
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370 274	rTrpGlySerArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyT :::::::	353 2697	
353 269	AlaLysGluArgLysPheAsnValThrLysGluHisArgAsnGlnCysTh	337 2650	
336 264	erSerCysTrpLeuCysLeuSerSerGlyProProTyrTyrGluGlyMet :: :::	320 2600	
320 259	ulleGlnGlyAlaPheGlnAlaIleAsnSerThrAspProAspAlaThrS	303 2550	
303 254	AsnSerProGlyValProValLysThrGlyGlnArgLeuPheSerLe :::	288 2506	
287 250	ThrAsnThrProA :::::: GCACAAACTCCCA	278 2456	
278 245	nLeuThrSerLeuArgProAspIleThrGlnProProSerAsnSerThrT:	261 2433	
261 243	GluProProHisAsnLeuProValProGl::: ::::: ::::: :::::	252 2383	
251 238	alAlaMetGlyProAspLysValLeuAlaGluGlnGlyProProAlaLeu ::: 	235 2333	

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; NAME/KEY: misc_feature
; LOCATION: 1..8535
; OTHER INFORMATION: /standard_name= "GaLV SEATO Genome"
US-08-716-351A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
; Sequence 1, Application US/08716351A
; Patent No. 6033905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-716-351A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                  TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Bas
TITLE OF INVENTION: Retroviral Vectors
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PCDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3547 CAGGCTTTAGTCCTGACTCAACAATACCACCAGCTA 3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3447 CATCGCTGGGCCCCTATTACTCCTCCTCTGTTGCTCATCCTCGGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3397 TATGAAGGATGGTTCAATAACTCCCCTTGGTTCACTACCCTGCTATCAAC 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3347 AAGAAAAACTGGATAAAAGACAGTTAGAGCGCCAGAAAAGCCAAAAACTGG 3396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3197 TGACTTCCCTGTCCGAGGTAGTGCTCCAAAATAGGAGAGGCCTTGACTTC 3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/U
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 GlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 648
                                                                                                     FEATURE:
                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 aLeuThrGlyProLeuValValLeuLeuLeuLeuLeuThrValGlyProC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 PheGluGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAl 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570 rgLysLysLeuGluArgArgArgGluArgGluAlaAspGlnGlyTrp 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 sPheTyrValAspHisSerGlyAlaIleArgAspSerMetAsnLysLeuA 570
                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTTACATAGACCACTCAGGTGCAGTACGGGACTCCATGAAAAACTCA 3346
                                                                                                                                                                      linear
                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibbon Ape Leukemia Virus-Based Retroviral Vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US94/03784
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188	1 uTyrLysAspLysSerCysSerProSerAspLeuAspTyrLeuLysIleS	` 17
6544	5 ACTGTAAAATGGGACCAAAATAGCGAATGGACTCAAAAATTTCAACAGTG	649
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121 6397	09 TyrGlyPheTyrCysCysPro	109 6348
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93	80 rgGlyThrTrpTrpProGluLeuHisPheCysLeuArgLeu	~
80 6147	63 eAspProAspThrGlyValThrValAsnSerThrArgGlyValAlaProA :::: :::	610
63 6100	48AspSerSerAsnProHisArgProLeuSerLeuThrTrpLeuIleII:::::::	609
47 6050	44 ysargLeuIle	600
44 6000	36 rIleThrProGlnAlaSerSerL ::::: ::: :::	591
36 5953	23 roleuSerPheAlaSerIleAlaTrpPhe.LeuThrLeuTh	591
23 5903	12 rArgGlyGlyGlyFloLysArgLeuArgIleP ::::	58
12 5853	2 HisProThrLeuSerargArgHisLeuProTh	58
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TyrTyrHi ::	HILLIAN CAG	YSILEGIY GCATAGGA GCATAGGA ValTyrG1 :: TCCATCAA	LysGluAr :::::: TCATCAGG TGATSerA	erCysTrp CTTGCTGG	eGlnGlyA : GCAGGGGG	AsnSerPr ::: AACACTCC	lyLeu] TGGCG#	uThrSerL C	стсест	laMetGly ::: CAGTAGGT	rThrLeuT ::: ACAGTTCA	uLeuGlyAs :: .ACGGGAAA	heThrGlu ::: TCACAGAC	:::: CCAGACCG
SProGluG : TCCTGAAG	SerLysası :::::::::::::::::::::::::::::::::::	AGGTGCC GlnAlas ::::::: TCCTCCG	gLysPheA::: AGAGGTCG AGASnLys ::::: AAGGAAAG	LeuCysLeu CTTTGTTTG	laPheGln	oGlyValF GC	ProThrAs ::::: AGTGCACA	euArgPro	CCCACCTC	ProAspLy CCTGACCT	hrIleArg	nSerPheL:::::: AACCTGGG	ArgLysTh ::: AAA	Ω
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.uTyrAspTyr. CTATGACAAT	/Svaiser	HILL TCTGCAA Valprog ::: :	ArgAsnG::::CTTGACC LSerGly	[yrTyrGlu ATTATGAA	spProAspA :: ACCCAGGGG	nArgLeuPh : CAGACTTTT	AAAACAATT	roSerAsnS ACTCTAACT	nLeuProVa : AGCGCCACC	GlyProPro GGACCTCC	lyThrGlui ::: AACATG	rGlyGlyG ::: GTCTGGAC	ValAspLys GAC	CTT/
ArgTy :: TCTCA	CCTCAG	SerThr:::: CAGACC YTyrAs::: CAACCA	nCysTh: : : : : : : : :	GlyMet :::::: GCAATA	laThrs : CCACTG	eSerLe ::: TGATCT	rgttacc	SerThrT : CCACAG	alProGl :: CGCCATC	oAlaLeu TAGAACG	ProProV CCAGCTG	lyAlaG1 ATCCAGG	STrpTyr CTGGATA	: AAAATAG
453 7372	7272 736 7322	1 2 0 P a	5 7	336 7025	320 6975	303 6925	287 6881	278 6831	261 6808	251 6758	235 6708	218 6664	204 6617	6579

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09075272 Patent No. 6136598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7673
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7823 CATCGCTGGGCCCCTATTACTCCTCCTTCTGTTGCTCATCCTCGGGCCAT
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APPLICANT: WOLGAMOT, GREG
APPLICANT: BONHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 lGlnIleMetValLeuArgGln 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 aLeuThrGlyProLeuValValLeuLeuLeuLeuThrValGlyProC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487 GlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetTh 503
                                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                               COUNTRY: UZIP: 94111
                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAATTCTGGTCCTTAGACAA 7944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgLysLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyTrp 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeu 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ysLeuIleAsnArgPheValAlaPheValArgGluArgValSerAla.Va 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTTTCTAAAAGAAGGTGGCCTCTGTGCGGCCCTAAAGGAAGAGTGCTG 7672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rGluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGACTTCCCTGTCCGAGGTAGTGCTCCAAAATAGGAGAGGCCTTGACTTG 7622
                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                      TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7872
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APPLICATION NUMBER: FILING DATE: 08-MAY

08-MAY-1998

US/09/075,272

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127 6196	115 ProGlyThrGluLysGluLysTyrCysGlyGlySerGl
114 6146	107ArgSerTyrGlyPheTyrCysCys
106 6096	96 oAlavalLysSerThrProProAsnLeuVal
96 6046	91LeuArgLeuIleAsnPr
90 5996	80 rgGlyThrTrpTrpProGluLeuHisPheCys
80 59 4 6	63 eAspProAspThrGlyValThrValAsnSerThrArgGlyValAlaProA ::::
63 5899	47 IleAspSerSerAsnProHisArgProLeuSerLeuThrTrpLeuIleIl ::: :::
46 5849	30 laTrpPheLeuThrLeuThrIleThrProGlnAlaSerSerLysArgLeu ::::: ::: 5824 CAGGAGCCCCCTCCATCACCCTGGAC
30 5823	G.
23 5773	10 LeuProThrArgGlyGlyGlyGluProLysArgLeuArgIlePro
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	alignment_block: US-09-171-553B-6 x US-09-075-272-1
	alignment_scores: 1431.00 Length: 727 Quality: 1431.00 Gaps: 25 Percent Similarity: 65.199 Percent Identity: 43.466
	CLASSIFICATION: PRIOR APPLICATION NUMBER: US 60/046,140 FILING DATE: 09-MAY-1997 ATTORNEY/AGENT INFORMATION: NAME: POOT, Brian W. REGISTRATION NUMBER: 32,928 REFERENCE/DOCKET NUMBER: 14538A-003710 FILLECOMMUNICATION INFORMATION: TELEPHONE: (206) 467-9600 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 8655 base pairs TYPE: nucleic acid STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: cDNA US-09-075-272-1

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380 6959	luValSerGlyLysGlyThrCysIleGlyLysAlaProProSerHisGln	364 6910
364 6909	uHisargAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeuThrG: :::	347 6863
347 6862	ProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnValThrLysGl	331 6813
330 6812	hrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyPro ::: :: ::: 	314 6763
314 6762	yGlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSerT::: :::	297 6713
297 6712	IleProThrAsnThrProArgAsnSerProGlyValProValLysThrGl	281 6690
280 6689	erLeuArgProAspIleThrGlnProProSerAsnSerThrThrGlyLeu ::	264 6643
264 6642	oProAlaLeuGluProProHisAsnLeuProValProGlnLeuThrS	248 6593
248 6592	GluProProValAlaMetGlyProAspLysValLeuAlaGluGlnGlyPr ::::::::::: ::: ::: CTGGCAGTAACATCCATAGGACCCAACAAGGTCCTTACGGAACAAGCCCC	232 6543
231 6542	lyGlyAlaGlySerThrLeuThrIleArgLeuArgIleGluThrGlyThr ::: :::::: GAGACCCTGGGTTTATCTTTACGATTAGACTGACAGTAAGAGAC	215 6499
215 6498	AspLysTrpTyrGluLeuGlyAsnSerPheLeuLeuTyrGlyG:::::::	201 6458
200 6457	IleSerPheThrGluArgLysThrGlyLysTyrSerLysVal ::: ::: ::: ATAAAATTCACTGAGAAAGGGAAACAAGCTCGCCTGAGTTGGCT	187 6414
186 6413	ds.	170 6384
170 6383	rGlyProGlyLysTyrLysMetMetL rgggTgTGCTCTTAAAAATTACAGCCCCCCAGGACCA	161 6347
161 6346	SerLeuGlnAspArgValLysPheSerPheValAsnSe	149 6297
148 6296	TPLYSTrpProIle	144 6247
6246	AGACTACTTTTGGGGTAAATGGACATGTGAAACAACAGGGGAAGCCTACT	6197

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-110-300A-8
                                                                                                                                                                                                    Sequence 8, Application US/08110300A Patent No. 5643756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7445 TGCTCTCAAAGAGGAATGTTGTTTCTATGTCGACCACTCGGGAGTGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7495 AAGATTCTATGGCCAAACTTAGAGAACGCCTAGATATACGTCAAAGAGAG
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                                APPLICANT: Pinter, Abraham APPLICANY: Kayman, Samuel TITLE OF INVENTION: FUSION NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7345 TAACCAAACTAGAAGAATCTTTAACTTCTCTGTCTGAGGTAGTACTGCAA 7394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 ArgGluArgValSerAlaValGlnIleMetValLeuArgGlnGlnTyrGl 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 aAlaLeuLysGluGluCysCysPheTyrValAspHisSerGlyAlaIleA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  530 AsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAl 546
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   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         G...GTCTTCCAGGAGGCCGAAAACTCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGAAAGAATAAATGCAGTACAGGTTATGGTATTAAAACAACAATATCA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTGCTTACTTTTGGCCCCTGCATTCTTAATAAGTTAGTAGCCTTTATT 7694
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Davis Hoxie Faithfull and Hapgood
                                                                                                      FUSION GLYCOPROTEINS
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alignment_block:
US-09-171-553B-6 x US-08-110-300A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-110-300A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 2.855
Percent Similarity: 64.175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-110-300A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-586-1461 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5787 ACGCTCTCAAAATCC.....CCTAAAGATAAGATTGACCCGCGGGACCT 5830
                                                                                                                                                                                                                                                                                                                       5901 CAGGTCTACAACATTACCTGGGAAGTGACCAATGGGGATCGG...GAGAC 5947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5831 CCTAATCCCCTTAATTCTC.......TTCCTGTCTCTC.... 5861
                                                                                                                                                                                                                                 5948 AGTATGGGCAATATCAGGCAACCACCCTCTGTGGACTTGGTGGCCAGTCC 5997
                                                   6048 CTAGAGTATCAGGCCCCCTATTCCTCGCCCCGGGGCCCCCTTGTTGCTC 6097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-AUG-19
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                20 uArgIleProLeuSerPheAlaSerIleAlaTrpPheLeuThrLeuThrI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ThrLeuSerArgArgHisLeuProThrArgGlyGlyGluProLysArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING YSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STRANDEDNESS: doub
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                                                                                                                                           TCACCCCAGATTTGTGTATGTTAGCTCTCAGTGGGCCGCCCCACTGGGGG 6047
                                                                                                                                                                                                                                                                                                                                                  ArgProLeuSerLeuThrTrpLeuIleIleAspProAspThrGlyValTh 70
                                                                                                                                                                                                                                                                        rValAsnSerThrArgGlyValAlaProArgGlyThrTrpTrpProGluL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                      leThrProGlnAlaSerSerLysArgLeuIleAspSerSerAsnProHis 53
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.....CysLeuArgLeuIleAsnProAlaV 98
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Gaps: 26
Percent Identity: 42.595
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361 T.HeUTHTGLIVAISeTGlyTySGlyThrCys1leGlyLysAlaProProS 378 ::: ::: :::		328 erGlyProProTyrTyrGluGlyMetAlaLySGluArgLySPheAsnVal 344	311 eAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerS 328 : ::: ::::::	295 LysThrGlyGlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaII 311 ::: ::: ::: :::	279 lyLeuIleProThrAsnThrProArgAsnSerProGlyValProVal 294	262 uThrSerLeuArgProAspIleThrGlnProProSerAsnSerThrThrG 279 :::	246 GlnGlyProProAlaLeuGluProProHisAsnLeuProValProGlnLe 262	229 hrGlyThrGluProProValAlaMetGlyProAspLysValLeuAlaGlu 245 ::: :::	212 uTyrGlyGlyGlyAlaGlySerThrLeuThrIleArgLeuArgIleGluT 229 :	196 ysTyrSerLysValAspLysTrpTyrGluLeuGlyAsnSerPheLeu.Le 212 :::: :::	180 erAspLeuAspTyrLeuLysIleSerPheThrGluArgLysThrGlyL 196	164 YLYSTYTLYSMETMETLYSLEUTYTLYSASPLYSSETCYSSETPTOS 180 ::: ::: :::::::	148 IleSerLeuGlnAspArgValLysPheSerPheValAsnSerGlyProGl 164	131 ysargargTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpPro 147	117 rGluLysGluLysTyrCysGlyGlySerGlyGluSerPheC 131 ::::::: ::: ::: ::: ::: ::: ::: :::	108SerTyrGlyPheTyrCysCysProGlyTh 117 6198 GACCAGGTAACTCATAAATCAAGTGAGGGATTTTATGTCTGCCCCGGGTC 6247	98 alLysSerThrProProAsnLeuValArg 107 ::
eq_documentation Sequence 8, App	641 LeuArgGlnGlnTyrGlnGlyLeu 648 ::: 7755 CTGACTCAACAATACCACCAGCTA 7778 seq_name: /cqn2 6/ptodata/2/ina/5B COMB.seq:US-08-886-642-8	624 rgPheValAlaPheValArgGluArgValSerAlaValGlnIleMetVal 640 ::: ::: ::: :::	607 oLeuValValLeuLeuLeuLeuLeuChrValGlyProCysLeuIleAsnA 624 ::::::: :::		574 luargargargargGlualgargGlualaaspGlnGlyTrpPheGluGlyTrp 590 ::::: :::: ::::		55 5	erGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArg	507 gAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrSerLeuS 524 : ::::::: ::::	LeuGlu :::::: TTTCAG	lavalg ::: CCGCGG	1SerLeu GTCCTT#	445 ValleuAspGluTyrAspTyrAsgTyrAsgArgFroLysArgGluProVa 461 ::::::::: :::	428 ysvalmetValGlnIleValProArgValTyrTyrHisProGluGluVal 444 ::: :::::	YLEUTHTPTOCYSVAlSerThrSerValPheAsnGlnSerLysAspPheO	395 ASSGLNTYYLLENVALPROGLYTYYASAARGTRPTRAALACYSASATARG1 411 ::::	CTCACC

70 rValAsnSerThrArgGlyValAlaProArgGlyThrTrpTrpProGluL 87	54 ArgProLeuSerLeuThrTrpLeuIleIleAspProAspThrGlyValTh 70 ::: :::	37 leThrProGlnAlaSerSerLysArgLeuIleAspSerSerAsnProHis 53 :::::::: 5862AAAGGGGCCAGATCCGCAGCACCCGGCTCCAC 59	20 uArgileProLeuSerPheAlaSerIleAlaTrpPheLeuThrLeuThrI 37	4 ThrLeuSerArgArgHisLeuProThrArgGlyGlyGluProLysArgLe 20	Align seg 1/1 to: US-08-886-642-8 from: 1 to: 8323	alignment_block: US-09-171-553B-6 x US-08-886-642-8	alignment_scores: Quality: 1299.00 Length: 709 Ratio: 2.855 Gaps: 26 Percent Similarity: 64.175 Percent Identity: 42.595	GENERAL INFORMATION: APPLICANT: Kayman, Samuel TITLE OF INVENTION: FUSION GLYCOPROTEINS NUMBER OF ESQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson P.C. STREET: 45 Rockefeller Plaza, Suite 2800 CITY: New York STATE: NY COUNTRY: USA ZIP: 10111 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows Version 2.0 CURRENT APPLICATION NUMBER: US/08/886,642 APPLICATION NUMBER: US/08/886,642 APPLICATION NUMBER: 00/110,300 FILING DATE: 20-AUG-1993 APPLICATION NUMBER: 07/938,100 FILING DATE: 28-AUG-1993 APPLICATION NUMBER: 07/938,100 FILING DATE: 28-AUG-1993 APPLICATION NUMBER: 07/938,100 FILING DATE: 28-AUG-1993 APPLICATION NUMBER: 07/63/010002 TELECOMMUNICATION INFORMATION: REGISTRATION NUMBER: 07/63/010002 TELECOMMUNICATION INFORMATION: TELEPHONE: 212/765-5070 TELEFAX: 212/765-5070 TELEFAX: 212/765-5070 TELEFAX: 212/765-5070 TELEFAX: 8323 base pairs TYPE: nucleic acid STRANDEDNESS: Single MOLECULE TYPE: Genomic DNA US-08-886-642-8
7 997	0 947	3 900	7	0830				

344	erGlvProProTvrTvrGluGlyMetAlaLysGluArgLysPheAsnVal	328
6828	eAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerS: ::::	311 6779
7	SerLeuIleGlnGlyAlaPheGlnAlaI 	295 6729
7	lyLeuIleProThrAsnThrProArgAsnSerProGlyValProVal	279 6685
279 6684	erLeuArgProAspIleThrGlnProProSerAsnSerThrThr ::: ::: ::: ::: ::: :::	262 6645
	GlnGlyProProAlaLeuGluProProHisAsnLeuProValProGlnLe	246 6612
	hrGlyThrGluProProValAlaMetGlyProAspLysValLeuAlaGlu ::: :: :: :: :: .AATCTAGGACCTCGGATCCCAATAGGACCAAACCCCGTCCTGGCAGAC	229 6564
229 6563	UTYIG1YG1YA1aG1YSerThrLeuThrI1eArgLeuArgI1eGluT:::	212 6515
212 6514	SerLys	196 6471
196 6470	erAspLeuAspTyrLeuLysIleSerPheThrGluArgLysThrGlyL	180 6435
180 6434	yLysTyrLysMetMetLysLeuTyrLysAspLysSerCysSerProS ::: :::::::: ::: CTCTAACCAGGCTGTTCAGGTATGCAAAGACAATAAGTGGTGCAATCCC.	164 6386
164 6385	IleSerLeuGlnAspArgValLysPheSerPheValAsnSerGlyProGl	148 6345
147 6344	ysArgArgTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpPro 	131 6298
131 6297	rGluLysGluLysTyrCysGlyGlySerGlyGluSerPheC:::::	117 6248
117 6247	SerTyrGlyPheTyrCysCysProGlyTh	108 6198
107 6197	ProProAsnLeuValArg	98 6148
98 6147	CysLeuArgLeuIleAsnProAlaV CAGGCTGTGCCAGAGACTGCAACGAGCCCT	90
6097	TAGAGTATCAGGCCCCCTATTCCTCGCCCCGGGGCCCCCCTTGTTGCTC	6048
89		89
89 6047	euHisPhe	87 5998

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7655 TCTCATTATACTCCTACTAATTCTGCTTTTTGGACCCTGCATTCTTAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7123 GCGTTCTCGTGGAATTATGGCCCAGGGTCACCTACCATCCTCCCAGTTAC 7172
624 rgPheValAlaPheValArgGluArgValSerAlaValGlnIleMetVal 640
                                                                                                                                                                                                                          591 PheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuThrGlyPr 607
                                                                                                                                                                                                                                                                                                                                                           574 luArgArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrp 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 erGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArg 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 ValleuAspGluTyrAspTyrArgTyrAsnArgProLysArgGluDroVa 461
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                                                                                                                                       oLeuValValLeuLeuLeuLeuThrValGlyProCysLeuIleAsnA 624
                                                                                                                                                                                                TTTAACAGATCCCCCTGGTTTACCACGTTGATATCCACCATCATGGGGCC
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alignment_block:
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                                                                                                                                                            Align seg 1/1 to: PCT-US93-08041-8
                                                                                                                                                                                              US-09-17\bar{1}-553B-6 \times PCT-US93-08041-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-08041-8
                                                                                                                                                                                                                                                        Ratio: 2.855
Percent Similarity: 64.175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application PC/TUS9308041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8:
  5831 CCTAATCCCCTTAATTCTC.......
                                                                        5787 ACGCTCTCAAAATCC.....CCTAAAGATAAGATTGACCCGCGGGACCT 5830
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7755 CTGACTCAACAATACCACCAGCTA 7778
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                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                        20 uArgIleProLeuSerPheAlaSerIleAlaTrpPheLeuThrLeuThrI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: The Public Health Research Institute APPLICANT: New York, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: FUSION GLYCOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 LeuArgGlnGlnTyrGlnGlyLeu 648
                                                                                                              4 ThrLeuSerArgArgHisLeuProThrArgGlyGlyGluProLysArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212 /- TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/938,100 FILING DATE: 28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jacobs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
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                                                                                                                                                                                                                                                                                                Quality: 1299.00
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45 Rockefeller Pl.
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20-AUG-1993
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                                                                                                                                                                                                                                                      Length: 709
Gaps: 26
Percent Identity: 42.595
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TTCCTGTCTCTC.... 5861
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279 6684	2 uThrSerLeuArgProAspIleThrGlnProProSerAsnSerThrThrG::: ::: :::	262 6645
262 6644	5 GlnGlyProProAlaLeuGluProProHisAsnLeuProValProGlnLe	246 6612
245 6611	hrGlyThrGluProProValAlaMetGlyProAspLysValLeuAlaGlu::: ::: ::: :::	229 6564
229 6563	2 uTyrG1yG1yG1yA1aG1ySerThrLeuThrI1eArgLeuArgI1eG1uT :::	212 6515
212 6514	ysTyrSerLysValAs::: ACCTCATGG	196 6471
196 6470	PerAspLeuAspTyrLeuLysIleSerPheThrGluArgLysThrGlyL	180 6435
180 6434	LyLysTyrLysMetMetLysLeuTyrLysAspLysSerCysSerProS ::: :::	164 6386
164 6385	IleSerLeuGlnAspArgValLysPheSerPheValAsnSerGlyProGl	148 6345
147 6344	ysargargTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpPro 	131 6298
131 6297	rGluLysGluLysTyrCysGlyGlySerGlyGluSerPhec::::::::::::::::::::::::::::::::::::	117 6248
117 6247	BSerTyrGlyPheTyrCysCysProGlyTh	108
107 6197	allysSerThrProPro	98 6148
98 6147)CysLeuArgLeuIleAsnProAlaV	9609
89 6097	CTAGAGTATCAGGCCCCCTATTCCTCGCCCCGGGGCCCCCCTTGTTGCTC	6048
	euHisPhe	87 5998
87 5997) rValAsnSerThrArgGlyValAlaProArgGlyThrTrpTrpProGluL 	70 5948
70 5947	ArgProLeuSerLeuThrTrpLeuIleIleAspProAspThrGlyValTh ::: ::::: ::: ::	54 5901
53 5900	LeThrProGlnAlaSerSerLysArgLeuIleAspSerSerAsnProHis	37 5862

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APPLICANT: Collins, Mary KL
APPLICANT: Wedss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER APPLICATION NUMBER: GB9517263.1
NUMBER OF SEO ID NOS: 29
COCTUALDE: DATE: 1995-08-23
NUMBER: DESCRIPTION OF THE NEW TOWNS TO THE NEW TOWNS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
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LENGTH: 6061
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                     NAME/KEY: misc_feature
LOCATION: (3996)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: FORMATION: Description of Artificial Sequence: Portion of OTHER INFORMATION: construct
NAME/KEY: misc_feature LOCATION: (3997)
                                                                                                                                                                                                                                                                          OTHER INFORMATION: n is any
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (3810)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (3808)
OTHER INFORMATION: n is any nucleotide
                                                                       FEATURE:
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LOCATION: (3995)
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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OTHER INFORMATION: n is any nucleotide
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LOCATION: (3807)
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142 yAspTrpLysTrpProIleSerLeuGlnAspAr :	126 SerGlyGluSerPheCysArgArgTrpSerCysValThrSerAsnAspGl ::: ::	112 yrcyscysProGlyThrGluLysGluLysTyrCysGlyGly	104 .AsnLeuValArgSerTyrGlyPheT ::::: 1756 GAACAGACTCAAGCTAGACCAGACAACTCATAAATCAAATGAGGGATTTT	1706 GACTGCGAAGAACCTTTAACCTCCCTCACCCCTCGGTGCAACACTGCCTG	103	102 roPro	88HisPheCysLeuArgLeuIleAsnProAlaValLysSerThrP	82 ThrTrpPrpProGluLeu	65 roAspThrGlyValThrValAsnSerThrArgGlyValAlaProArgGly	48 pSerSerAsnProHisArgProLeuSerLeuThrTrpLeuIleIleAspP ::: ::: ::: ::::::::	43 SerLysArgLeuIleAs 1 1 1 1	26 heAlaSerIleAlaTrpPheLeuThrLeuThrIleThrProGlnAlaSer ::::::::::::::::::::::::::::::::::::	12 rArgGlyGlyGluProLysArgLeuArgIleProLeuSerP ::: ::: :::	2 HisProThrLeuSerArgArgHisLeuProTh	Align seg 1/1 to: US-09-011-745-6 fro	alignment_block: US-09-171-553B-6 x US-09-011-745-6	alignment_scores: Quality: 1258.00 Ratio: 2.759 Percent Similarity: 62.466 Percent I	FEATURE: NAME/KEY: misc_feature LOCATION: (3998) OTHER INFORMATION: n is any nucleotide US-09-011-745-6
gValLysPheSerPheV TTCATCACAG						> .					GGGGTCAGTACTGCTTCGCC	hrIleThrProGlnAlaSer ::::: :::: AGGTTAACCCGCGAGGCCCC	eProLeuSerP ::::: CCTCTAGACTGACATGGCGC	LeuProTh TTGGATACACGCCGCCCACG	rom: 1 to: 6061	•	Length: 730 Gaps: 26 Identity: 40.822	ide e
159 1943	142 1905	125 1855	112 1805	1755	103	103 1705	102 1655	87 1611	81 1561	65 1514	48 1464	42 1414	26 1364	12 1314				

456 2756	rHisProGluGluValValLeuAspGluTyrAspTyrAsgTyrAsnArgP (439 2710
439 2709	GlnSerLysAspPheCysValMetValGlnIleValProArgValTyrTy .::	423 2660
422 2659	<pre>rpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAsn ::: </pre>	406 2610
406 2609	rGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrpT .:::::::	389 2566
389 2565	GlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValValTy ::: :::	373 2516
372 2515	erArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysIle :::::: :: ::: CCCAACACAAGTTGACCCTGTCCGAAGTGACCGGACAGGGACTCTGCATA	356 2466
356 2465	UArgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlyS::::::::::::::::::::::::::::::::::::	339 2416
339 2415	TrpLeuCysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGl	323 2366
322 2365	lyAlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCys 	306 2316
306 231	rProGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleGl 	289 2276
289 227	ProSerAsnSerThrThrGlyLeuIleP 	273 2240
272 223	snLeuProValProGlnLeuThrSerLeuArg	256 2210
256 220	OASPLYSVALLEUALAGIUGINGIYPTOPTOAIALEUGIUPTOPTOHISA ::: ::: ::: AAACCCCGTTCTGGCAGACCAACAGCCAGTCTCCAAGCCCAAA.	239 2167
239 216	3 IleArgLeuArgIleGluThrGlyThrGluProProValAlaMetGlyPr	223 2120
222 211	euGlyAsnSerPheLeuLeuTyrGlyGlyGlyAlaGlySerThrLeuT 	206 2072
206 207	ArgLysThrGlyLysTy	191 2029
191 202	LysSerCysSerPro:	175 1994
174 199	9 alAsnSerGlyProGlyLysTyrLysMetLysLeuTyrLysAsp	159 1944

	635 aValGlnIleMetValLeuargGlnGlnTyrGlnGlyLeu 648 : :::	
635 329]	619 ProCysLeuIleAsnArgPheValAlaPheValArgGluArgValserAl 6	
618 324:	602 erAlaLeuThrGlyProLeuValValLeuLeuLeuLeuLeuThrValGly 6	
602 319:	585 yTrpPheGluGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuS (
585 314:	569 LeuArgLysLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGl 5	
568 309	552 ysCysPheTyrValAspHisSerGlyAlaIleArgAspSerMctAsnLys !	
552 304	535 pLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluC :	
535 299	519 SerleuThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAs:	
518 294	502 etThrGluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGlu::::::::::::::::::::::::::::::::	
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485 285	471LeuGlyThralaValGlyValGlyThrGlyThrAlaAlaLeuIl	
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Perfect score:
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             Pred. No.
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            Match
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US-08-766-528-2

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US-09-376-781-25

US-09-011-745-7

US-09-011-745-5

US-09-015-483-310

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2160	gaaagagaggctgaccaggggtggtttgaaggatggttcaaccaggtctcctttggatgacc	10	Qy
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1860	.cagggacagctgccctgatcacaggaccacagcagctagagaaaaggacttggtga	1801	Qy
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2047	gggaaggggacatgcataggaaaagctcccccatc	1988	Db
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                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 2, Application US/08766528 Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: cDNA US-08-766-528-2
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2641 totcaactgcaatotgtcactotgcccaggagcccacgcaggtgcggacctccggagcta 2700
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                                                                            REFERENCE/DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       STREET: 60 St.
CITY: Boston
STATE: Massac
                                                                                                                                                                                                              APPLICATION NUMBER: US/08/766,528 FILING DATE:
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                                                                                                                                              REGISTRATION NUMBER: 35,965
                                         TOPOLOGY:
                                                   STRANDEDNESS:
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                                                             nucleic acid
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                                                                          7333 base pairs
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                                           linear
                                                                                                                                                                                                                                                                                  Floppy disk
                                                     single
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Length 7333;
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Query Match

63.7%;

Score 1882.8; DB 4;

4d 4d 4d 60 60 60 60 60 60 60 60 60 60 60 60 60	40 40 40 40 40 40 40 40 40 40 40 40 40 4	Best Matc Qy
5220 TCTTTGTTAACAAT 5220 TCTTTTGTTAACAAT 843 ttccggcccgggca 7 843 ttccggcccgggca 7 903 agacttagattatct 9 903 agacttagattatct 1111 111111111111111111111111111111	61 acgggggaccccccccgttgtagaaattgccccyattgctaftillillillillillillillillillillillillill	Local Similarity 80.1%; Pred. No. 0; hes 2409; Conservative 0; Mismatches 402; Indels 195; C hes 2409; Conservative 0; Mismatches 402; Indels 195; C 1 tgctttttagggttaggaacacccctggacagtttgggctgaccccctatgaattgctc 1 tgctttttagggttaggaacacccctggacagtttgggcTgaccccCTATAAATTGCTC 1

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6428 CTCAGGAGCCATCAGAGACTCCATGAGCAAGCTTAGAGAAAGGTTAGAGAGGCGTCGAAG 6487
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GENERAL INFORMATION:
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APPLICANT: Stoye, Jonathan p
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
FILE REFERENCE: 4238/75168
FILE REFERENCE: 4238/75168
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CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
BARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                     TYPE: DNA ORGANISM: Porcine retrovirus
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                    Similarity
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US-09-111-085-1
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                                    gcttagaaaaaagttagagaggcgtcgaagggaaagagaggctgaccaggggtggtttga 2129
                                                                         1926 gcttagagaaaggttagagaggcgtcgaagggaaagaggctgaccaggggtggttga 1985
                                                                                                            2130 aggatggttcaacaggtctccttggatgaccaccctgcttctgctctgacggggccct 2189
1866 aaaagagaatgetgettetatgtagateacteaggageeateagagaetecatgagea 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jay A. Fishman IIILE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS IIILE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MGP-038CP TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/766,528
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Patent No. 6190861
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REGISTRATION NUMBER: 35,965
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CORRESPONDENCE ADDRESS:
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US-08-766-528-3
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Pred. No. 0;
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                       LENGTH: 8132 base pairs
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                         MOLECULE TYPE: CDNA
                                                                               ; MOLECULE TO
US-08-766-528-3
                                                                                                                             Query Match
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27.4	3 tatggoggggagoagggtccactttaaccattcgccttaggatagagacggggacagaa 1062
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386	I I I I I I I I I I I I I I I I I I I
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6446	-CGACTAAAATGGGGGCAAAACTTTTAGCCTCATCCAGGGGGGGCTTTTCAACTCTTAAC 650
1303	tecacegacectgatgecaettettettgttggetttgtetatecteagggeeteettat 1362
363	tatgagggatggctaaagaaagaaaattcaatgtgaccaaagagcatagaaatcaatgt 142
423	acatgggggtcccgaaataagcttacctcactgaagttccgggaagggacatgcata
483	aaaagctcccccatcccaccaacacctttgctatagtactgtggtttatgagcaggcc 154
i 7	GAAANGITUCCCCAICCCACCAACACCITIGIAACCACACGAAGCCITIAAICAAACC 674
	Ccagaaaatcagtatttagtacctggttataacaggtggtgggcatgcaatactgggtta 1602
603	acccctgtgtttccacctcaqtcttcaaccaatccaaaatttgtgtgtcatggtccaa 1662
663 865	atcgtccccgagtgtactaccatcctgaggaagtggtccttgatgaatatgactatcgg 1722
723	Cogtatecettaecetagetgtaatgeteggattaggg 178.
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843 045	Oggccatgacagaagatctccgagccttaaaggagtct 19
03	.tctttgtctgaagtggttctacagaaccggagg 196.

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2023 tgcttctatgtagatcactcaggagccatcagagactccatgaacaagcttagaaaaag 2082
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1963 ggattagatctgctgtttctaagagaaggtgggttatgtgcagccttaaaagaagaatgt 2022
                  2143 aggietectiggaigaecaccetgetitetgetetgaeggggeecetagiagteetgete 2202
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US-08-766-528-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.7%; Score 1231.8; DB 4; Length 8060; 69.8%; Pred. No. 0;
                APPLICANT: Jay A. Fishman .
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MGP-038CP
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/766,528
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>=</u>
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 8060 base pairs
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Matches 1873; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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                                                                                                                                                                                                          02109-1875
GENERAL INFORMATION:
                                                                                                                                                       Boston
                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                            COUNTRY:
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                                                                                                                              816 ggaccgggtaaaattctcctttgtcaa-----ttccggcccgggcaagtacaa 863
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478 TAAACAATGGAACTGTGTAACCTCTAATGATGGATATTGGAAATGGCCAACCTCTCAGCA 537
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                          1821 cacaggaccacagcagctagagaaaggacttggtgagctacatgcggccatgacagaaga 1880
                                       1881 totccgagccttaaaggagtctgttagcaacctagaagagtccctgacttctttgtctga 1940
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TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of TITLE OF INVENTION: Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 32.9%; Score 973.8; DB 4; Length 2000; Local Similarity 70.2%; Pred. No. 1.2e-305; nes 1461; Conservative 0; Mismatches 532; Indels 88;
2896 cagcgcgcttggaataaaaatcctcttgctgtttgcatcaaaa 2938
                          2551 CAGCGCGCTTGGAATAAAATCCTCTTGCTGTTTGCATCAAGA 2593
                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
                                                                                                                                               Sequence 25, Application US/09376781 Patent No. 6261806
                                                                                                                                                                                                                                                     APPLICANT: Andersson, Goran K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                           APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive
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SEQ ID NO 25
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APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of
Patent No. 6261806
TITLE OF INVENTION: Use
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Indels 88; Gaps
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70.2%; Pred. No. 1.2e-305;
tive 0; Mismatches 532;
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CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
                                                                                                                                                     ; Sequence 30, Application US/09376781
; Patent No. 6261806
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Qy Db	622 ctgcatti 301 ctatatgi	Typectecgattgattaacccgctgttaaaagcacacctcccaacctagtc 68
Οy	682 cgtagtta	999ttctattgctgcccaggcacagagaaagaaatactgtgggggt 73:
Ob	358 cgtgct	
Qy Dp	739 tctggggaa 418 cctagagat	octtctgtaggagatggagctgcgtcacctccaacgatggagactggaaa 79
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Qy Dp	919 aagataagt 598 aaaataagt	aaaaaggaaaacaggaaatattcaaaagtggataaatggtatg 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of Partent No. 6261806
TITLE OF INVENTION: 02686
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
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; Patent No. 6261806
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APPLICANT: Banerjee, Papia T.
APPLICANT: Patience, Clive
APPLICANT: Andersson, Goran K.
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US-09-376-781-24
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                                                                                                                                                                                                                                               Query Match 24.0%; Score 710.4; DB 4; Length 1493; Best Local Similarity 70.7%; Pred. No. 3.4e-220; Matches 1069; Conservative 0; Mismatches 361; Indels 82; Gaps
                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:Nucleotide OTHER INFORMATION: sequence of the 3' end of the PERV-D env region. US-09-376-781-24
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EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEO ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                       LENGTH: 1493
                                                                                         SEQ ID NO 24
                                                                                                                          TYPE: DNA
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                                                         815 atcgacaaaagaaaaaacccatatccctgacactcgcagtaatgctcggactcggagtga
                                                                                                     Sequence 7, Application US/09011745

Sequence 7, Application US/09011745

Patent No. 6165715

GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Welss, Robin A
TITLE OF INVENTION: Expression systems
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011.745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06.22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER PILING DATE: 1996-08-23
EARLIER PILING DATE: 1996-08-23
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO?

FEMALUM NO?
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                                      OTHER INFORMATION: Description of Artificial Sequence: Portion OTHER INFORMATION: construct
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15.4%; Score 455; DB 4; L
Best Local Similarity 53.0%; Pred. No. 8.5e-137;
Matches 1261; Conservative 0; Mismatches 1030;
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LOCATION: (4058)
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LOCATION: (4246)
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LOCATION: (4247)
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LOCATION: (4248)
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LOCATION: (4249)
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                                                                                                                                                                                ccctgtgtttccacctcagtcttcaaccaatccaaagatttgtgtgtcatggtccaaat 1664
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1485 aaaageteeeceateecaceacaacacetttgetatagtaetgtggtttatgageaggeete 1544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT:
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5704 CCCTGTCTTATTTACTCACTTAAAGGCTTTAGAAATTGTAAGGACCCAAAATCTGGGACCA 5763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /standard_name= "GaLV SEATO Genome"
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                                                                                                                                                                         15280-128-1PC
APPLICATION NUMBER: US/08/716,351A
                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                          NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 15280
TELECOMMUNICATION INPORMATION:
TELEFAX: (415) 543-5043
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8535 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
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LOCATION: 1..8535
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                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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1725 taaccgaccaaaaagagaacccgtatcccttaccctagctgtaatgctcggattagggac 1784
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RESULT 11
US-09-075-272-1
US-09-075-272-1
Sequence 1, Application US/09075272
Patent No. 6136598
GENERAL INFORMATION:
APPLICANT: MILLER, A. DUSTY
APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BONNAM, LYNN
TITLE OF INVENTION: PACKAGING CELL LINES
ITTLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO EMBATCAGENC Center, 8th Floor
CITY: San Francisco
STREET: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: ELDPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 372.2; DB 3; 62.1%; Pred. No. 8.3e-110; tive 0; Mismatches 383;
                                                                                                                                                                                                                                                         14538A-003710
                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,140
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POOF, Brian W.
REGISTRATION NUMBER: 32,928
                                    UMBER: US/09/075,272
08-MAY-1998
                                                                                                                                                                                                                                            REFERENCE/DOCKET 1453
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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Best Local Similarity
                                                                                       CLASSIFICATION:
                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Retroviral Vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/716,351A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bastian,, Kevin L.
REGISTRATION NUMBER: 34,77
REFERENCE/DOCKET NUMBER: 15280-128-1PC
TELECOMNUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03784
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08716351A; Patent No. 6033905; GENERAL INFORMATION:
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nucleic acid
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-716-351A-5
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                                                                                                                                                                       ATCAATTCCTCTAAAAACCATCAGTATCTGCTCCCCTCAAACCATAGCTGGTGGGGCCTGC 6552
                                                                                                                                                                                                               aatactgggttaaccccctgtgtttccacctcagtcttcaaccaatccaaagatttgtgt 1650
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                                                              gggacatgcataggaaaagctcccccatcccaccaacacctttgctatagtactgtggtt 1530
                                                                                               6433 GGGCCATGCATAGGGAAGGTGCCTCTTACCCATCAACATCTTTGCAACCAGACCTTACCC 6492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGGTTAGGGATTGCGGCAGGTATAGGTACTGGCTCAACCGCCCTAATTAAAGGGCCC 6792
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                         12;
                         Indels
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     Pred. No. 4.7e-105;
0; Mismatches 337;
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; Sequence 18, Application US/09376781
; Patent No. 6261806
; GENERAL INFORMATION:
     62.9%;
                       592; Conservative
Best Local Similarity
Matches 592; Conserv
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                                                       Methods
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                                               TITLE OF INVENTION MOLECULAR Sequence of Swine Retrovirus and Neterin No. 6254806
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT APPLICATION NUMBER: 60/097,015
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER PILING DATE: 1998-08-18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 18
                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 343; DB 4; Length 69
Pred. No. 4.1e-101;
0; Mismatches 191; Indels
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                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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al Similarity 71.0%;
483; Conservative
APPLICANT: Banerjee, Papia T.
APPLICANT: Patience, Clive
APPLICANT: Andersson, Goran K.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     Patent No. 6261806
                                                                                                                                                                                                                                                         LENGTH: 698
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                                                                                                                   APPLICANT: COLLINS, MATY KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REPERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEO ID NOS: 29
NUMBER OF SEO ID NOS: 29
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; JCCATION: (3965)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-5
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INFORMATION: n is any nucleotide
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Best Local Similarity 56.7<sup>3</sup>
Matches 631; Conservative
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LOCATION: (3775)
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LOCATION: (3962)
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LOCATION: (3963)
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LENGTH: 6028
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1551 tcagtatttagtacctggttataacaggtggtgggcatgcaatactgggttaaccccctg 1610
                           1188 CTACTACCTTGCAGCACCCGCCGGACAACTGGGCCTTGCAGCATGGATTGACTCCCTG 1247
                                                                                                 1671 cogagigitaciaccaiccigaggaagiggicciigaigaataigaciaioggiataaccg 1730
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                                                                          APPLICANT: Nienhuis, Arthur W.
APPLICANT: Vanin, Elio F.
TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR and Retroviral Vecto
                                                                                                                                                                              ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1191 cagtaccactggattgattcctaccaacacgcctagaaactccccaggtgttcctgttaa 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1251 gacaggacagagactcttcagtctcatccagggagctttccaagccatcaactccaccga 1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 303.8; DB 1; Length 1965; 56.5%; Pred. No. 4.6e-88; tive 0; Mismatches 472; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271010-208
                                                                                                                                                                                                                                                                                    COMPOTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
                      Sequence 9, Application US/08258420 Patent No. 5710037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: -Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COPERATING SYSTEM: MS-DOS
COPERATE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-258-420-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 629; Conservative
                                                                                                                                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                            CITY: Roseiana
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1965 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                          GENERAL INFORMATION:
                                                                                                                                                                                       STREET: 6 BECALLITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                          07068
  US-08-258-420-9
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Sequence | Strid Orig | Sixto | Strid Orig | Sixtore | Escore | Len | Documentation | Sequence | Se
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Database length: 113238999
Search time (sec): 134.760000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -Q-G9n2_1/USPT0_Spool/US9917153/runat_22022002_122826_11171/app_query.fasta_1.3312
-DB=Issued_Patents_NA -QPMT=fastap -SUFFIX=feb22std.rni
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.000 -GAPOP=4.500 -GAPEXT=7.000 -YGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cd1-LIST=45 -DOCALIGN=200
-THR_SCORE=PCt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09171553 -GCN1_1_158 -NCPU=6 -LOPU=3 -LONGLOG
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LENGTH: 3482
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                 rpSerCysValThrSerAsnAspGlyAspTrpLysTrpProIleSerLeu 150
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alignment_block:
US-09-171-553B-10 x US-09-111-085-3
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-007-282B-1 + 426.50
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-716-351A-3 + 420.50
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-376-781-7 + 389.00
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-078-311-20 + 297.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 3484.00
Ratio: 5.319
Percent Similarity: 99.696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: Specific sequences
FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION UMBER: GB 9710154.7
EARLIER APPLICATION UMBER: GB 9710154.7
EARLIER APPLICATION UMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ. ID NOS: 16
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APPLICANT: Weiss, Robin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
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                              rGluLysGluLysTyrCysGlyGlySerGlyGluSerPheCysArgArgT •134
                                                                                                                                                                                                                                                      rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLysSer 100
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                                                                                                               ACACCTCCCAACCTAGTCCGTAGTTATGGGTTCTATTGCTGCCCAGGCAC
                                                                                                                                                                  ThrProProAsnLeuValArgSerTyrGlyPheTyrCysCysProGlyTh 117
                                                                                                                                                                                                                              GGCCTGAACTGCATTTCTGCCTCCGATTGATTAACCCCGCTGTTAAAAGC
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Percent Identity: 98.478
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1310
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434 leValProArgValTyrTyrHisProGluGluValValLeuAspGluTyr
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                                                                                                                                          ProGlyTyrAsnArgTrpTrpAlaCysAsnThrGlyLeuThrProCysVa 417
                                                                                                                                                                                                                                                                                                                                        hrAsnThrProArgAsnSerProGlyValProValLysThrGlyGlnArg 300
                                                                        lSerThrSerValPheAsnGlnSerLysAspLeuCysValMetValGlnI 434
                                                                                                                                                                                                                ysTyrSerThrValValTyrGluGlnAlaSerGluAsnGlnTyrLeuVal 400
                                                                                                                                                                                                                                                                    CGGGAAGGGGACATGCATAGGAAAAGCTCCCCCATCCCACCAACACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyProProTyrT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTAAAGATAAGTTTCACTGAAAAAGGAAAACAGGAAAATATTCAAAAG
                                                   TTCCACCTCAGTCTTCAACCAATCCAAAGATTTCTGTGTCATGGTCCAAA
                                                                                                                         CCTGGTTATAACAGGTGGTGGGCATGCAATACTGGGTTAACCCCCTGTGT
                                                                                                                                                                                              GCTATAGTACTGTGGTTTATGAGCAGGCCTCAGAAAATCAGTATTTAGTA
                                                                                                                                                                                                                                                                                     rGlyLysGlyThrCysIleGlyLysAlaProProSerHisGlnHisLeuC
                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGGGGATGGCTAAAGAAGGAAAATTCAATGTGACCAAAGAGCATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                 yrGluGlyMetAlaLysGluArgLysPheAsnValThrLysGluHisArg 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATGCCACTTCTTGTTGGCTTTGTCTATCCTCAGGGCCTCCTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTCAGTCTCATCCAGGGAGCTTTCCAAGCCATCAACTCCACCGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSerThrAspPr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAACACGCCTAGAAACTCCCCAGGTGTTCCTGTTAAGACAGGACAGAGA 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTGGAGCCACCGCATAACTTGCCGGTGCCCCAATTAACCTCGCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTGTGGCAGTGGGACCCCGATAAAGTACTGGCTGAACAGGGGCCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roProValAlaMetGlyProAspLysValLeuAlaGluGlnGlyProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGATGAAACTATATAAAGATAAGAGCTGCTCCCCATCAGACTTAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt sMetMetLysLeuTyrLysAspLysSerCysSerProSerAspLeuAspT}
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seq_documentation_block:
                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-111-085-1
                                                 GENERAL INFORMATION:
                                                                             Sequence 1, Application US/09111085 Patent No. 6100034
APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
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                                                                                                                                                                                                                                           2861 AGCCAAGGAGAAACTGACCTC 2881
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                                                                                                                                                                                                                                                                                                                                                                           alSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rValGlyProCysLeuIleAsnArgPheValAlaPheValArgGluArgV 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluGluCysCysPheTyrValAspHisSerGlyAlaIleArgAspSerMe
                                                                                                                                                                                                                                                                                                SerGlnGlyGluThrAspLeu 657
                                                                                                                                                                                                                                                                                                                                                    TGAGTGCAGTCCAGATCATGGTACTTAGGCAACAGTACCAAGGCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAGGGGTGGTTTGAAGGATGGTTCAACAGGTCTCCTTGGATGACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArgGluAlaA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeuLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuSerAlaLeuThrGlyProLeuValValLeuLeuLeuLeuLeuTh, 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spGlnGlyTrpPheGluGlyTrpPheAsnArgSerProTrpMetThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCAAGCTTAGAGAAAGGTTAGAGAGGCGTCGAAGGGAAAGAGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGAATGTTGCTTCTATGTAGATCACTCAGGAGCCCATCAGAGACTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTAGATCTGCTGTTTCTAAGAGAAGGTGGGTTATGTGCAGCCTTAAAA
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TITLE OF INVENTION: Detection of retroviral sulfittle OF INVENTION: Specific sequences; FILE REFERENCE: 4238/75168; CURRENT APPLICATION NUMBER: US/09/111,085; CURRENT FILING DATE: 1998-07-07; EARLIER APPLICATION NUMBER: GB 9710154.7; EARLIER FILING DATE: 1997-05-16; NUMBER OF SEQ ID NOS: 16; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 1

subtypes

based

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; TYPE: DNA; ORGANISM: PC
US-09-111-085-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-171-553B-10 x US-09-111-085-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 2631.50
Ratio: 4.468
Percent Similarity: 86.745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-111-085-1 from: 1 to: 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Porcine retrovirus
                                                                                                           215 lyGlyGlyAla..........
                                                                                                                                                                                                                                                                                                       661 GTCTCTCAGCAAGACAGAGTAAGTTACTCTTTTGTTAACAATCCTACCAG
                                                                                                                                                                                                                                                                                                                                                                                      131 ysArgArgTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpPro 147
                                                                                                                                                                                                                                                                                                                                                                                                                                     561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AACTCCCATAAACCCTTATCTCTCACCTGGTTACTTACTGACTCCGGTAC
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                                                                                                                                                                                                        170 ysLeuTyrLysAspLys......SerCysSerProSerAsp 181
                                                                                                                                                                                                                                         711 TTATAATCAATTTAATTATGGCCATGGGAGATGGAAAGATTGGCAACAGC
                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                       115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 ATGCATCCCACGTTAAGCCGGCGCCCCCCCCCGATTCGGGGTGGAAAGCC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AsnProHisArgProLeuSerProThrTrpLeuIleIleAspProAspTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oGly...ThrGluLysGluLysTyrCysGlyGlySerGlyGluSerPheC 131
                                           TCAAAAGTGGGTAAATGGTATATCTTGGGGAATAGTGTAC.....TATG 904
                                                                eGlnLysTrpIleAsnGlyMetSerTrpGlyIleValPheTyrLysTyrG 215
                                                                                                                                                                                                                                                          GCAAGCAATGGAGCTGCATAACTTCTAATGATGGGAAATTGGAAATGGCCA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGACCCCCAAATAATGAAGAATATTGTGGAAATCCTCAGGATTTCTTTT 610
GlySerThrLeuThrIleArgLeuArgIle 228
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905	GAGGCTCTGGGAGAAAGAAAGGATCTGTTCTGACTATTCGCCTCAGAATA	954
229 955	GluThrGlyThrGluProProValAlaMetGlyProAspLysValLeuAl ::: ::: GAAACTCAGATGGAACCTCCGGTTGCTATAGGACCAAATAAGGGTTTGGC	245 1004
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1005	ACAG	1032
262 1033	.nLeuThrSerLeuArgProAspTleThrGlnProProSerAsnSerThr ::: :: AGGCCATCTCCTAACCCCTCTGATTACAATTACAACC	278 1068
	rGlyLeuIleProThrAsnThrProArgAsnSerProGlyValProVa::: ::: ::::::::::::::::::::::::	295
29	LysThrGlyGlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaI 	12
0	AAAACAGGGGCGAAACTTTTTAGCCTCATCCAGGGAGCTTTTCAAGCTC	-
312 1154	leAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSer:: :::	328 1203
329 1204	SerGlyProProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnVa TCGGGCCCACCTTACTATGAGGGGAATGGCTAGAGGAGGGAAATTCAATGT	345 1253
345 1254	1ThrLysGluHisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuT	362 1303
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379 1354	SerHisGlnHisLeuCysTyrSerThrValValTyrGluGlnAlaSerGl 	395 1403
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479 1654	GlyThrGlyThrAlaAlaLeuileThrGlyProGlnGlnLeuGluLysGl 	495 1703
495 1704	yLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysG :::::: ACTTAGTAACCTACATCGAATTGTAACGGAAGATCTCCAAGCCCTAGAAA	512 1753
512 1754	luSerValSerAsnLeuGluGluSerLeuThrSerLeuSerGluValVal:::	528 1803

linear

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                       TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2104
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                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004
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                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pair
                                                                                                                                       TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JAY A. FISHMAN
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 PheValArgGluArgValSerAlaValGlnIleMetValLeuArgGlnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 uCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHisSerGlyA 562
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 LeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLe 545
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                              NAME: Louis Myers REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nTyrGlnGlyLeuLeuSerGlnGlyGluThrAspLeu 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTCCTGTTACTTACAGTTGGGCCTTGCTTAATTAATAGGTTTGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euLeuLeuLeuThrValGlyProCysLeuIleAsnArgPheValAla 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTTGGATGACCACCCTGCTTCTGCTCTGACGGGGCCCCTAGTAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCAGAGACTCCATGAGCAAGCTTAGAGAAAGGTTAGAGAGGCGTCGA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACCAAGGCCTTCTGAGCCAAGGAGAAACTGACCTC 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGTTAGAGAACGAGTGAGTGCAGTCCAGATCATGGTACTTAGGCAACA 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLeuValValL 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPheAsnArgSe 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTGTAGCCTTAAAAGAGGAATGCTGCTTCTATGTAGATCACTCAGGAG 1903
                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08766528
                                           7333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 State Street
                                                                                                               (617)227-5941
single
                                                                                                                                                                                                                                                                                                                                                                            US/08/766,528
                                                                                                                                                                                                           35,965
                                                                                                                                                                                        MGP-038CP
                                                                                                                                                                                                                                                                                                                                                                                                                          #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2103
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-766-528-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 86.626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-171-553B-10 x US-08-766-528-2
                                                                                              5450 AAAGAAAGGATCTGTTCTGACTATTCGCCTCAGAATAGAAACTCAGATGG 5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5156
                                                                                                                                                                                                                                                                                                                                       5356 AAATAAGTTTCACTGAAAAAGGAAAACAAGAAAATATTCAAAAGTGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5006 TGTCTGCCTTCGATCAGTAATCCCTGGTCTCAATGACCAGGCCACACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4956 AACAGCACTCAAGGGGAGGCTCCCTTGGGGACCTGGTGGCCTGAATTATA 5005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4906 CCTTATCTCTCACCTGGTTACTTACTGACTCCGGTACAGGTATTAATATT 4955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4856 TCCTCAAGTTAATGGTAAACGCCTTGTGGACAGCCCGAACTCCCATAAAC
233 luProProValAlaMetGlyProAspLysValLeuAlaGluGlnGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LysGluLysTyrCysGlyGlySerGlyGluSerPheCysArgArgTrpSe 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 rProGlnAlaSerSerLysArgLeuIleAspSerSerAsnProHisArgP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 IleProLeuSerPheAlaSerIleAlaTrpPheLeuThrLeuThrIleTh
                                                                                                                             ......GlySerThrLeuThrlleArgLeuArgIleGluThrGlyThrG 233
                                                                                                                                                                                                               AATGGTATATCTTGGGGAATAGTGTAC.....TATGGAGGCTCTGGGAG 5449
                                                                                                                                                                                                                                                  AsnGlyMetSerTrpGlyIleValPheTyrLysTyrGlyGlyGlyAla..
                                                                                                                                                                                                                                                                                                                                                                   ysIleSerPheThrGluLysGlyLysGlnGluAsnIleGlnLysTrpIle 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCATAACTTCTAATGATGGGAATTGGAAATGGCCAGTCTCTCAGCAAG 5205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rCysValThrSerAsnAspGlyAspTrpLysTrpProIleSerLeuGlnA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGATGTACTCCGTGCTTACGGGTTTTACGTTTGCCCAGGACCCCCAAAT 5105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sPheCysLeuArgLeuIleAsnProAlaVal....LysSerThrProP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roLeuSerProThrTrpLeuIleIleAspProAspThrGlyValThrVal 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTACGAAATAAGCAAATAAGCTGTCATTCGTTAGACCTAGATTACTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pLys.....SerCysSerProSerAspLeuAspTyrLeuL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTATGGCCATGGGAGATGGAAAGATTGGCAACAGCGGGTACAAAAAGA 5305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......GlyProGlyLysTyrLys.....MetMetLysLeuTyrLysAs 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGAGTAAGTTACTCTTTTGTTAACAATCCTACCAGTTATAATCAATTT 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spArgValLysPheSerPheValAsnSer..........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 2537.50
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                                  249
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549 6398	rgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeu 	533 6349
533 6348	nLeuGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnArgA 	516 6299
516 6298	HisalaalametThrGluAspLeuArgAlaLeuLysGluSerValSerAs ::: ::: ::: CATCGAATTGTAACGGAAGATCTCCCAAGCCCTAGAAAAATCTGTCAGTAA	500 6249
499 6248	laAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeu 	483 6199
483 6198	uAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrGlyThrA 	466 6149
466 6148	TyraspTyrargTyrasnargProLysargGluProValSerLeuThrLe	450 6099
449 6098	InIleValProArgValTyrTyrHisProGluGluValValLeuAspGlu	433 6049
433 6048	SVA1SerThrSerVa1PheAsnG1nSerLysAspLeuCysVa1MetVa1G	416 5999
416 5998	ValProGlyTyrAsnArgTrpTrpAlaCysAsnThrGlyLeuThrProCy 	400 5949
399 5948	euCysTyrSerThrValValTyrGluGlnAlaSerGluAsnGlnTyrLeu 	383 5899
383 5898	5 lSerGlyLysGlyThrCysIleGlyLysAlaProProSerHisGlnHisL 	366 5849
366 5848) ArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeuThrGluVa ::: :::	350 5799
349 5798	3 yrTyrGluGlyMetAlaLysGluArgLysPheAsnValThrLysGluHis 	333 5749
333 5748	5 PProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyProProT :::	316 5699
316 5698	0 ArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSerThrAs :::	30 564
299 5648	hrProArgA	28 561
283 5613	:InProProSerAsnSerThrThrGlyL ::: ::: CCTCTGATTACAATACAACCTCTGGAT	26 556
266 5564	.euProValProGlnLeuThrs	555
5549	AACCTCCCGTTGCTATAGGACCAAATAAGGGTTTGGC	1 0

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US-08-766-528-1
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    Sequence 1, Application US/08766528
    Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                           TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616 uThrValGlyProCysLeuIleAsnArgPheValAlaPheValArgGluA 633
                     TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6699 CTGAGCCAAGGAGAAACTGACCTC 6722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6649 GAGTGAGTGCAGTCCAGATCATGGTACTTAGGCAACAGTACCAAGGCCTT 6698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6499 CTGACCAGGGGTGGTTTGAAGGATGGTTCAACAGGTCTCCTTGGATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 LeuSerGlnGlyGluThrAspLeu 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 rgValSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583 laAspGlnGlyTrpPheGluGlyTrpPheAsnArgSerProTrpMetThr 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566 rMetAsnLysLeuArgLysLysLeuGluArgArgArgArgArgGluArgGluA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550 LysGluGluCysCysPheTyrValAspHisSerGlyAlaIleArgAspSe 566
                                       LENGTH: 8060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/766,528
                                                                                                                                                                                                                                              MGP-038CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
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alignment_block: US-09-171-553B-10 x US-08-766-528-1 alignment_scores: Quality: 2402.00 Ratio: 4.312 Percent Similarity: 85.038 Align seg 1/1 to: US-08-766-528-1 from: 1 to: 8060 ||:::|||:::
777 TCAAAATAAACCAG...CTGGAGCCTCCAATGGCTATAGGACCAAATACG 823 164 yLysTyrLysMetMetLysLeuTyrLysAspLysSer.....CysSerP 179 243 ValLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeuPr 259 226 euArgIleGluThrGlyThrGluProProValAlaMetGlyProAspLys 242 731 TATGGAGGCTCGGGTAAACAACCAGGCTCCATTCTAACTATTCGCC 212 rLysTyrGlyGlyAla........GlySerThrLeuThrIleArgL 226 683 GAAAATATCCTAAAATGGGTAAATGGTATGTCTTGGGGAATGGTATAT.. 730 196 GluAsnIleGlnLysTrpIleAsnGlyMetSerTrpGlyIleValPheTy 212 633 CTTCAGACCTAGATTACCTAAAAATAAGTTTCACTGAGAAAGGAAAACAA 179 roSerAspLeuAspTyrLeuLysIleSerPheThrGluLysGlyLysGln 195 583 ACAATTTAATTACCTGACCTGGATTAGAACTGGAAGCCCCCAAGTGCTCTC 483 AATGGAACTGTGTAACCTCTAATGATGGATATTGGAAATGGCCAACCTCT 532 433 ACCAAATAATGGAAAACATTGCGGAAATCCCCAGAGATTTCTTTTGTAAAC 482 117 rGluLysGlu...LysTyrCysGlyGlySerGlyGluSerPheCysArgA 133 336 236 AACTCCCATAAACCCTTATCTCTCACCTGGTTAATTACTGACTCCGGCAC 285 186 CTCTGTCAATAACCTCTCAGACTAATGGTATGCGCATAGGAGACAGCCTG 235 84 rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLysSer 100 51 AsnProHisArgProLeuSerProThrTrpLeuIleIleAspProAspTh 67 34 hrLeuThrIleThrProGlnAlaSerSerLysArgLeuIleAspSerSer 50 86 ATGCATCCCACGTTAAGCCGGCGCCACCTCCCGATTCGGGGTGGAAAGCC 135 1 MetHisProThrLeuSerTrpArgHisLeuProThrArgGlyGlyGluPr 17 GCCTGATCTATACGTTTGCCTCAGATCAGTTATTCCTAGTCTGACCTCA 385 Percent Identity: 68.702 Gaps: 776 682

824	GTCTTGACGGGTCAAAGACCCCCAACCCCAAGGACCA	859
259	roProSerA	276
860		872
7	erThrThrGlyLeuIleProThrAsnThrProArgAsnSerProGly	وتد
7	CATAACTTCTGGATCAGACCCCCACTGAGTCTAGCAGCACGACT	·
293 917	ValLySThrGlyGlnArgLeuPheSerLeuIleGlnGlyAlaPh	309 957
309 958	GlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTrpLeuC :::	326 100
326 1008	ysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluArgLys ::	342 105
343 1058	ThrLysGluHisArgAsnGlnCysThrTrpGlySerArgAs ::: ACAAAAGAACATAGAGACCAATGCACATGGGGATCCCAAAA	359 110
359 1108	nLysLeuThrLeuThrGluValSerGlyLysGlyThrCysIleGlyLysA	376 115
376 1158	laProProSerHisGlnHisLeuCysTyrSerThrValValTyrGluGln::	392 120
393 1208	AlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCy:::: :::	409 125
409 1258	sAsnThrGlyLeuThrProCysValSerThrSerValPheAsnGlnSerL 	426 130
426 1308	pLeuCysvalMetValGlnIleValProArgValTyrTyrHisPro ::: :::	442 135
443 1358	GluGluValValLeuAspGluTyrAspTyrAsgTyrAsnArgProLysAr :::::::	459 140
459 1408	gGluProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaV :::	476 145
476 1458	alGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeu::	492 150
493 1508	GluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAl 	509 155
509 1558	aLeuLysGluSerValSerAsnLeuGluGluSerLeuThrSerLeuSerG ::::::	526 160
526 1608	LUValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGlu AGTAGTCCTACAGAATAGAAGAGGGTTAGATTTATTATTCTAAAAGAA	542 165
543 1658	GlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHi :::	559 170

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alignment_scores:
                                                                                                                           US-08-766-528-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-766-528-3
                                                                                                                                                                                                                                                                               NAME: LOUIS MYERS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08766528 Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentTn Bollo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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       Quality: 2395.00
Ratio: 4.292
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                          Length:
Gaps:
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alignment_block:
US-09-171-553B-10 x US-08-766-528-3
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                                                    6358 GTCTTGACGGGTCAAAGACCCCCAACCCAAGGACCA......6393
                                                                                                                                                                                     6311 TCAAAATAAACCAG...CTGGAGCCTCCAATGGCTATAGGACCAAATACG 6357
                                                                                                                                                                                                                                                                                                            6265 ....TATGGAGGCTCGGGTAAACAACCAGGCTCCATTCTAACTATTCGCC 6310
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                                                                                                                      243 ValLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeuPr 259
                                                                                                                                                                                                                                             226 euArgIleGluThrGlyThrGluProProValAlaMetGlyProAspLys 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 GluAsnIleGlnLysTrpIleAsnGlyMetSerTrpGlyIleValPheTy 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 roSerAspLeuAspTyrLeuLysIleSerPheThrGluLysGlyLysGln 195
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259 oValProGlnLeuThrSerLeuArgProAspIleThrGlnProProSerA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 LeuGlnAspArgValLysPheSerPheValAsn....SerGlyProGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 rGluLysGlu...LysTyrCysGlyGlySerGlyGluSerPheCysArgA 133
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                                                                                                                                                                                                                                                                                                                                                                          rLysTyrGlyGlyGlyAla......GlySerThrLeuThrIleArgL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCAGACCTAGATTACCTAAAAATAAGTTTCACTGAGAAAGGAAAACAA 6216
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6592 TTCAATGTGACAAAAGAACATAGAGACCAATGCACATGGGGATCCCAAAA 6641
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      7242
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                                                                                                                       7192 GGAGGATTATGTGTAGCCTTGAAGGAGGAATGCTGTTTTTATGTGGATCA 7241
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                                                                                                                                                    543 GlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHi 559
                                                                                                                                                                                                                                                                        526 luValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGlu 542
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                                                        559 sSerGlyAlaIleArgAspSerMetAsnLysLeuArgLysLysLeuGluA 576
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......GGACCATCCTCA 6406
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GENERAL INFORMATION:
APPLICANT: Banerjee, Papia T.
APPLICANT: Patience, Clive
APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of Patent No. 6261806
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
TITLE REPERENCE: 61750-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:Contiguous ; OTHER INFORMATION: compilation of SEQ ID NOs: 18, 22, and 24. US-09-376-781-25
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                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block: us-09-171-553B-10 \times us-09-376-781-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-09-376-781-25 from: 1 to: 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09376781 Patent No. 6261806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7492 AGACAACAGTACCAA 7506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7342 AACAGGTCTCTTTGGTTGGCTACCCTACTTTCTGCTTTAACAGGACCCTT 7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 uValValLeuLeuLeuLeuThrValGlyProCysLeuIleAsnArgP 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 AsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLe 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 rgArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPhe 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  626 heValAlaPheValArgGluArgValSerAlaValGlnIleMetValLeu 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 ArgGlnGlnTyrGln 647
                                                    143 CTCTGTCAATAACCTCTCAGACTAATGGTATGCACATAGGAGACAGCCTG 192
                                                                                                                                                   93 AAAAAGACTAAAAATCCCCTTAAGCTTCGCCTCCATCACATGGTTCCTTA 142
                                                                                                                                                                                                                                                       43 ATACATCCCACGTTAAGCCGGCGCCACCTCCTGATTCAGGGTGAAAAGCC 92
                                                                                              34 hrLeuThrIleThrProGlnAlaSerSerLysArgLeuIleAspSerSer 50
                                                                                                                                                                             17 oLysargLeuArgIleProLeuSerPheAlaSerIleAlaTrpPheLeuT 34
51 AsnProHisArgProLeuSerProThrTrpLeuIleIleAspProAspTh 67
                                                                                                                                                                                                                                                                                                         1 MetHisProThrLeuSerTrpArgHisLeuProThrArgGlyGlyGluPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 2169.00
Ratio: 4.032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.515
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 11
Percent Identity: 64.571
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363	LysGluHisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLe	347
346 1008	lyProProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnValThr :: ::::	
330 958	hrSerSerCysTrpLeuCysLeuSerSerG 	
313 908	InArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAs 	
858		UT (
o on a	::: ::	α <u>μ</u> α
1 6	InGlyProProAlaLeuGluProProHisAsnLeuProValProGlnL	247 781
246 780	ac GG	w w
230 730	.TyrGlyGlyGlyAlaGlySerThrLeuThrIleArgLeuArgIleGluT:::	21 4 684
213 683	IleGlnLysTrpIleAsnGlyMetSerTrpGlyIleValPheTyrLys	198 634
197 633	leSerPheThrGluLysG { TAAGTTTCACCGAAAAAA	181 584
181 583	letLysLeuTyrLysAspLysSerC 	166 534
166 533	LeuGlnAspArgValLysPheSerPheValAsnSerGlyProGlyLysTy	150 490
149 489	:rAsnAspGlyAspTr ::: !TAATGATGGAAATCG	
133 439	LysTyrCysG1yG1ySerc ::: ::: GGAAAACACTATGGAAATCCT1	117 390
117 389	OProAsnLeuValArgSerTyrGlyP ::::::: :: CCAGATATCCTCCGTGCTTACGGAT	101 343
100 342	eCysLeuArgLeuIleAs CTGCCTCAGATCAGTCAT	84 293
84 292	rGlyValThrValAsnSerThrArgGlyValAlaProArgG	67 243
242	AACTCCCATAAACCCTTAT	193

613 euLeuLeuThrValGlyProCysLeuIleAsnArgPheValAlaPh	563 eArgAspSerMetAsnLysLeuArgLysLysLeuGluArgArgArgArg	1509 TGTCAGTAACCTGGAAAAATCCCTAACCTCCTTATCTGAAGTAGTTCTA 530 InAsnargArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCy	59 CCTGACACTCGCAGTAATGCTCGGACTGGAGTGATAACAGGTGTGAG R0 hrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyL	209 AACCCCTTGTGTTTCCACCTTGGTTTTCAACCAAACTAAAGACTTTTTAC 430 AIMELVALGAINII LEVALDTOARGVATTYYTHISPTGALUGLUVALVA ::	AAAAACATAGAGACCAATGTACATGGGGATCCCAAAATAAGCTTACCC (ThrGluValSerGlyLysGlyThrCysIleGlyLysAlaProProSer
185 185 646 190	G 580 G 1708 G 1708 F 596 C 1758 C 1758	T 1658	14 49 14 51	125 446 130 130 463 135	T 1058 H 380 C 1108 C 1108 in 396 in 1158 in 413 r 11208 V 430

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seq_documentation_block:
; Sequence 30, Application US/09376781
; Patent No. 6261806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide ; OTHER INFORMATION: consensus sequence of PERV-D. US-09-376-781-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block: us-09-171-553B-10 \times us-09-376-781-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-376-781-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-376-781-30 from: 1 to: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 2169.00
Ratio: 4.032
Percent Similarity: 82.515
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TITLE OF INVENTION: USE
TITLE REFERENCE: 61750-267
CURRENT TELLING DATE: 1999-08-18
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
TENCTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Banerjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Andersson, Goran K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2000
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                143 CTCTGTCAATAACCTCTCAGACTAATGGTATGCACATAGGAGACAGCCTG 192
                                                                   390 ACCAAATAATGGAAAACACTATGGAAATCCTAGAGATTTCTTTTACAAAC 439
                                                                                                                      117 rGluLysGlu...LysTyrCysGlyGlySerGlyGluSerPheCysArgA 133
                                                                                                                                                                                                                                                                                                             293 GGCCTGATCTATATGTCTGCCTCAGATCAGTCATTCCTAGTCTGACCTCA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AGGTATTAATATCCACAGCGCTCGAGGGGAGGCTCCTTTAGAAACCTGGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AACTCCCATAAACCCTTATCTCTGACCTGGTTAATTACTGACTCTGACAC 242
                                                                                                                                                                                                                                                                                                                                          84 rpProGluLeuHisPheCysLeuArgLeuIleAsnProAlaValLysSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AsnProHisArgProLeuSerProThrTrpLeuIleIleAspProAspTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 hrLeuThrIleThrProGlnAlaSerSerLySArgLeuIleAspSerSer 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 oLysArgLeuArgIleProLeuSerPheAlaSerIleAlaTrpPheLeuT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rGlyValThrValAsnSerThrArgGlyValAlaProArgGlyThrTrpT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AAAAAGACTAAAAATCCCCTTAAGCTTCGCCTCCATCACATGGTTCCTTA 142
rgTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpProIleSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 652
Gaps: 11
Percent Identity: 64.571
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446	0 alMetValGlnIleValProArgValTyrTyrHisProGluGluValVal ::	43
125	3 UTNIPIOCYSVALSETINISEIVAL 	120
י וֹט יי	7 GlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCysAsnThrolyL	5 9
396 115) isGlnHisLeuCysTyrSerThrValValTyrGluGlnAlaSerGluA 	
380 110	SIleGlyL CATAAAAA	367 1059
363 105	7 LysGluHisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLe :: ::	347 1009
346 100	0 lyProProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnValThr :::	33(95)
330 958	3 nSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerG :::	31; 909
	nArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaI :::	297 859
G		UI (
855 296	AGCACGACT	817
280	. CAAAGAACCCCAACCCCAGGACCATCCTCTGATATA	781 263
9	GlnGlyProProAlaLeuGluProProHisAsnLeuProValProGlnL	4
246 780	0 hrGlyThrGluProProValAlaMetGlyProAspLysValLeuAlaGlu :: ::: ::: ::: ::: 1 GCCAGCTAGAGCCTCCAATGGCTATAGGACCGAATACGGTCTTAACGGGT	23(73)
230 730	4 .TyrGlyGlyGlyAlaGlySerThrLeuThrIleArgLeuArgIleGluT :::	214 684
683	8 IleGinlysTrpileAsnGlyMetSerTrpGlyIleVaiPneTyrLys	198
و بن د	SpLeuAspTyrLeuLysIleSerPheThrGluLysGlyLysGlnGluA	œ œ
181 583	Ö.	166 534
166 533	· B	15(49(
489	::	440

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Patent No. 6261806

TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267

CURRENT APPLICATION NUMBER: US/09/376,781

CURRENT FILING DATE: 1999-08-18

EARLIER APPLICATION NUMBER: 60/097,015

EARLIER FILING DATE: 1998-08-18

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-376-781-24
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/09376781 Patent No. 6261806
                                                                                                                                                                                                                                APPLICANT: Banerjee, Papia T.
APPLICANT: Patience, Clive
APPLICANT: Andersson, Goran K.
TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 ValArgGluArgValSerAlaValGlnIleMetValLeuArgGlnGlnTy 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 luArgGluAla.AspGlnGlyTrpPheGluGlyTrpPheAsnArgSerPr 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497 GlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSe 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646 rGln 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTAGAAAACGAATAAGTGCAGTCCAGATCATGGTACTTAGACAACAGTA 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euLeuLeuThrValGlyProCysLeuIleAsnArgPheValAlaPhe 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLeuValValLeuL 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAGACTCCATGAACAAGCTTAAAAAAAGGTTGGAGAAACGTCGAAGGG 1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAlaLeuLysGluGluCysCysPheTyrValAspHisSerGlyAlaII 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeu 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAspGluTyrAspTyrArgTyrAsnArgProLysArgGluProValSe 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGTTACTCACAGTTGGGCCATGTATTATTAACAAGTTAATTGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGTTGGCTACCTACTTTCTACTTTAACAGGACCCTTAATAGTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAGGAAACTTACTCAAAGATGGTTTAAAAGATGGTTCAACAGGTCTCC 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eArgAspSerMetAsnLysLeuArgLysLysLeuGluArgArgArgArgG 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAATAAAAAAGGGTTAGATTTATTTCTAAAAAAAAAGAAGATTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATGGTCCAAATTGTTCCCCGAGTATATTACTATCCCAAGAAAACAATT 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCys 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTAACCTACATCAAATTGTAACAGGAAATCTCCAAGCCCTAAAAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1808
                                                                                                                                                                                                                                                 and Methods
                                                                                                                                                                                                                                                 Of.
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; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide; OTHER INFORMATION: sequence of the 3' end of the PERV-D env regions-09-376-781-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block: US-09-171-553B-10 \times US-09-376-781-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 83.640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 24
LENGTH: 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
376 aProProSerHisGlnHisLeuCysTyrSerThrValValTyrGluGlnA 393
                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 ProGlyLysTyrLysMetMetLysLeu...TyrLysAspLysSer...Cy 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 alLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 PheTyrLys...TyrGlyGlyGlyAlaGlySerThrLeuThrIleArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CCCAATAACCACCGGACCTGGAAAACGTCATACAGGTACCATTCTGGGTG 53
                                                                                                                                                                                                                                                                                                                                                                                           GlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCy
                                                                                LysLeuThrLeuThrGluValSerGlyLysGlyThrCysIleGlyLysAl
                                                                                                                                                                                                                                                                                        sLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluArgLysP
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                                                   AAGCTTACCCTTACTGAGGTTTCTGGAAAGGACACCTGCATAAAAAAGGT
                                                                                                                                                                                                                                                               CTTAACTTCGGGCCCACCTTACTATAAGAAAATGGCTAAAAGAGAAAAAT
                                                                                                                                                                                                                                                                                                                                                                   CAAGCTCTTAACTCCACGACTCCAGAGGCTACCTCTTCTTGTTGGCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sSerProSerAspLeuAspTyrLeuLysIleSerPheThrGluLysGlyL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValProGlnLeuThrSerLeuArgProAspIleThrGlnProProSerAs 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTAACGGGTCAAAGAACCCCCAACCCCAGGACCATCCTCTGATATA...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAAGAAATATCCTAAAATGGATAAATGGTATGTCCTGGGGAATAATA
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                                                                                                                                                    626 heValAlaPheValArgGluArgValSerAlaValGlnIleMetValLeu 642
                                                                                                                                                                                                                                                                      609 uValValLeuLeuLeuLeuLeuThrValGlyProCysLeuIleAsnArgP 626
                                                                                                                                                                                                                                                                                                                                                                                                                       593 AsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLe 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            929 AAACAGGACTTAGTAACCTACATCAAATTGTAACAGGAAATCTCCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    879 AGGTGTGAGAACAGGAACTGCAGCTTTAGTTACAGGACCTCAGCAGCTAG
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                                                        643 ArgGlnGlnTyrGln 647
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                                                                                                                                                                                                                                                                                                                                                                     AACAGGTCTCCTTGGTTGGCTACCCTACTTTCTACTTTAACAGGACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGTCGAAGGGAAAAGGTTACTCAAAGATGGTTTAAAAGATGGTTC
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AGACAACAGTACCAA 1393
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-011-745-7
seq_documentation_block:
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seq_documentation_block:
 Sequence 7, Application US/09011745
 Patent No. 6165715
 GENERAL INFORMATION:

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alignment_block:
US-09-171-553B-10 x US-09-011-745-7
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                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                          Align seg 1/1 to: US-09-011-745-7
                                                                                                                                                                                                                                                                  Ratio: 3.300 Percent Similarity: 70.909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Expression systems FILE REFERENCE: 09/011,745 CURRENT APPLICATION NUMBER: US/09/011,745 CURRENT FILING DATE: 1998-06-22 EARLIER APPLICATION NUMBER: PCT/GB96/02061 EARLIER FILING DATE: 1996-08-23 EARLIER APPLICATION NUMBER: GB9517263.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1995-08-23 NUMBER OF SEQ ID NOS: 29
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APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (4249)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (4247)
OTHER INFORMATION: n is
1725 GTCC...CAAACTGGAGACGTTGTCTGGGATACAAAGGCAGTCCAGCCCC
                                                                              1675 CTGCAAAATAAGAACCCCCACCAGCCCATGACCCTCACTTGGCAGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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OTHER INFORMATION: n is any nucleotide
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                                      63 eAspProAspThrGlyValThrValAsnSerThrArgGlyValAlaProA 80
                                                                                                                    47 IleAspSerSerAsnProHisArgProLeuSerProThrTrpLeuIleIl
                                                                                                                                                                                                                                                                                   Quality: 1544.50
Ratio: 3.300
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Gaps: 15
Percent Identity: 46.970
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of

323 2605	nGlyAlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerC ::::: :::	306 2556
306 2555	SerProGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleGl:::	290 2512
289 2511	euIleProThrAsnThrProArgAsn :::::: CGACTAGTGCACAAACTCCCACGGTGAGAAAAAAAAATTGTTACCCTAAAC	281 2462
281 2461	rSerLeuArgProAspIleThrGlnProProSerAsnSerThrThrGlyL ::: CCCGACTCTAACTCCACAGCCCTGG	264 2437
264 2436	ProProHisAssnLeuProValProGlnLeuTh ::::: ::: CCCCCAAGGGAAGCGCCACCGCCATCTCTC	25 4 2389
253 2388	etGlyProAspLysValLeuAlaGluGlnGlyProProAlaLeuGlu :: :: raggTCCTgACCTCGTCCTTGTGGAACAAGGACCTCCTAGAACGTCCCTC	238 2339
238 2338	rLeuThrIleArgLeuArgIleGluThrGlyThrGluProProValAlam ::: ::: GTTCACCATTCGCTTAAAAATCACCAACATGCCAGCTGTGGCAG	221 2295
221 2294	MetSerTrpGlyIleValPheTyrLysTyrGlyGlyGlyAlaGlySerTh ::: ::	205 2248
20 4 22 4 7	erPheThrGluLysGlyLysGlnGluAsnIleGlnLysTrpIleAsngly:: ::: ::: ::: ATTTCACAGACAAAGGAAAATTATCCAAGGACTGGATAACGGGA	188 2204
188 2203	. uTyrLysAspLysSerCysSerProSerAspLeuAspTyrLeuLysI1eS 	171 2169
171 2168	LysPheSerPheValAsnSerGlyProGlyLysTyrLysMetMetLysLe:::::::::::::::::::::::::::::::::::	155 2119
154 2118	hrSerAsnAspGlyAspTrpLysTrpProIleSerLeuGlnAspArgVal :::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	138 2072
138 2071	STyrCysGlyGlySerGlyGluSerPheCysArgArgTrpSerCysValT::::::::::::::::::::::::::::::::::::	121 2022
121 2021	TyrGlyPheTyrCysCysPro	109 1972
108 1971	GGGGAGCCATAGGGTGCAGCTACCCTCGGGCTAGGACTAGAATGGCAAGC	105 1922
104 1921	SSETThrProProAsn	99 187.2
99 1871	AGTCTTGAGTCCTGGGATATCCCGGGAACCGATGTCTCGTCCTCTAAACG	94 1822
93 1821	rgGlyThrTxpTxpProGluLeuHisPheCysLeuArgLeu	80 1772

959	leAsnArgPheValAlaPheValArgGluArgValSerAlaValGlnTle	623	
	rGlyProLeuValValLeuLeuLeuLeuThrValGlyProCysLeuI: :::: ::: :	606 3453	
606 345	GlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuTh	590 3403	
589 340	ysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyTrpPheGlu :::::: :::	573 3353	
573 335	rValaspHisSerGlyAlaIleArgAspSerMetAsnLysLeuargLysL ::: ::: ::: CATAGACCACTCAGGTGCAGTACGGGACTCCATGAAAAAACTCAAAGAAA	556 3303	
556 330	LeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTy :::	540 3253	
539 325	erLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPhe - - - - - - - - - - - - -	523 3203	
523 320	PLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrS	506 3153	
506 315	GlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAs ::: ::: ::: aTAGACCTCCAGCAAGGCCTGACAAGCCTCCAGATCGCCATAGATGCTGA	4 90 3103	
489 310	1yThralaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyPro	473 3053	
473 305	gProLysArgGluProValSerLeuThrLeuAlaValMetLeuGlyLeuG 	456 3003	
456 300	TyrHisProGluGluValValLeuAspGluTyrAspTyr ::: ::: ::: TACTATCCTGAAGAAGTTTTGTTACAGGCCTATGACAAT	440 2953	
439 295	snGlnSerLysAspLeuCysValMetValGlnIleValProArgValTyr ::::: ::::	423 2903	
423 290	pTrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheA 	406 2853	
406 285	TyrCluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTr:::::::::::::::::::::::::::::::::::	390 2803	
389 280	leGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValVal :::	373 2753	
373 275	SerArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysI	356 2703	
356 270	GluArgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGl :::	340 2656	
339 265	STRPLeuCysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLys	323 2606	

640 MetValLeuArgGlnGlnTyrGlnGlyLeu 649 ::: ::: 3553 TTAGTCCTGACTCAACAATACCACCAGCTA 3582
q_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-716-351A-1
<pre>q_documentation_block: Sequence 1, Application US/08716351A Patent No. 6033905 GENERAL INFORMATION: APPLICANT:</pre>
NVENTION: Gibbo NVENTION: Retro SEQUENCES: 5 EADABLE FORM:
COMPUTER: FLOPPY GLEK COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
ICATION DATA: NN NUMBER: US/08/716,351A TE:
SIFICATI APPLICAT
: 06-APR-1994 I INFORMATION:
TRATION NUM
ŧ
FOR SEQ HARACTEF 8535 be
TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
TYPE:
NAME/KEY: misc_feature LOCATION: 18535 OTHER INFORMATION: /standard_name= "Galv SEATO Genome"
ignment_score Qua R ercent Simila
.ignment_block: JS-09-171-553B-10 x US-08-716-351A-1
vlign seg 1/1 to: US-08-716-351A-1 from: 1 to: 8535
47 IleAspSerSerAsnProHisArgProLeuSerProThrTrpLeuIleIl 63 ::::::::::::::::::::::::::::::::::::
63 eAspProAspThrGlyValThrValAsnSerThrArgGlyValAlaProA 80 :::: :: ::: :::
80 rgGlyThrTrpTrpProGluLeuHisPheCysLeuArgLeu 93

94	IleAsnProAlaValLy :::::: :: ::	9
6198	TCTCGTCCTCTAAAC	24
99	ThrProProA	04
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6495	GGGACCAAAATAGCGAATGGACTCAAAATTTCAACA	54
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188 6580		62
20	SerTrpGlyIleValPheTyrLysTyrGlyGlyGlyAlaGlySerTh	N
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221 6671	rLeuThrIleArgLeuArgIleGluThrGlyThrGluProProValAlaM 2 :: :::	571
238	tGlyProAspLysValLeuAlaGluGlnGlyProProAlaLeuG	ΐ
6715	GTCCTGACCTCGTCCTTGTGGAACAAGGACCTCCTAGAACGTC	76
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6765	CCCCAAGGGAAGCGCCACCGC	81
264	GlnProProSerAsnSerThrT	281
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281	ulleProThrAsnThrProArgAsn	æ
6838	CACAAACTCCCACGGTGAGAAAAACAATTGTTACCCTAAA	88
290 6888	ScrProGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleGl 3 :::	93
306 6932	nGlyAlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerC 3 :::::: ::: ::: GGGGCCTTCCTAACCTTAAATGCTACCAACCCAGGGGCCACTGAGTCTT 6	98
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- 00	.CTGGCTTTGTTTGGCCATGGGCCCCCCTTATTATGAAGCAATAGCCTC	703
340	hrLysGluHisArgAsnGlnCysThrTrpGl	G

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7629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7479 ATAGACCTCCAGCAAGGCCTGACAAGCCTCCAGATCGCCATAGATGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7329 TACTATCCTGAAGAAGTTTTGTTACAGGCCTATGACAATTCTCACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7279 ATCAGACTAGAGATTTCTGTATCCAGGTCCAGCTGATTCCTCGCATCTAT 7328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7229 GTGGGCTTGCAGCACTGGCCTCACCCCTTGCCTCTCCACCTCAGTTTTTA 7278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7179 ATCAATTCCTCCGGAGACCATCAGTATCTGCTCCCCTCCAACCATAGCTG 7228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7129 TAGGAAAGGTGCCCTTTACCCATCAGCATCTCTGCAATCAGACCCTATCC 7178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 GlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAs 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 lyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyPro 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 TyrHisProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnAr 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 snGlnSerLysAspLeuCysValMetValGlnIleValProArgValTyr 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 TyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTr 406
                                                                                                                                                                   GlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuTh 606
                                                                                                                                                                                                                                                                                                                                                                                                                               ysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyTrpPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rValAspHisSerGlyAlaIleArgAspSerMetAsnLysLeuArgLysL 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrS 523
eMetValLeuArgGln 644
                                                           TCAATAAGTTAGTTCAATTCATCAATGATAGGATAAGTGCATGTTAAAAT 7928
                                                                                                          leAsnArgPheValAlaPheValArgGluArgValSerAla.ValGlnIl 639
                                                                                                                                                                                                                                                                                    GGATGGTTCAATAACTCCCCTTGGTTCACTACCCTGCTATCAACCATCGC
                                                                                                                                                                                                                                                                                                                                                                                                 AACTGGATAAAAGACAGTTAGAGCGCCAGAAAAGCCCAAAACTGGTATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAAAAGAAGGTGGCCTCTGTGCGGCCCTAAAGGAAGAGTGCTGTTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTy 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPhe 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCGGGCCCTCCAAGACTCAGTCAGCAAGTTAGAGGACTCACTGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pTrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValVal 389
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alignment_block:
US-09-171-553B-10 x US-09-075-272-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-075-272-1
                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-075-272-1 from: 1 to: 8655
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                            5811 TTCGCTTGCGTCGCAGGAGCCCCCCCCATCACCCTGGAC......
                                                                                                                                   5761 AACCCACGAAGACAACTGGGCTGTGGAAGCCACTGATAACCCTCTTAAGC 5810
                                                                                                                                                                                                                         5711 TCCTGGATCCACGCTTCACACGTCAAGAGGGCCCCCAGTCAAGATGAAGA 5760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7929 TCTGGTCCTTAGACAA 7944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION UDATA:
APPLICATION UNMBER: US 60/046,140
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MILLER, A. DUSTY APPLICANT: WOLGAMOT, GREG APPLICANT: BONHAM, LYNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MUS DUNNI ENDOGENOUS TITLE OF INVENTION: PACKAGING CELL LINES
                                                                                      26 PheAlaSerIleAlaTrpPheLeuThrLeuThrIleThrProGlnAlaSe 42
                                                                                                                                                                             22 lePro.....LeuSer 25
42 rSerLysArgLeuIleAspSerSerAsnProHisArgProLeuSerProT 59
                                                                                                                                                                                                                                                                 6 SerTrpArgHis.LeuProThrArgGlyGlyGluProLysArgLeuArgI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1478.50
Ratio: 3.080
milarity: 65.934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 728
Gaps: 24
Percent Identity: 44.368
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8899	CATTAGAGACAAC	6642
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264 6641	roProAlaLeuGluProProHisAsnLeuProValProGlnLeuThr	249 6592
UT I	CTGGCAGTAACATCCATAGGACCCAACAAGGTCCTTACGGAACAGGC	.4-
249	AltaGACTGACAGTAAGAG OAspiysVallenalaGlnGlnGlv	222
nω	GlyAlaGlySerThrLeuThrIleArgLeuArgIleGluThrGlyT	216
6497	InLySTrpIleAsnGlyMetSerTrpGlyIleValPheTyrLySTyrGly ::: :::::	199 6450
4	TCATAAAATTCACTGAGAAAGGGAAACAAGCTCGCCTG	6408
199	sIleSerPheThrGluLysGlyLysGlnGluAsnIl	182
6407	TyrLysMetMetLysLeuTyrLysAspLysSerCysSerProSerAspLe	166 6384
6383	ATACCTAGATTCTGGGTGTGCTCTTAAAAATTACAGCCCCCCAGGACC	6334
165	PheValAsnSerGly	157
w i	GTGGTAGTGGTTATGATAAGCCAAAGCAAGGAGAAAGAAA	6284
157	SerLeuGlnAspAl	149
148 6283	AsnAspGlyAspTrpLysTrpProIle	140 6234
6233	GGCATCAGACTACTTTTGCGGTAAATGGACATGTGAAACAAC	6184
139	sGlyGlySerGlyGl	123
123 6183	yPheTyrCysCysProGlyThrGluLysGluLysTyrC 	110 6134
6133	GCAGTTCTATCGAGCTAATCTTAGGGC	6084
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6083	TGAATAACCCACCCTCTGAACAAAAGTGTGTCCCAAACGGGGTAGGAAGC	6034
, c	HAMITABCABCABCATCTCCCAMITAGGACCTICCCGAICAIACIGAC	0 40
ο	LeuA	9
5983	GGCCTGATCTCACAC	5934
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75 5933	hrTrpLeuIleIleAspProAspThrGlyValThrValAsnSerThrArg :: ::::::: :: ::: CTTGGGAAGTGCTTAATGAAAAGGGAGACGTTGTATGGGTAGCCACT	59 5887
5886	::: ::: :::::: : 	5850

597 7593	UATGG1UA1AASpG1nG1yTrpPheG1UG1yTrpPheAsnArgSerProT ::: 	580 7544
580 7543	ArgAspSerMetAsnLysLeuArgLysLysLeuGluArgArgArgArgGl:::	564 7494
563 7493	laAlaLeuLysGluGluCysCysPheTyrValAspHisSerGlyAlaIle 	547 7444
547 7443	nAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysA 	530 7394
530 7393	ValSerAsnLeuGluGluSerLeuThrSerLeuSerGluValValLeuGl:::::::::	514 7344
513 7343	SGluS ::: ACACT	497 7296
497 7295	· 产	480 7256
480 7255	ThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyTh	465 7206
464 7205	SpGluTyrAspTyrArgTyrAsnArgProLysArgGluProValSerLeu ::::::::	448 7159
448 7158	tValGlnTleValProArgValTyrTyrHisProGluGluValValLeuA: ::::: ::: :::::	431 7109
431 7108	ProCysValSerThrSerValPhcAsnGlnSerLysAspLeuCysValMe ::: ::: ::: CCTTGTAFATCTATGTCTGTTTTCAATAGCTCCAAAGATTTCTGTATTTT	415 7059
414 7058	YrLeuValProGlyTyrAsnArgTrpTrpAlaCysAsnThrGlyLeuThr 	398 7009
398 7008	nHisLeuCysTyrSerThrValValTyrGluGlnAlaSerGluAsnGlnT 	381 6959
381 6958	GluValSerGlyLysGlyThrCysIleGlyLysAlaProProSerHisGl ::: ::: :::: ::: GCAGTTTCAGGAAATGGGCTTTGTTTAGGTCAGGTGCCCCCAGGATAAATG	365 6909
364 6908	luHisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeuThr:: :::	348 6862
348 6861	OPTOTYTTYTG1UG1YMETA1ALYSG1UATGLYSPHEASNVA1ThrLYSG ::: ::: ::: ::: ::: CCTTATTATGAAGGAATTGCTCAGACTAGAACTTACAATATTACTTCAG	331 6812
331 6811	ThraspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyPr ::: :::	315 6762
314 6761	lyGlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSer::::	298 6712
6711	CTCCCCACCACTCCTAGATACAG	6689

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alignment_scores:
Quality: 1329.00
Ratio: 2.973
~:--11arity: 64.224
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,300A
FILING DATE: 20-ANG-1993
FILING DATE: 20-ANG-1993
CLASSIFICATION: 45
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H.
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER: 32,140
REFERENCE/DOCKET NUMBER: 11698A50
TELEFONMUNICATION INFORMATION:
TELEFAX: 212-557-2200
TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8323 base pairs
TYPE: nnc leic a sid
                                                                                        alignment_block:
US-09-171-553B-10 x US-08-110-300A-8
                                                                                                                                                                                                                                                                                          US-08-110-300A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-110-300A-8
                                             Align seg 1/1 to: US-08-110-300A-8 from: 1 to: 8323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08110300A Patent No. 5643756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7744 AG...GTCTTCCAGGAGGCCGAAAACTCGCTC 7772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7694 TAGAGAAAGAATAAATGCAGTACAGGTTATGGTATTAAAACAACAATATC 7743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            647 lnGlyLeuLeuSerGlnGlyGluThrAspLeu 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 lArgGluArgValSerAlaValGlnIleMetValLeuArgGlnGlnTyrG 647
16 GluProLysArgLeuArgIleProLeuSerPheAlaSerIleAlaTrpPh 32
                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 45 Rocke
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EE: Davis Hoxie Faithfull and Hapgood
45 Rockefeller Pl.
                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                    Length: 696
Gaps: 23
Percent Identity: 42.816
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275	euArgProAspIle:	259	
258 5635	ysValLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeu 2	242 6598	
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225 6550	IleValPheTyrLysTyrGlyGlyGlyAlaGlySerThrLeuThrTleAr 2 :::	209 6501	
208 6500	LysTrpIleAsnGlyMetSerTrpGly ::: ::: CATGGACAACTGGACACTATTGGGGT	192 6457	
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126 628	CysCysProGlyThrGluLysGluLysTyrCysGlyGlySe 	113 6234	
112 623:	SnLeuValargSerTyrGlyPheTyr	104 6184	
104 618	ulleAsnProAlaValLysSerThrProProA	93 6134	
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808		6034	
87 603	TTEPTEPETGLILEU	5984 5984	
82 598	ASPThrGlyValThrValAsnSerThrArgGlyValAlaProAr		
65 593	.sArgProLe ::: .CCAGGTCTA	588	
49 588	hrE	585	
585	7 GACCCGCGGGACCTCCTAATCCCCTTAATTCTCTT	581	

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6965 AACAGTCCCAAAAACTCACCAGGCCCTGTGCAACACTACCCTT...... 7008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7256 TATGGGTGGCATCGCCGCGGGAGTAGGGACAGGAACTACCGCCCTGGTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7159 ATCCTCCCAGTTACGTCTATAGCCAGTTTGAA...AAATCCCATAGACAT 7205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7109 CACCACTGACTATTGCGTTCTCGTGGAATTATGGCCCAGGGTCACCTACC 7158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7059 GCATGTAACACTGGACTCACTCCATGCCTATCTGCCACCGTGCTTAATCG 7108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6915 CAACACAAGCTGACCCTGTCCGAAGTGACTGGACGGGGACTCTGCATAGG 6964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6865 GTACTTATTCCAACCATACCTCTGCCCCAGCTAACTGCTCCGTGGCCTCC 6914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6815 GTTATGCCTAGTGTCTGGACCCCCCTATTACGAGGGGGTTGCCGTCCTAG 6864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6765 GCTTACCAGGCACTCAACCTTACCAACCCTGATAAAACTCAAGAGTGCTG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6721 CG.....CCAGCAGGAACGGGAGACAGATTACTAAATCTAGTACAGGGA 6764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6671 TAGTTCGACTCCCACATTGATTTCCCCGTCCCCCACTCCCACTCAGCCCC 6720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6636 CCCCTACCC......AAACCTGCCAAGTCTCCCCCCGCCTC 6670
                                                                                                                                                                                                                                                                                                                                                              7391 TCTTACTTCGTTGTCTGAGGTTGTACTGCAGAATCGACGAGGCCTAGACC 7440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7341 CAAGATGATCTCAAAGAAGTCGAAAAGTCAATTACTAACCTAGAAAAGTC 7390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7206 AAAAGAGAACCAGTGTCCTTAACCTTGGCCTTATTATTAGGTGGGCTAAC 7255
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                                                                                                                                                                                                                         537 euLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCys 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 ....LeuGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 nSerLysAspLeuCysValMetValGlnIleValProArgValTyrTyrH 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 yLysAlaProProSerHisGlnHisLeuCysTyrSerThrValValTyrG 391
                                               554 CysPheTyrValAspHisSerGlyAlaIleArgAspSerMetAsnLysLe 570
                                                                                                                                                                                                                                                                                                                                                                                                                                              520 rLeuThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspL 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 ThrGluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSe 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 hrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMet 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 LysArgGluProValSerLeuThrLeuAlaValMetLeuGly..... 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 isProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnArgPro 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 AlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 roGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleGlnGly 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 luGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrp 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 ArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysIleGl 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 rgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySer 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 rAsnSerThrThrGlyLeuIle...ProThrAsnThrProArgAsnSerP 291
                                                                                                                                                                               TGTTGTTCCTAAAAGAGGGAGGACTGTGTGCTGCCCTAAAAGAAGAATGT 7490
TGTTTCTATGCTGACCATACAGGCCTAGTAAGAGATAGTATGGCCAAATT 7540
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; MOLECULE TYPE: US-08-886-642-8
                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-886-642-8
    Ratio: 2.973
Percent Similarity: 64.224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08886642 Patent No. 5952474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7741 TCCAGGCTTTAGTCCTGACTCAACAATACCACCAGCTA 7778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7691 CTGCATTCTTAATCGATTAGTTCAATTTGTTAAAGACAGGATCTCAGTAG 7740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7641 ACCATCATGGGGCCTCTCATTATACTCCTACTAATTCTGCTTTTTGGACC 7690
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 07 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pinter, Abraham
APPLICANT: Kayman, Samuel
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637 alGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 AlaLeuThrGlyProLeuValValLeuLeuLeuLeuLeuThrValGlyPr 620 :::::: |||||||||::::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             570 uArgLysLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-JUL-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620 oCysLeuIleAsnArgPheValAlaPheValArgGluArgValSerAlaV 637
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           TELEPHONE: 212/258-2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/1: FILING DATE: 20-AUG-1993 APPLICATION NUMBER: 07/9: FILING DATE: 28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hone, William J. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                        LENGTH: 8323 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                              Quality: 1329.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1011
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                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
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JMBER: 07/938,100
                                                                                                                                                     Genomic DNA
                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                  26,739
Length: 696
Gaps: 23
Percent Identity: 42.816
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59	25 gLeuArgIleGluThrGlyThrGluProProValAlaMetGlyProAspL
225 6550	209 IleValPheTyrLysTyrGlyGlyGlyAlaGlySerThrLeuThrIleAr ::: :::
208 6500	leGln :: TCACC
192 6456	175 SSerCysSerProSerAspLeuAspTyrLeuLysIleSerPheThrGluL
175 6421	G — ⊅
159 6371	143 SpTrpLysTrpProIleSerLeuGlnAspArgValLysPheSerPheVal
143 6333	126 rGlyGluSerPheCysArgArgTrpSerCysValThrSerAsnAspGlyA ::: ::: ::: ::::: 6284 AGACTCCTTCTACTGTGGCTCTTGGGGCTGCGAGACAACCGGTAGAGTAT
126 6283	113 CysCysProGlyThrGluLysGluLysTyrCysGlyGlySe
112 6233	104 snleuvalargSerTyrGlyPheTyr
104 6183	93 ulleasnProAlaValLysSerThrProProA
93 6133	90
89 6083	HisPhe ::: CACTGGGGGCTAGAGTATCA
87 6033	82 rTrpTrpProGluLeu
82 5983	66 ASPThrGlyValThrValAsnSerThrArgGlyValAlaProArgGlyTh
65 5936	Pro
49 5886	ysArgLeu :: GATCCGCA
32 5851	16 GluProLysArgLeuArgIleProLeuSerPheAlaSerIleAlaTrpPh ::: ::: ::: 5817 GACCCGCGGGACCTCCTAATCCCCTTAATTCTCTT
	Align seg 1/1 to: US-08-886-642-8 from: 1 to: 8323
	alignment_block: US-09-171-553B-10 x US-08-886-642-8
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3	euLeuPheLeuArqGluGlyGlyLeuCysAlaAlaLeuLysGluGluCys	537
537 7440	rLeuThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspL 	520 7391
520 7390	ThrGluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSe ::: :: :::::: CAAGATGATCTCAAAGAAGTCGAAAAGTCCAATTACTAACCTAGAAAAGTC	504 7341
503 7340	hrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMet ::: ::::::GCCACCCAGCAGTTTCAG	487 7305
487 7304	LeuGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleT ::: ::: :: TATGGGTGGCATCGCCGCGGGAGTAGGGACAGGAACTACCGCCCTGGTC.	472 7256
471 7255	> - ⊏	458 7206
457 7205	. isProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnArgPro 	441 7159
441 7158	nSerLysAspLeuCysValMetValGlnIleValProArgValTyrTyrH	424 7109
424 7108	AlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAsnGl 	408 7059
407 7058	l luGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrp :: ::::: AGGCAGGCAAAGGGTCTTACTATCTAGTTGCCCCCACAGGAACTATGTGG	391 7009
391 7008	YLYSALAPTOPTOSETHISGLNHISLEUCYSTYTSETTHTVALVALTYTG	374 6965
374 6964	3 ArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCyslleGl ::::::	358 6915
357 6914	1 rgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySer 	3 4 1 6865
341 6864	4 pLeuCysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluA 5 GTTATGCCTAGTGTCTGGACCCCCCTATTACGAGGGGTTGCCGTCCTAG	324 6815
324 6814	8 AlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTr ::: ::: ::: 5 GCTTACCAGGCACTCAACCTTACCAACCCTGATAAAACTCAAGAGTGCTG	301 676!
307 6764	1 roGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleGlnGly	29 672
291 6720	LeuI TTGA	27 667.
275 6670	ThrSerLe	25 663
258 6635	2 ysValLeuAlaGluGlnGlyProProAlaLeuGluProProHisAsnLeu 	2 4 659

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seq_documentation_block:
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                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8323 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application PC/TUS9308041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,100
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H.
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER: 11698A50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7541 AAGAGAGAGACTCTCTCAGAGACAAAAACTATTTGAGTCGAGCCAAGGAT 7590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7691 CTGCATTCTTAATCGATTAGTTCAATTTGTTAAAGACAGGATCTCAGTAG 7740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7641 ACCATCATGGGGCCTCTCATTATACTCCTACTAATTCTGCTTTTTGGACC 7690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7491 TGTTTCTATGCTGACCATACAGGCCTAGTAAGAGATAGTATGGCCAAATT 7540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Public Health Research Institute of the City APPLICANT: New York, Inc.
TITLE OF INVENTION: FUSION GLYCOPROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 alGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 oCysLeuIleAsnArgPheValAlaPheValArgGluArgValSerAlaV 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 AlaLeuThrGlyProLeuValValLeuLeuLeuLeuLeuThrValGlyPr 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 CysPheTyrValAspHisSerGlyAlaIleArgAspSerMetAsnLysLe 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                  TOPOLOGY: li
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Davis Hoxie Faithfull and Hapgood STREET: 45 Rockefeller Pl.
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                   STRANDEDNESS: double
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                                            linear
Ö
                    DNA (genomic)
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ANTI CT-US93-	1-SENSE: NO -08041-8	
lignment Percent	L_scores: Quality: 1329.00 Length: 696 Ratio: 2.973 Gaps: 23 Similarity: 64.224 Percent Identity: 42.816	
ılignment US-09-17	_block: 1-553B-10 x PCT-US93-08041-8	
Align se 16	eg 1/1 to: PCT-US93-08041-8 from: 1 to: 8323 GluProLysArgLeuArgIleProLeuSerPheAlaSerIleAlaTrpPh 3 ::: :: CACCGCGGGGACCTCCTAATCCCCTTAATTTC	851
32 5852	OGlnAlaSerSerLysAr :::::::: AAAGGGGCCAGATC	9886
49 5887	roHisArgProL ::: CTCACCAGGTCT	55 5936
66 5937	AspThrGlyValThrValAsnSerThrargGlyValAlaProArgGlyTh 8	32 5983
82 5984	TTTpTTpProGluLeu8	37 5033
88 6034	HisPhe	39 5083
90 6084	CCCCCTTGTTGCTCAGGGAGCAGCGGGAACGTTGCAGGCTGTGCCAGAGA 6	93 5133
93 6134	ulleasnProAlaValLysSerThrProPro	L04 5183
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. 160 6372	ASnSerGlyProGlyLysTyrLysMetMetLysLeuTyrLysAspLy ::::::::::::::::::::::::::::::::::	175 6421
175 6422	SSerCysSerProSerAspLeuAspTyrLeuLysIleSerPheThrGluL	192 6456
192 6457	ysGlyLysGlnGluAsnIleGlnLysTrpIleAsnGlyMetSerTrpGly	208 6500

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7109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6865 GTACTTATTCCAACCATACCTCTGCCCCAGCTAACTGCTCCGTGGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6721 CG.....CCAGCAGGAACGGGAGACAGATTACTAAATCTAGTACAGGGA 6764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6765 GCTTACCAGGCACTCAACCTTACCAACCCTGATAAAACTCAAGAGTGCTG 6814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 yLysAlaProProSerHisGlnHisLeuCysTyrSerThrValValTyrG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 ArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysIleGl 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 rgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySer 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 pLeuCysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluA 341
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                         hrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMet 503
                                                                                                                                                                                                                                                                                             LysArgGluProValSerLeuThrLeuAlaValMetLeuGly.....
                                                                                                                                                                                                                                                                                                                                                              ATCCTCCCAGTTACGTCTATAGCCAGTTTGAA...AAATCCCATAGACAT 7205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCACTGACTATTGCGTTCTCGTGGAATTATGGCCCAGGGTCACCTACC
..GCCACCCAGCAGTTTCAG......
                                                                                                                   TATGGGTGGCATCGCCGCGGGAGTAGGGACAGGAACTACCGCCCTGGTC.
                                                                                                                                                   ....LeuGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleT 487
                                                                                                                                                                                                                                                                                                                                                                                                                       isProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnArgPro 457
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                                                                                                                                                                                                                                          AAAAGAGAACCAGTGTCCTTAACCTTGGCCTTATTATTAGGTGGGCTAAC
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.CAGCTCCATGCTGCCGTA 7340
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: GB9
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/011,745 CURRENT FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
                                            NAME/KEY: misc_feature LOCATION: (3808) OTHER INFORMATION: n is
                                                                                                                                               LOCATION: (3807)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Portion OTHER INFORMATION: construct
                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (3807)
                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
NAME/KEY: misc_feature
                               FEATURE:
                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7641 ACCATCATGGGGCCTCTCATTATACTCCTACTAATTCTGCTTTTTGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637 alGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 oCysLeuIleAsnArgPheValAlaPheValArgGluArgValSerAlaV 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               520 rLeuThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspL 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 ThrGluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGGCTTTAGTCCTGACTCAACAATACCACCAGCTA 7778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCATTCTTAATCGATTAGTTCAATTTGTTAAAGACAGGATCTCAGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCGAAGGATGGTTTAACAGATCCCCCCTGGTTTACCACGTTGATATCC 7640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpPheGluGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSer 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uArgLysLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTTCTATGCTGACCATACAGGCCTAGTAAGAGATAGTATGGCCAAATT
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                                                                                                                                                                                                                                                                                                                                                                                  6061
                                                                                                                                                    any
                                                    any nucleotide
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386 255	GlyThrCysIleGlyLysAlaProProSerHisGlnHisLeuCysTyrSe	370 2504
369 250	ysThrTrpGlySerArgAsnLysLeuThrLeuThrGluValSerGlyLys :: ::	353 2454
353 245	yMetAlaLysGluArgLysPheAsnValThrLysGluHisArgAsnGlnC ::: GGTTGCCGTCCTGGGTACCTCCAACCATACCTCTGCTCCAGCCAACT	336 2404
336 240:	ThrSerSerCysTrpLeuCysLeuSerSerGlyProProTyrTyrGluGl :::::: ACCCAAGAGTGCTGGTTGTGTCTAGTAGGGGGACCCCCCTACTACGAAGG	320 2354
319 235	IlyAlaPheGlnAlaIleAsnSerThrAspProAspAla ::	303 2304
303 230	erProGlyValProValLysThrGlyGlnArgLeuPheS	286 2272
286 227:	roSerAsnSerThrThrGlyLeuIleProThrAsnTh ::: ::: CAGTGGGACTCCTCTCTCCCCTACCCAACT	270 2228
269 222	LeuProValProGlnLeuThrSerLeuArgProAsp	253 2199
253 219	roAlaLeuG : CTCT	236 2155
236 215,	OProVa	220 2108
219 210	leValPheTyrLysTyrGlyGlyGlyAlaGly :: :: TACGTTTGTATGTCTCCGGACAAGATCCAGGG	203 2058
203 2057	ASnIleGlnLySTrpIleA::: ::: :::: :::::::::::::::::::::	186 2014
186 201:	.LysSerCysSerProSerAspLeuAspTyrLeuLy 	171 1979
170 1978	roGlyI	154 1934
154 1933	AspargV 	137 1891
137 189(ysVa GTGA	121 1841
120 1840	TyrCysCysProGlyThrGluLysGlu	108 1791
107 1790	GACCAG	104 1741
1740	CCAGGCTGTTCCAGAGACTGCGAAGAACCTTTAACCTCCCTC	1691

	eu 649 	649 3330
649 3329	UATGVALSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGlyL: ::: ::: ::: :::	632 3280
632 3279	LeuThrValGlyProCysLeuIleAsnArgPheValAlaPheValArgGl	616 3230
615 3229	hrThrLeuLeuSerAlaLeuThrGlyProLeuValValLeuLeuLeuLeu	599 3180
599 3179	uAlaAspGlnGlyTrpPheGluGlyTrpPheAsnArgSerProTrpMetT :::	582 3130
582 3129	SerMetAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArgGl	566 3080
565 3079	euLysGluGluCysCysPheTyrValAspHisSerGlyAlaIleArgAsp	549 3030
549 3029	gArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaL 	532 2980
532 2979	AsnLeuGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnAr	516 2930
515 2929	euHisAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValSer ::: ::: :: ::::::: ::: ::: ::: TCCAAGCCGCAGTACAGGATGATCTCAGGGAGGTTGAAAAATCAATC	499 2880
499 2879	rAlaAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluL ::: ::: ::: :::::: HITTACTGCTCTAATGGCCACTCAGCAATTCCAG	482 2845
482 2844	LeuGlyLeuGlyThrAlaValGlyValGlyThrGlyTh	470 2795
469 2794	rgTyrAsnArgProLysArgGluProValSerLeuThrLeuAlaValMet 	453 2745
453 2744	OARGVAITYRTYRHISPROGLUGLUVALVALLEUASPGLUTYRASPTYRA	436 2698
436 2697	ServalPheAsnGlnSerLysAspLeuCysValMetValGlnIleValPr:::::::	420 2648
419 2647	yrAsnArgTrpTrpAlaCysAsnThrGlyLeuThrProCysValSerThr:::	403 2598
403 2597	rThrValValTyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyT: :::::::::	386 2554

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Minimum
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Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                        US-09-009-913-1
US-08-766-528-14
US-08-766-528-13
US-08-800-2918-7
US-08-808-949-1
US-08-308-949-1
US-08-658-136-2
US-08-658-136-2
US-08-658-136-3
US-08-658-136-3
US-08-944-495-3
US-08-95-588-3
US-09-075-272-1
US-08-925-588-3
US-09-075-272-1
US-08-157-005-1
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PCT-US95-17026-8
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US-08-766-528-3
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21.294 Million cell updates/sec
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Sequence 1, Appli	US-08-399-561-1	Ъ	4928	71.0	14.2	45	C
Sequence 18, Appl	US-09-162-484-18	4	4024	71.0		44	
Sequence 130, App	US-09-050-159-130	4	4020	71.0	14.2	43	
Sequence 1, Appli	US-08-293-284A-1	N	3083	71.0		42	c
Sequence 1, Appli	US-08-346-849-1	Н	3083	71.0		41	С
Patent No. 5187079	5187079-3	σ	1470	71.0		40	C
Sequence 5, Appli	US-08-955-138-5	N	1160	71.0		39	
Sequence 4, Appli	US-08-993-260-4	ω	2567	72.0		38	c
Sequence 5, Appli	US-09-360-197-5	4	1666	72.0	14.4	37	C
Sequence 1, Appli	US-08-828-596-1	N	1539	72.0	14.4	36	C
Sequence 2, Appli	US-09-184-445-2	4	7886	74.0	14.8	35	
Sequence 2, Appli	US-09-060-836-2	N	7886	74.0	14.8	34	
Sequence 2, Appli	US-08-751-189-2	N	7886	74.0	14.8	w	
Sequence 44, Appl	US-09-201-912-44	4	569	74.0	14.8	32	a
`	US-08-487-231-44	N	569		14.8	31	C
Sequence 44, Appl	US-07-965-285-44	N	569	74.0	14.8	30	a
Sequence 44, Appl	US-08-483-695-44	N	569	74.0	14.8	29	O
Sequence 9, Appli	US-08-449-093A-9	1	489	74.0	14.8	28	C

ALIGNMENTS

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US-08-766-528-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08766528
Patent No. 6190861
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF
TITLE OF INVENTION: AND METHODS OF USE
                                                         Matches
                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                           TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                LENGTH: 7333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/766,528 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 60 S
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
1 gatggctctcctgccctttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                       Conservative
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                                                                       Score 20; DB 4
Pred. No. 0.85;
                                                       Mismatches
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                                                                                          DB 4;
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                                                                                        Length 7333;
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US-09-111-085-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09111085 Patent No. 6100034
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: specific sequences FILE REFERENCE: 4238/75168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                      TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Porcine retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3482
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
                                                                                                                 REFERENCE/DOCKET NUMBER: MG TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE
                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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LENGTH:
TYPE: n
                                                                                                                                                   NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
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                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                            TELEPHONE:
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            8060 base pairs
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                                                                                               (617)227-7400
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US-09-009-913-1/c
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                                                                                                                             Best Local Similarity Matches 19; Conserv
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Best Local Similarity
                                                                                                                                                         Query Match
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APPLICANT: Jay A. Fishman

TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS

TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7763 GATAGCTCTCCTGCCCTTTG 7782
                                                             5237 GATAGCTCTCCTGCCCTTTG 5256
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LENGTH: 8132 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                    NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGI
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                                                                                                                                                                                                                                                                      nucleic acid
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(617)227-5941
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                                                                                                                                                                                                                                         linear
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Pred. No. 4.7;
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; Sequence 1, Application US/09009913
; Patent No. 6087485

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GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: CITY: F

Palo Alto

285 Hamilton Ave, Suite 200

Bozicevic & Reed, LLP

NUMBER OF SEQUENCES:

339

APPLICANT: AxyS Pharmaceuticals, Inc. TITLE OF INVENTION: Asthma Related Ge

Asthma Related Genes

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; MOLECULE TYPE: Genomic DNA US-09-009-913-1
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                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08766528 Patent No. 6190861
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Jay A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,528
                                                                                                                                                                                                                                     TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 72928 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 36,677
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CITY: Boston
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                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                    STATE:
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Pred. No. 32
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US-08-766-528-15
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; MOLECULE TYPE: US-08-766-528-15
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
APPLICANT: Jay A. Fishman
APPLICANT: Jay A. Fishman
APPLICANT: Jay A. Fishman
APPLICANT: OF USE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                   TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                        NAME: Louis Myers
REGISTRATION NUMBER:
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CITY: Boston
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STRANDEDNESS: single
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                                                                                                                                                                                            MGP-038CP
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                                                                                                                                                                                                                                                                                                                                                                Version #1.25
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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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В
                                                                                                                      US-08-800-291B-7
                                                                                                                                          RESULT
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PCT-US93-12464-1/c

Sequence 1, Application PC/TUS9312464

GENERAL INFORMATION:
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                                                                                     Sequence 7, Application US/08800291B Patent No. 6153740
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Best Local Similarity
                                                                                                                                                                                                                                                           Matches
                                                                       GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
               APPLICANT: J.D. Young & C.E. Cass
TITLE OF INVENTION: cDNA ENCODING NUCLEOSIDE TRANSPORTER
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                       1851 GCTCTCCTGCCCTTTG 1836
      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: The Regents of the University of California, et al. TITLE OF INVENTION: METHOD FOR INHIBITION OF CELL TITLE OF INVENTION: ADHESION TO RECEPTORS CONTAINING SELECTINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 455-5100
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NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,
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ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: ALPHA-L-FUCOSIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                    80.0%; Score 16; DB 5;
100.0%; Pred. No. 53;
tive 0; Mismatches
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Pred. No.
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. 34;
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US-08-308-949A-1
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CLASSIFICATION:
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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Sequence 1, Application US/08308949A Patent No. 5580703
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INFORMATION FOR SEQ ID NO:
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Adeno-Associated Virus Integration TITLE OF INVENTION: Site DNA and Uses Thereof
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/499,314
FILING DATE: 7-JULY-1995
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APPLICATION NUMBER: US/08/800,291B
FILING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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LENGTH: 2400 base pairs
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MEDIUM TYPE: Floppy
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SOFTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE:
                APPLICATION NUMBER:
                                                                                                                                                                                  STREET: Two Mili
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TELEFAX: 619/678-5099
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Two Militia Drive
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                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                               Kotin, Robert M.
Berns, Kenneth I.
                                                                                                                                                                                                                                                                                                             Linden, Ralph M.
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September 20, 1994
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                US/08/308,949A
                                                                                                                                                                                                                        Brook, Smith & Reynolds, P.C
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

September 27, 1992

07/947,127

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                                                                                  TELEFAX: (212) 753-6237 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                           NAME: LIGHTY, S. Peter REGISTRATION NUMBER: 25,351 REFERENCE/DOCKET NUMBER: 03.
TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 527-7700
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: QIAN, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KLINGER, KATHERINE W. APPLICANT: LANDES, GREGORY M. APPLICANT: BURN, TIMOTHY C.
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REFERENCE/DOCKET NUMBER: ACC
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
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                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08
FILING DATE: 12-OCT-1994
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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STRANDEDNESS: single
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BURN, TIMOTHY C.
CONNORS, TIMOTHY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DACKOWSKI, WILLIAM R. GERMINO, GREGORY
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DNA (genomic)
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Db 14923 GCTGGCTCTCCTGCCCT 14907
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MOLECULE TYPE:
US-08-658-136-2
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US-08-658-136-2/c
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                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                Query Match
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GE
                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                               1 gatggctctcctgccct 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 01701
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Local Similarity 94.1%;
les 16; Conservation
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                                                                                                                                         Conservative
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LANDES, GREGORY M
BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                       77.0%; Score 15.4; DB 3; 94.1%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYCYSTIC KIDNEY DISEASE GENE 58
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                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                 Length 53526;
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US-08-658-136-1/c
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                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                          Sequence 3, Application US/08826246 Patent No. 6048709
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Best Local
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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NAME: LASSEN, ELIZABETH
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                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/658,136 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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les 16; Conserv
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           COUNTRY:
                                  STATE:
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MASSACHUSETTS
10036-2711
                                               New York
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                                                                1155 Avenue of the Americas
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CONNORS, TIMOTHY D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LANDES, GREGORY M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLINGER, KATHERINE W
                  USA
                                                                                                                                                                               Falb, Dean
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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94.1%;
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                                                                                                                            COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
                                                                                                                44
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US-08-826-246-3
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REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,
                                                                                                                                    ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                               APPLICANT: Falb, Dean TITLE OF INVENTION: CCTTITLE OF INVENTION: THE TITLE OF INVENTION: CA
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FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
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CORRESPONDENCE ADDRESS:
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                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                              CITY:
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                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
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                                    FILING DATE:
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                  CLASSIFICATION:
                                                                                                                                                                            10036-2711
                                                                                                                                                                                                                                New York
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(212)8699741
                                                                                                                                                                                               USA
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                                                                                                                       IBM Compatible
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                                                                                                                                                                                                                                                                                                                   COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
                                                                                                                                                                                                                                                                                                      44
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                                                     US/08/944,495
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Gaps

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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                 nucleic search, using sw model
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/ina/backfiles1.seq:*
           DВ
  US-09-111-085-3
US-08-766-528-2
US-08-766-528-3
US-08-766-528-61
US-09-766-528-61
US-09-150-141-8
US-09-150-141-8
US-09-374-492-8
US-09-374-492-8
US-09-374-492-8
US-09-374-492-8
US-08-0812-29-2
US-08-0812-29-2
US-08-08-755-587-27
US-08-483-553-2
US-08-483-553-2
US-08-488-01118-20
US-08-488-0118-20
US-08-488-0118-20
US-08-488-0120-20
US-08-850-727-20
US-08-850-727-20
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US-08-95-1200-20
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US-08-95-1020-20
US-09-006-535-7
US-09-006-535-7
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Compugen Ltd
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71.1	71.1	71.1	72.2	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	74.4	74.4	74.4	74.4	74.4	74.4
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US-08-545-809A-62	US-08-905-223-150	US-08-680-326-46	US-08-961-083-181	US-09-103-840A-1	US-09-090-793-12	US-08-785-420-1	US-09-013-881-14	PCT-US95-02303-21	US-08-485-657A-22	PCT-US95-02303-25	US-08-485-657A-17	US-09-103-840A-1	US-09-301-665-3	US-09-081-320-1	US-09-081-320-2	US-08-818-112-106	US-09-006-535-1
62,	150			Sequence 1, Appli	Sequence 12, Appl	1,	14	21	22		Sequence 17, Appl	Sequence 1, Appli		Sequence 1, Appli	Sequence 2, Appli		Sequence 1, Appli

ALIGNMENTS

RESULT 1 US-09-111-085-3/c

Sequence 3, Application US/09111085 Patent No. 6100034

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US-08-766-528-2/c
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APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
APPLICANT: Weiss, Robin A
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
TITLE OF INVENTION: Specific sequences
FILE REFERENCE: 4238/75168
CURRENT PPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                             Sequence 2, Application US/08766528 Patent No. 6190861 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Porcine retrovirus
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3482
                                                                                                                                                                                            APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                            COUNTRY: USA
ZIP: 02109-1875
                                                                                      CITY: Boston
STATE: Massachusetts
                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD, STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 3 100.0%; Pred. No. 0.72;
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US-08-766-528-1/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08766528 Patent No. 6190861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                 REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jay A. Fishman TITLE OF INVENTION: MOLECUTITLE OF INVENTION: AND MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
             SEQUENCE CHARACTERISTICS:
LENGTH: 8060 base pairs
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                                                                                                                                                                                 APPLICATION NUMBER: US 01 FILING DATE: 14-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
7.IP: 02109-1875
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Louis Myers
REGISTRATION NUMBER: 35,965
TYPE:
                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ccacagtcgtacaccacg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   NUMBER: US 08/572,645
14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR SEQUENCE OF SWINE RETROVIRUS
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RESULT 5
US-08-766-528-61
; Sequence 61, Application US/08766528
; Patent No. 6190861
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US-08-766-528-3/c
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                                                                                                                                                                       Query Match
Best Local :
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-594: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
TYPE: nucleic acid
                                                                                             8080 CCACAGTCGTACACCACG 8063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109-1875
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                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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18; Conserv
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                                                                                                                                                        Conservative
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                                                                                                                                                       Score 18; DB 4
Pred. No. 0.75;
Mismatches
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Pred. No. 0.75;
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                                                                                                                                                                                   DB_4; Length 8132;
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GENERAL INFORMATION:

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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-111-085-15
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                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/09111085 Patent No. 6100034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                       TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: specific sequences
FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER: OF SED ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                  LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
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PRIOR APPLICATION DATA:
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
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US-09-374-493-8
; Sequence 8, Application US/09374493
; Patent No. 6204016
                                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Mus musculus US-09-150-141-8
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; Sequence 8, Application US/09150141B
; Patent No. 6071732
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-150-133-8
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GENERAL INFORMATION:
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APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERAES, AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.504
                                                                                                                                                                                                Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERAES, AND METHODS OF USE THEREOF
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SOFTWARE: Wordperfect 5.1 (saved in ASCII format)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/150,133B CURRENT FILING DATE: 1998-09-09
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nes 15; Conserv
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                                                                                                                                                                                                              76.7%;
88.2%;
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88.2%;
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100.0%; Pred. No.
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                                                                                                                                                                                                              Score 13.8; DB 3; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus US-09-374-493-8
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                                                                                                                                                                                   US-09-374-492-8
                                                                                                                                                                                                     RESULT
                                            GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
SEQ ID NO 8
LENGTH: 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09374824 Patent No. 6207414
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                                                                                                                                    Sequence 8, Application US/09374492 Patent No. 6207432
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Best Local Similarity
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EARLIER FILING DATE: 1998-09-09
EARLIER PPLICATION NUMBER: 09/072,994
EARLIER FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: PCT/US99/16750
EARLIER FILING DATE: 1999-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.547
CURRENT APPLICATION NUMBER: US/09/374,824
CURRENT FILING DATE: 1999-08-13
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EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 60/072,994
EARLIER FILING DATE: 1998-01-29
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CURRENT APPLICATION NUMBER: US/09/374,493
CURRENT FILING DATE: 1999-08-13
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TITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
  CURRENT FILING DATE:
                         CURRENT
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APPLICATION NUMBER: US/09/374,492 FILING DATE: 1999-08-13
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Pred. No. 1:1e+02;
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Pred. No. 1.1e+02;
0; Mismatches 2;
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LENGTH: 1760
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EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 60/072,994
EARLIER FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: PCT/US99/16750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows DEMONSTRATION Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Modified Lepidopteran Receptors
TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcript
TITLE OF INVENTION: and Transgene Expression Regulation
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2711 base pairs
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gage, Frederick H. APPLICANT: Suhr, Steven T.
                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                  TOPOLOGY:
                                                                                                                                             TYPE:
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                                                                                                                    STRANDEDNESS: single
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                                                                                                                                                                                                                                           619-677-1465
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Pred. No. 1.1e+02;
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Best Local
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REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haymond, W. Bradley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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166 CGCGGTCGTACACCACG 150
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CTTY: San Antonio
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TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Hilliard, Julia K.
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269..2941
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 Mismatches

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Pred. No. 1.1e+02;
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APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
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APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael D
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
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Skolnick, Mark I
Goldgar, David I
Miki, Yoshio
Swenson, Jeff
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14-DEC-1995
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; ORIGINAL SOURCE:
; ORGANISM: Hom
US-08-480-784-20
Search completed: February 24, 2002, 03:01:32 Job time: 21443 sec
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Matches 15; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994

PRIOR APPLICATION NUMBER: US 08/289,221
PRIOR APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2484-10934
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
DELICATION NUMBER: US 08/308,104
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Susceptibility Gene
TITLE OF SEQUENCES: 85
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CORRESPONDENCE ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wiseman, Roger W. APPLICANT: Futreal, P. Andrew
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965 CTACAGGCGTACACCAC 949
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STRANDEDNESS: doub
TOPOLOGY: linear
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Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
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88.2%;
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                                                                                                                                                                                                             Score 13.8; DB 1; Length 6769; Pred. No. 1.1e+02;
                                                                                                                                                                                          0; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 482											Match Length DB	ÿ
10 AA529580	13 AQ920035	11 BF442561	13 вн059214	13 AZ730616	13 AZ380763	13 AZ891915	10 AW447645	11 BI183551	10 BE013835	11 BF709087	DB ID	
AA529580 vi41d04.r	AQ920035 RPCI-23-2	BF442561 259390 MA	BH059214 RPCI-24-3	AZ730616 RPCI-24-1	AZ380763 1M0136B22		AW447645 89634 MAR		BE013835 125326 MA	BF709087 MI-P-AY0-	Description	

ALIGNMENTS

BF709087 391 bp mRNA EST 02-JAN-2001
MI-P-AY0-nae-c-07-0-UI.Sl MI-P-AY0 Sus scrofa cDNA clone
MI-P-AY0-nae-c-07-0-UI 3', mRNA sequence.
BF709087
BF709087.1 GI:12008564
EST.
pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 391)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene

JOURNAL MEDLINE COMMENT

Res. 6 (9), 791-806 (1996)

Animal Science

REFERENCE AUTHORS

TITLE

VERSION KEYWORDS

LOCUS
DEFINITION
ACCESSION

SOURCE

ORGANISM

RESULT 1 BF709087/c

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DLINE 97044477
Contact: Tuggle CK
Molecular Genetics Laboratory, Department of
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252

Fax: 5152942401

Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized placenta library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward

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FEATURES
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                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 52 row: B column: 23
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Re
PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE013835 545 bp mRNA EST (
125326 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BE013835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE013835.1 GI:8274822 EST.
                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                         and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                          PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYA-Yes.
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/clone_lib="MI-P-AY0"
/lab_nost="DH10B (Life Technologies)"
/lab_nost="DH10B (Life Technologies)"
/lab_nost="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: EcoRI; The MI-P-AY0 library is derived from placenta. For a detailed description of the library from which this clone was derived, please visit our web site at http://plqest.genome.lastate.edu/. The procedure used to create this library has been previously described (Bonaldo , Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=MI-P-AY0
                                                  /clone_lib="MARC 1PIG"
                                                                                    /db_xref="taxon:9823"
                                                                                                       /organism="Sus scrofa"
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_TISSUE=placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 g
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NE 68933-0166, USA
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Pomp, D
Department of Animal Sci
University of Nebraska,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library from swine ovarian follicles Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI183551
BI183551.1 GI:14657960
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caetano, A.R., Johnson, R.K. and Pomp, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA=No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 -29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo-dT track not found, Not I site shown is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dpomp@unl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation and sequence characterization of a normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                 /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
                                           TAG_SEQ=None found"
a 83 c 92 g
                                                                                                                                                                of the pig estrous cycle. This library was derived the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as despite the 
                                                                                                                                       by Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="ph10B"
/note="Vector: pcMV SPORT6; Site_1: xbaI; Site_2: xhoI;
/inote="Vector: pcMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
a 120 c 129 g 168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UNL-P-FN-by-g-02-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain="University of Nebraska, Lincoln Swine Selection/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                 1996.
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Pred. No.
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s a string of 5-6
                                                                                                                                          Genome Research 6: 791-806
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                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                   2461 gagtgggtgaggcagcgagcgtggaagcagctccgggaggcctactcaggag 2512
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                                                                              302 GAGTGGGTGAGCGAGCGTGGAAGCAGCTCCGGGAGGCCTACTCAGGAG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegraid, W.W., Rohrer, G.A., Chilko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 70 row: L column: 19 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW447645
AW447645.1 GI:6989432
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
134 c 124 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
/lab_host="DH10B"
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100.0%; Pred. No.
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3.5e-05;
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hes 0;
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         2420 tgctgctttcccagcctttgttctctaggctcaaggcgctcgagtgggtgag 2471
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                                                                                                                                                                                                                                                                                                                                                     304 TGCTGCTTTCCCAGCCTTTGTTCTCTAGGCTCAAGGCGCTCGAGTGGGTGAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , DNA sequence.
AZ891915
Dunn, D., Aoyagi, A.,
                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 549)
                                                                                      Mus musculus
                                                                                                                                 GSS
                                                                                                                                                                            AZ380763
                                                                                                                                                                                               1M0136B22R \ \mbox{Mouse} \ 10\mbox{kb} \ plasmid \ \mbox{UUGC1M library} \\ \mbox{clone} \ \mbox{UUGC1M0136B22} \ \mbox{R, DNA sequence.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Other_GSSs: RPCI-24-172A20.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ891915 451 bp DNA GSS 05-MAR-2001 RPCI-24-172A20.TV RPCI-24 Mus musculus genomic clone RPCI-24-172A20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 172 row: A column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.
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الم
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA."
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="RPCI-24-172A20"
/clone_lib="RPCI-24"
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                                                                                                                                                      GI:10494463
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100.0%; Pr
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  Barber, M., Beacorn, T., Duval, B.,
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Pred. No. 3.2e-05;
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                                                                 Euteleostomi;
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                                                                                                                                                                                            RPCI-24-149D1.TJ RPCI-24 Mus musculus genomic clone RPCI-24-149D1,
1 (bases 1 to 576)
                                         Eukaryota; Metazoa;
                                                              Mus musculus
                                                                                                                                AZ730616.1 GI:12491859
                                                                                                                                                         AZ7306:
                                                                                                                                                                            DNA sequence.
                                                                                                                                                                                                                        AZ730616
                    Mammalia;
                                                                                        house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                  Eutheria;
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/strain="C57BL/6J"
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                                                                                                                                                  Unpublished (1999)
Other_GSSs: RPCI-24-326H3.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Tel: 301 838 0200 Fax: 301 838 0208
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                                                                         9712 Medical Center Dr., Rockville,
                                                                                                                 The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 704)
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
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Class: BAC ends.
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Other_GSSs: RPCI-24-149D1.TV
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Clones are derived from the mouse BAC library RPCI-24. For BAC
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
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/note="Vector pTARBAC1; Site_1: BamH1;
/note="Vector pTARBAC1; BamH1; BamH1;
/note="Vector pTARBA
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/clone="RPCI-24-149D1"
/clone_lib="RPCI-24"
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF442561 100 bp mRNA EST (259390 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                    and -minmatch 12 options.
                                                                                                                                                                                                                              Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                 Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                            Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; veiteriata, successiona Suidae; Sus. Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF442561.1 GI:11502653
                                                                                                                                   BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                     EST discovery in swine
                                                                                        primer: ATTTAGGTGACACTATAG
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site BamH1; Sites using wboI partially digested male C57BL/6JDNA."
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/clone="RPCI-24-326H3"
/clone_lib="RPCI-24"
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/db_xref="taxon:9823"
                     /organism="Sus scrofa"
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100.0%; Pred. No.
                                                                                                                column: 16
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RPCI-23-273D7.TV RPCI-23 Mus musculus genomic clone RPCI-23-273D7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 482)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 273 row: D column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
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                     128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from poled tissue from testis, ovary, endometrium, hypothalanus, pituitary, and placenta." a 24 c 26 g 21 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                      selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                         /note="Organ: Kidney/Brain; Vector: pBACc3.6; Site_1: ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of ECORI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                 1. .482
                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="RPCI-23-273D7"
                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                     /clone_lib="RPCI-23"
                                                                                                                                                                                                     /lab_host="DH10B"
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Query Match

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Score 37;

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                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 326.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashIngton University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This_clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 545)
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                                                                                                                                                                                                                                        developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)" 130 c 127 g 145 t
                                                                                                                                                                                                                                                                                                                 /note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Gastrulating embryos were collected at 7.5dpc from C57BL6 x DBA matings, excluding embryos that had
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:906343"
/clone_lib="Beddington mouse embryonic region"
                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="DH12S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="pooled"
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                                                                                                                                                 Score 36; Pred. No.
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                                                                                                                                             0.78;
                                                                                                                                                             DB 10; Length 545;
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P21414 POL POLYPROTEIN
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                                                                                                                         0;
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В QΥ

Matches

Local Similarity 36;

Conservative

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Mismatches

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ORIGIN
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                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0300 row: M column: 05
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 575)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ479717.1 GI:10639886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone UUGC1M0300M05 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ479717 575 bp DNA GSS 04-OCT-2000 1M0300M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                     136 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308,
                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: PWD42nv; Purified genomic DNA from M musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0300M05"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
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  Score 36;
Pred. No.
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DB 13;
0.75;
                          Length 575;
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193 CAMAGCTCAGGACAGGTAGAGAGGATGAATAGAACC 158
                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C
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                                                                                                                             Similarity
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                                                                                                                                                                                                                                                           146
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                                                                                                     Conservative
                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PW042nv; Purified genomic DNA from M.
musculus CSTBL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC1M0190M06"
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/strain="C57BL/6J"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                        100.0%;
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                                                                                                                        Score 36; DB 13;
Pred. No. 0.74;
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                                                                                                     Mismatches
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                                                                                                                                                Length 583;
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334 CAAAGCTCAGGACAGGTAGAGAGGATGAATAGAACC 369

Matches

Conservative

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Mismatches

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LOCUS
                                                                                                                                      BASE COUNT
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Contact: Robert B.
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2M0205L23R Mouse 10kb plasmid UUGC2M library Mus musculus
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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                                                                                                                              adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

136 c 151 g 152 t
                                                                                                                                                                                                                                      was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0205L23"
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  1.1%;
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  Score 36;
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Std Error: 0.00
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AZ859488
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/sex="Male"
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/db_xref="taxon:10090"
/clone="UUGC2M0165D07"
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FEATURES Source	TITLE JOURNAL COMMENT	VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 BI182930/c LOCUS DEFINITION
Department of Animal Science University of Nebraska, Lincoln Lincoln, NE 68583-0908, USA Tel: 402 472 6416 Fax: 402 472 6362 Email: dpomp@unl.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized porcine ovarian follicles library Seq primer: M13 -29 POLYA-Yes. Location/Qualifiers 1564 /organism="Sus scrofa"	Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles Unpublished (2001) Contact: Pomp, D. Contact: Pomp, D.	BI182930.1 GI:14657339 ESST. pig. Sus scrofa Sus scrofa Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 564)	BI182930 564 bp mRNA EST 10-JUL-2001 UNL-P-FN-br-h-08-0-UNL-ST UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-br-h-08-0-UNL 3', mRNA sequence.

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                          Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                         Design and use of two pooled tissue normalized EST discovery in swine
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                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 86 row: C column: 8
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                    Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 467)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegre and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore v0.980904.e. Vector v0.980904.e. V0.980904.e. Vector v0.980904.e. Vector v0.980904.e. Vector v0.980904.e. V0.980904.e. V0.980904.e. V0.980904.e. V0.980904.e. V0.98
                                                                                                                                                                                                                                                           Single pass sequencing. Bases ov v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pig.
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BF441465.1 GI:11501629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 86 row: D column: 8 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                         and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for
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                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
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                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
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/lab_host="DH10B"
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100.0%;
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Pred. No. 4.3e-26;
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                                                                                                                                                                                                                                                                                                  called and alt_trimmed with phred
                                                                                                                                                                                                                                                           cross_match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pig.
Sus scrofa
                                                                                                                                                                                                                                                             Email: cktuggle@lastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 59-132,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tuggle CK Molecular Genetics Laboratory, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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                                                                                                                                                                                                 Seq primer: M13 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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                                                                                                                                                                                                                                             >GC_rich#Low_complexity
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(bases 1 to 532)
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/clone="MI-P-AY1-nga-b-06-0-UI"
/clone_lib="MI-P-AY1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
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/clone_lib="MARC 2PIG"
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                                                                                      /strain="crossbreed"
/db_xref="taxon:9823"
                                                                                                                                  /organism="Sus scrofa"
                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                           Forward
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rismatches 0;
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 CTTTTGCCTGCTTGTGGAAGACGCGGACGGGTCGCGTGTGTCTGGATCTGTTTGGTTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180;
                                                                                      Email: cktuggle@lastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 59-132,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF711018 408 bp mRNA EST 02-JAN-MI-P-AY1-nrb-h-02-0-UI.S1 MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-nrb-h-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                      Iowa State University
201 Kildee Hall, Ames,
Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig.
Sus scrofa
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                                                                 >GC_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                          Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                 Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, M.F.,
                                                                                                                                                                                                                                                     Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 408)
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                                            primer: M13
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Location/Qualifiers
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Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                               IA 50011-3150, USA
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/organism="Sus scrofa" /strain="crossbreed"

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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 CTGTCGGTCAGAGGACCGAGTTCTGTTGTTGAAGCGAAAGCTTCCCCCTCCGCGGCCGTC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 ctgtcggtcagaggaccgagttctgttgttgaagcgaaagcttccccctccgcggccgtc 478
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                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                              Oligo-dT track not found, Not I si is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 564)
Caetano, A.R., Johns
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BI181099.1 GI:14655508
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                                                                                                                                                                                                                                                                                                Seq primer: M13 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and sequence characterization of a normalized library from swine ovarian follicles
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                                                                                                                                                                                                                                                                                                                                                                                                 Email: dpomp@unl.edu
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TAG_SEQ-None found"

139 c 122 g 52 t 1 others
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/clone_lib="MI-P-AY1"
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/lab_host="PH10B (Life Technologies)"
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/note="Vector: pH10B-Pac (Pharmacia) with a modified
/note="Vector: pH10B-Pac (Pharmacia) with a modified
/labaray ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia)
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                                                                                                         /clone="UNL-P-FN-ab-d-02-0-UNL"
                                                                                                                                                              Lines"
                                                                                                                                                                                    /organism="Sus scrofa"
/strain="University of Nebraska, Lincoln
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                    /db_xref="taxon:9823"
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; Pred. No. 1.6e-22;
0; Mismatches 0;
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  (Pharmacia) with a modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library from swine ovarian follicles
Unpublished (2001)
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13
POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dpomp@unl.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pt7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_SEQ=None found"
196 c 143 g
                                                                                                                                                                                                                                                                                                                                 Lines"
                                                                                                                                                                                                                                                    /clone="UNL-P-FN-ab-d-02-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                          /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
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Pred. No. 1.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                        Matches
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                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1204 gccaattgcagcccctccagtattggcccttttcttctgcagatctctataattggaaaa 1263
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 GCCAATTGCAGCCCCTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGGAAAA 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 376)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF441469.1 GI:11501633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257863 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
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                                        Conservative
                                                                                                                                                        91
                                                                                                                                                    /note="Yector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 94 c 108 g 83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_SEQ=None found"
196 c 144 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                                                                                                                                                                                                                                /clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/db_xref="taxon:9823"
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                                                          6.4e-15;
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                                                                                                                                                                   8158 tggaataaaaatcctcttgctgtttgcatcaa 8189
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                                                                                                                                                  192 TGGAATAAAATCCTCTTGCTGTTTGCATCAA 223
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
             BF712162 602 bp mRNA EST 02-J MI-P-E6-acx-e-11-1-UM.S1 MI-P-E6 Sus scrofa cDNA clone MI-P-E6-acx-e-11-1-UM 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Sus scrofa
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BI360879.1 GI:15056907
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388957 MARC 2PIG Sus scrofa
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Mammalia;
BF712162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 142
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                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pCMV SPORT6; Site_1: Xba1; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 123 c 119 g 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="DH10B"
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  acccctgcgtggtgtacgactgtgggccccagcgcgcttggaataaaaatcctcttgctg 8179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTTTGTTGTGAACCCCCATAAAAGCTGTCCCGATTCCGCACTCGGGGCCGCAGTCCTCT
                                                                                                                                                                                                                                                      TTTGCATCAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                 ACCCCTGCGTGGCGTACGACTGTGGGGCCCCAGCGCGTTGGAATAAAAATCCTCTTGCTG
            BF441466 452 bp
257857 MARC 2PIG Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized fetus at gestational day 20 library cDNA Library reparation: RJ Woods, JA Green, RS Frather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cktuggle@iastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first oligonucleotide that was present in the
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Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iowa State University
201 Kildee Hall, Ames, IA 50011-3150,
Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 5152942401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 602)
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/dlone="MI-P-E6-acx-e-11-1-UM"
/clone="MI-P-E6-acx-e-11-1-UM"
/clone="Ib="MI-P-E6"
/lab_host="DH10B (Life Technologies)"
/lab_host="TH10B (Life Technologies)"
/lab_host="TH10B (Life Technologies)"
/lab_host="TH10B (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://pigest.genome.iastate.edu/
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scrofa cDNA 5', mRNA sequence
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Pred. No.
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4.3e-14;
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          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett Casas, E., Wray, J.E., White, J., Rohrer, G.A., Chitko-McKown, C.G.
                                                                                                                                                           Bos taurus
                                                                                                                                                                                COW
                                                                                                                                                                                                AW657531
AW657531.1 GI:7423429
EST.
                                                                                                                                                                                                                                                     AW657531 549 bp mRN/
110922 MARC 1BOV Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
Pertea, G., Holt, I., Karamycheva, S.,
                                                                           Bovidae; Bovinae; B
1 (bases 1 to 549)
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research
PO Box 166, Clay Center, NE 68933-C
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases call
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 86 row: C column: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 452)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 118 c 125 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
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/lab_host="DH10B"
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Pred. No. 5.8e-11;
                                                                                                                                                                                                                                                                            mRNA
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d by cross_match with the -minscore
Liang, F., Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 452;
                                                                                                                  Pecora; Bovoidea;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6640 aaattcaatgtgaccaaagagcatagaaatcaatgtacatgggggtcccggaaataagctt 6699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6760 cacctttgc 6768
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                                                     Contact: Pomp, D
Department of Animal Science
University of Nebraska, Linco
Lincoln, NE 68583-0908, USA
                                                                                                                                                                                                    1 (bases 1 to 857)
Caetano, A.R., Johnson, R.K. and Pomp, D.
                                                                                                                                                                                                                                                                                                                                                                                       BI184013 EST 10-JUL UNL-P-FN-cf-b-12-0-UNL-S1 UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-cf-b-12-0-UNL 3', mRNA sequence.
Email: dpomp@unl.edu
                                                                                                                                               Unpublished (2001)
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                Generation and sequence characterization of a normalized cDNA
                                                                                                                                                                                                                                                                                                                                                        BI184013.1 GI:14658422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 94 row: E column: 12 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                   library from swine ovarian follicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
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                   402 472 6416
402 472 6362
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Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
144 c 121 g 139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
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Pred. No. 1.6e-10;
                                                                                 Lincoln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
Email: cktuggle@lastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the
                                                                                                                                                                                                                                Contact: Tuggle CK Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF709087 391 bp mRNA EST 02-JAN-MI-P-AY0-nae-c-07-0-UI.sl MI-P-AY0 Sus scrofa cDNA clone MI-P-AY0-nae-c-07-0-UI 3', mRNA sequence.
                                                                                                                                                     Fax: 5152942401
                                                                                                                                                                        201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
                                                                                                                                                                                                                                                                                          97044477
                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                   discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF709087.1 GI:12008564
                                                                                                                                                                                                                    Iowa State University
                                                                                                                                                                                                                                                                                                                                                      Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_SEQ=None found"
a 217 c 248 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UNL-P-FN-cf-b-12-0-UNL"
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                                                                                                                                                                                                                                                                                                                                                                              Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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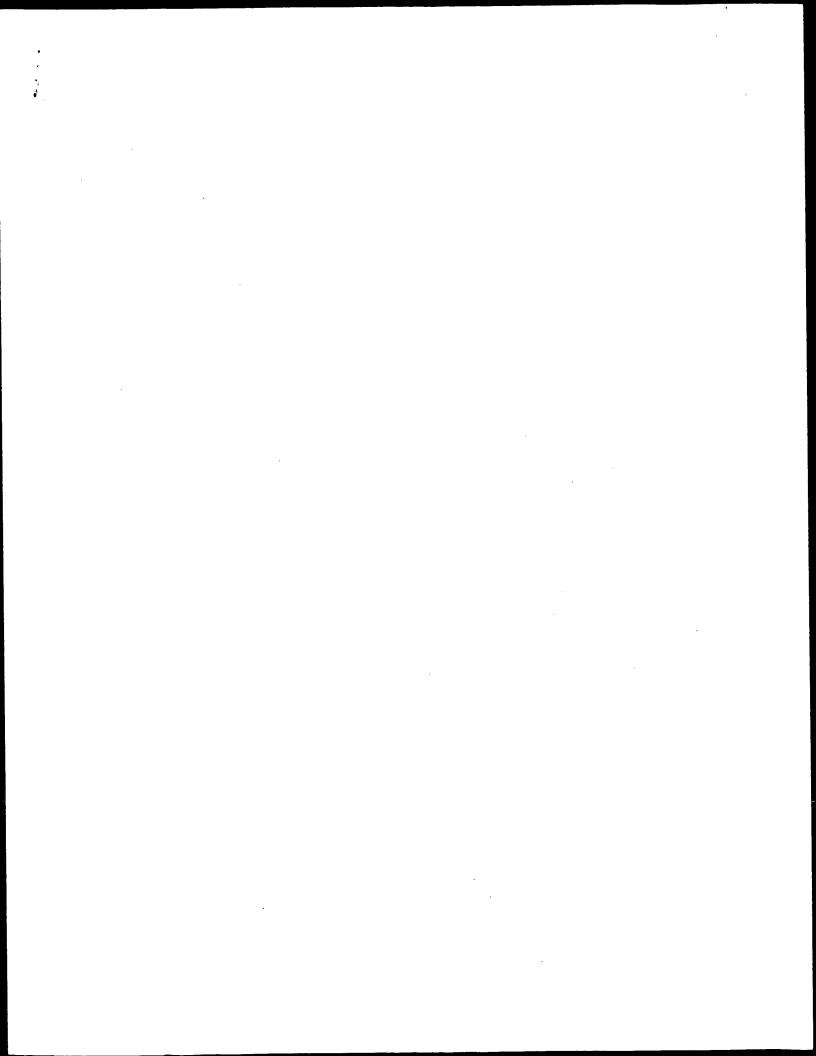
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FEATURES
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                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 545)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 52 row: B column: 23
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST discovery in swine Unpublished (2000)
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                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                  PCR PRimers
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//lab_host="PHIOB (Life Technologies)"
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//lab_host="PHIOB (Life Technologies)"
//lab_host="Phiopies"
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/clone_lib="MI-P-AYO"
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                                                                                                                                                                                               0.9%; Score 74; DB 10; ilarity 100.0%; Pred. No. 1.6e-0; Conservative 0; Mismatches
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a 120 c 129 g 168 t
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/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
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/lab_host="DH10B"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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73 M 911. 7717 7717 -24- 070E	1M0152P16 1M0152P15 RPCI-24-3 2M0236A21	29231 MAR UNL-P-FN- 2M0018A11 119054 MA	1M0498123 RPCI-24-1 1M0092E07 1M0053G10 UNL-P-FN-	MA 23- 04. 5D0 4F2	RPCI-24-1 UNL-P-FN- 29171 MAR MI-P-E3-a	-E3-

ALIGNMENTS

source	FEATURES		JOURNAL COMMENT	TITLE	AUTHORS	REFERENCE	ORGANISM	SOURCE	VERSION KEYWORDS	ACCESSION	LOCUS DEFINITION	RESULT 1 BI182930/c
1564 /organism="Sus scrofa"	University of Nebraska, Lincoln Lincoln, NE 68583 0908, USA Tel: 402 472 6416 Fax: 402 472 6416 Email: dpomp@unl.edu Email: dpomp@unl.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized porcine ovarian follicles library Seq primer: M13 -29 POLYA-Yes. Location/Qualifiers	Department of Animal Science	Unpublished (2001) Contact: Pomp. D	Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles	Caetano, A.R., Johnson, R.K. and Pomp, D.	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 564)</pre>	Sus scrofa	pig.	BI182930.1 GI:14657339 EST.	BI182930	BI182930 564 bp mRNA EST 10-JUL-2001 UNL-P-FN-br-h-08-0-UNL-S1 UNL-P-FN Sus scrofa cDNA clone	

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Local Similarity 99.3%;
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USDA, ARS, US Meat Animal Re
PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                          Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                          pig.
Sus scrofa
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388957 MARC 2PIG Sus scrofa cDNA
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                                                                                             Contact: Smith TPL
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                                                                                                                                                                    Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                          Mammalia;
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//lab_host="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE-porcine ovarian follicles
TAG_SEQ=CACACT"
129 c 143 g 151 t
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/clone_lib="UNL-P-FN"
/dev_stage="ADULT"
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Pred. No. 5.4e-37;
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                                                                         Research Center
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 TGGAATAAAATCCTCTTGCTGTTTGCATCAA 223
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EST.
                                                             Email: cktugdle@iastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized fetus at gestational day 20 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 142 row: B column: 4 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR PRimers
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                                       Missouri-Columbia, 65211 Clone distribution: clones available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 Kildee Hall, Ames, IA 50011-3150, USA Tel: 5152944252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 602)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF712162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iowa State University
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/lab_host="hH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
/inote="Vector: pCMV SPORT6; Site_1: XbaI; Site_1: XbaI; Site_2: XhoI;
/inote="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
/inote="vector: pCMV SPORT6; Site_1: XbaI; Si
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Pred. No. 2.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142;
                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Cass, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW657531 549 bp mrNA EST 110922 MARC 1BOV Bos taurus cDNA 5', mrNA sequence.
                           BACKWARD: GTTTTCCCAGTCACGACG
                                                                                               and -minmatch 12 options.
                                                                                                                                                                                                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                               FORWARD: AGGAAACAGCTATGACCAT
                                                                           PCR PRimers
                                                                                                                                                                                                                                                                                                                    21180013
                                                                                                                                                                                                                                                                                                                                                                                                                    Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
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/note="Vector: pT7T3D-pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E6 library is derived from fetus at gestational day 20. I a detailed description of the library from which this clone was derived, please visit our web site at http://pigest_genome.iastate.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=fetus at gestational day 20 TAG_SEQ=AGGAA"
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/clone_lib="MI-P-E6"
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row: E column: 12
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99.3%;
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Pred. No. 2.1e-13;
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                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 CACCTTTGC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128;
                                                                                                                                                                                                                                                                                               Email: dpomp@unl.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first
                                                                                                                                                                                                                                                                                                                                                                Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 468)
Caetano, A.R., Johnson, R.K. and Pomp, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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BI186066.1 GI:14660475
                                                                                                                                                                                                                                         Seq primer: M13 -29
                                                                                                                                                                                                                                                                                     strand cDNA and therefore this may represent a bonafide poly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Pomp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation and sequence characterization of a normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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144 c 121 g 139 t
                                                          /clone="UNL-P-FN-bo-a-05-0-UNL'
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                     /dev_stage="ADULT"
                                                                                                      /db_xref="taxon:9823"
                                                                                                                                         /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                /organism="Sus scrofa"
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. 5.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tuggle CK Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                          Seq primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF704354.1 GI:11989756
                                                                                                                                                                                                                                                                                                                                                            will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 Kildee Hall, Ames, IA 50011-3150, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iowa State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
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98 c 97 g
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/Clone="MI-P-03-aba-g-01-1-UM"
/Clone_lib="MI-P-03"
/Clone_lib="MI-P-03"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-03 library is derived from ovary at estrus day 12. For a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the pig estrous cycle.
the library UNL-P-F2. The
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                                                                                                                                                                   /db_xref="taxon:9823"
                                                                                                                                                                                               /strain="crossbreed"
                                                                                                                                                                                                                        /organism="Sus scrofa"
                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lennon, G. and Soares, M.B.
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The tag is a string of
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9.3e-08;
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RESULT 6 BF704354/c

DEFINITION

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BASE COUNT

Matches

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cktuggle@iastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized placenta library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI399852 521 bp mRNA EST 14-AUG MI-P-AY1-nrv-d-03-0-UI.S1 MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-nrv-d-03-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tuggle CK Molecular Genetics Laboratory, Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97044477
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                                                                 /lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EccRI; The MI-P-AY1 plbrary is normalized library derived from the MI-P-AY0 library ultimately derived from placenta tissue. For a detailed description of the library from which this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://pigest.genome.iastate.edu/.
TAG_SEQ=None found"
a 104 c 107 g 152 t 4
was derived, please visit our web site at http://pigest.genome.lastate.edu/. The procedure used to create this library has been previously described (Bonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detailed description of the library from which this clone
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                                                                                                                                                                                                                                /strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-AY1-nrv-d-03-0-UI"
                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa'
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8.8e-08;
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UNL-P-FN-cx-a-05-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-cx-a-05-0-UNL 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dpomp@unl.edu
Oligo-dT track not found, Not I si
is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 730)
Caetano, A.R., Johns
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llarity 100.0%;
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                      TAG_
                                                                          of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described
                                                                                                                                                    /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
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TAG_TISSUE=placenta
TAG_SEQ=ATTGG"
                                                           by Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                /clone="UNL-P-FN-cx-a-05-0-UNL"
/clone_lib="UNL-P-FN"
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                                                                                                                                                                                                                                                                              /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                            /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sus scrofa"
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UNL-P-FN-bo-a-05-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-bo-a-05-0-UNL 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Animal Science
University of Nebraska, Linco
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Pomp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library from swine ovarian follicles Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caetano, A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI182727.1 GI:14657136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: dpomp@unl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and sequence characterization of a normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: M13 -29
                  127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                 /lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a String of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
               TAG_SEQ=None found"
98 c 97 g
                                                                               by Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                            /clone="UNL-P-FN-bo-a-05-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="University of Nebraska, Lincoln Lines"
                                                                                                                                                                                                                                                                                                                          /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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 Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lincoln
                    145
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6.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 730;
                                                                                    Genome Research 6: 791-806
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Query Match

Best Local Similarity

2.3%; 100.0%;

Score 68; Pred. No.

DB 11; 1.6e-07;

Length 468;

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RESULT 10
BF703671/c
                                                                                                                                     BASE COUNT
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    Matches
                         Best Local Similarity
                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized embryo at gestational day 14 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be
  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missouri-Columbia, 65211 Clone distribution: clones available through Research Genetics (www.resgen.com)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: Ml3 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF703671.1 GI:11989079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iowa State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Normalization and subtraction: two approaches to facilitate gene
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Conservative
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                                                                                                                                                                                                                                                              /clone="MI-P-E4-abp-c-04-1-UM"
/clone_lib="MI-P-E4"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E4 library is derived from embryo at gestational day 14. a detailed description of the library from which this
                                                                                                                                 TAG_TISSUE-embryo at gestational day 14
TAG_SEQ=ACTCAC"
114 c 109 g 119 t 1 othe
                                                                                                                                                                                                    TAG_LIB=MI-P-E4
                                                                                                                                                                                                                                             a detailed description of the library from which
                                                                                                                                                                                                                           http://pigest.genome.iastate.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="crossbreed"
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                         100.0%;
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  0;
                       Score 64; DB 11;
; Pred. No. 1.4e-06;
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1.3e-06; hes 0;

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Matches

Local

Similarity

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RESULT 11
BF703805/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cktuggle@iastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized ovary at estrus day 5 library cDNA Library preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF703805 554 bp mRNA EST 22-DI MI-P-02-abs-a-11-1-UM.s1 MI-P-02 Sus scrofa cDNA clone MI-P-02-abs-a-11-1-UM 3', mRNA sequence.
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Sus scrofa
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201 Kildee Hall, Ames,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                      158
2.2%; Score 64; DB 11; ilarity 100.0%; Pred. No. 1.3e-06 Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                /db_xref="taxon:9823"
/clone="MI-P-02-abs-a-11-1-UM"
/clone="MI-P-02"
/clone="MI-P-02"
/lab_host="PH10B (Life Technologies)"
/lab_host="PH10B (Life Technologies)"
/lab_host="PH10B (Life Technologies)"
/lab_host="Nettor: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-02 polylinker; Site_1: Not I; Site_2: EcoRI; The MF-P-02 library is derived from ovary at estrus day 5. For a detailed description of the library from which this clone was derived, please visit our web site at
                                                                                                                                                                 TAG_TISSUE=ovary at estrus day
TAG_SEQ=ATCATC"
a 128 c 122 g 146 t
                                                                                                                                                                                                                                                   TAG_LIB=MI-P-02
                                                                                                                                                                                                                                                                               http://pigest.genome.iastate.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="crossbreed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sus scrofa"
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Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65211 Clone distribution: clones will be
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                                                        Length 554;
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В
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                                     DEFINITION
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                                                                                                                                                                       112 tgctgctttcccagcctttgttctctaggctcaaggcgctcgagtggggtggag 163
                                                                                                                                                  304 TGCTGCTTTCCCAGCCTTTGTTCTCTAGGCTCAAGGCGCTCGAGTGGGTGAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2879 tgta 2882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AACCCCATAAAAGCTGTCCCGATTCCGCACTCGGGGCCGCAGTCCTCTACCCCTGCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 TGTA 71
  BF701947 545 bp mRNA EST 22-D MT-P-E3-aag-c-06-1-UM.sl MT-P-E3 Sus scrofa cDNA clone MT-P-E3-aag-c-06-1-UM 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 172 row: A column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Other_GSSs: RPCI-24-172A20.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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301 838 0208
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-172A20"
/clone=lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The Library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Spleen/Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                    DB 13;
. 0.0012;
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                                                                                                                                                                                                                                                                       Length 451;
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                                                SOURCE
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                                                                                                                                                DEFINITION
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KEYWORDS
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Best Local
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ACCESSION
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                                                                                                          BI184279 300 bp mRNA E51
UNL-P-FN-Ck-g-02-0-UNL,S1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-Ck-g-02-0-UNL 3', mRNA sequence.
                                                        EST
                                                                                 BI184279
BI184279.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized fetus at gestational day 45 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular Genetics Laboratory, Department of Animal Science
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 Kildee Hall, Ames, IA 50011-3150, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E3 library is derived from fetus at gestational day 45. I a detailed description of the library from which this clone was derived, please visit our web site at beth //site for the library from which this clone was derived, please visit our web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=fetus at gestational day 45 TAG_SEQ=CGCGAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_LIB=MI-P-E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://pigest.genome.iastate.edu/.
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/clone_lib="MI-P-E3"
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/db_xref="taxon:9823"
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                 GI:14658688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 11;
Pred. No. 0.0018
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RESULT 15
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Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6362
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
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BI182742.1 GI:14657151
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Contact: Pomp, D
Department of Animal Science
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/clone_lib="UNL-P-FN"
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/strain="University of Nebraska, Lincoln Swine Selection
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Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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/lab_host="Molicial (Life Technologies)
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/strain="University of Nebraska, Lincoln Swine Selection
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AZ717731 RP	AZ897994 RP	AZ827524 2M		AZ715272 RP						_	AZ730616 RP	Description
RPCI-24-1	CI-24-1	2M0104E02	CI-24-2	RPCI-24-1	CI-24-1	RPCI-24-3	1M0067L03	2894023	1M0053G10	RPCI-24-9	RPCI-24-1	!

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ALIGNMENTS

PEATURES TO DO	TITLE M JOURNAL U COMMENT O	REFERENCE 1 AUTHORS 2 R	ACCESSION A VERSION A KEYWORDS G SOURCE h ORGANISM M	RESULT 1 AZ730616 LOCUS A DEFINITION R
Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tlgr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 149 row: D column: 1 Seq primer: SP6 Class: BAC ends. Location/Qualifiers	MOUSE BAC End Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-149D1.TV	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 576) 2 (bases 1 to 576) 2 (bases 1 to 576) 3 (bases 1 to 576) 4 (bases 1 to 576) 5 (bases 1 to 576) 5 (bases 1 to 576) 6 (bases 1 to 576) 7 (bases 1 to 576) 8 (bases 1 to		AZ730616 576 bp DNA GSS 25-JAN-2001 RPCI-24-149D1.TJ RPCI-24 Mus musculus genomic clone RPCI-24-149D1,

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                                                                                                                                                                                                                                                                                                                                  AGAGAAGACCTGGAAGCCCCACATCTCTTCCAAGTTATAGATTCAGTCTACATTAGACGC
                                                                                                                                                                                                                                                                                                                                                                                               CTCAAGGTGCTCGAATGGGTGAGACAGCAAGTATAGAAGCAGCTCCAGAATGCCTACTCA
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
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/note="Vector: pTARBAC1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_2: BamH1; Sites using MboI partially digested male C57BL/6JDNA."
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="RPCI-24-149D1"
   Metazoa; Chordata;
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361 GTTAAAGATACTGGCAAGCTTACTCTAGGTCAGCATGTGAGTGTAATCACTCCCCATGCG
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                       gtcaaggacgctgacaaattgactttggggacagaatataactgtaatagccccccatgca
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                                                                                                                                                                                                                                             CCATATTTGACTAAGCCTTTCACCATATACGTTGATGAGCCAGCTGGAGTAGCCCGCAGA
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-94C16.TJ RPCI-24-94C16.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 0200 Fax: 301 838 0208
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1 (bases 1 to 864)
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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/strain="057BL/6J"
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/clone="UgCIM0053G10"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2020 tatcctactaagaaagagacttcaaccgtggtggctaagaaaatactggaggaaattttt 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1960 aaatacggaaacaaatatctattggtttttgtagacaccttttcaggatgggtagaggct 2019
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                                        2492 tccgggaggcctactcaggag--gagacttgcaagttccacatcgcttccaagttggaga 2549
                                                                                                                          2436 tttgttctctaggctcaaggcgctcgagtgggtgaggcagcga----gcgtggaagcagc 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              672 CTCAGGGATGGCCTGGAAGCCTACTGGGAGGTAGAGTTTACAGAATCTAAGCCAGCT 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 AGATACGGCAACAAGTACTTATTAGTGTTTATAGATACCTTTTCAAGGTGGATAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 GTAAGTCAGGGACTGGCCAAGATATTAGAGATTGGTTAGAAGTTACATTGTGCATACAGG
                                                                                                                                                                                                                                                                                            265
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85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCCTACCAGGACTGAGAC-------GGCCAATATGATCCTAGACGAAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                    ttgaccacagagactggcattaatgattggatggctctccttgccctttgtgctttttagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGGCTCCACTGGTAAAAATAGCCTCTGTACATAGTGCTGACATGCTGCTTTCCCAGCC 146
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                                                                                                                                                                                                                                                                                         gtgaggaacaccctggacagtttgggctgaccccctatgaattgctctac----ggggg 2375
                                                                                                                                                                                                                                                                                                                                                                                           TTGGCAGCTGAGACTAGAGCTAATGATAAGATAGCTCTCCTACCCTTTGTGCTCTTCAGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCAAAGCTCAGGACAGGTAGAGAGAACGAATAGAACCATT - AAGAGACCCTTACCAAA
TCCAGAAGGCCTACTCAAGAGAAGACCTGCAAGCCCCACATCTCTTACAAGTTAGAGA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "
173 c 149 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant,
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78.1%;
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259 AGTAAGTTTTGCACCCCAGCCATTCTCAACCCCGCCTCCTTACTACCT---GAGGCTGA 315
                     969 ggtcactttcgctccaccagccgctctcaaccctgccactcttctgcctgaagagactga 1028
                                                                               199 GGACCGCTGGATGACCAACGCCCGAATGACGCACTACCAGAGCCTATTGCTGACAGAGCG
                                                                                                    909 agaccgatggatgaccaacgcccgcatgacccactatcaaagcctgcttctcacagagag 968
                                                                                                                                                                                         849 gggacagaatataactgtaatagccccccatgcattggagaacatcgttcggcagccccc 908
                                                                                                                                                                                                                                                                                                                                                   729 gaggagacctgttgcctacctgtcaaagaagcttgatcctgtagccagtggttggcccgt 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BI107577
BI107577.1 GI:14558470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11107 row: n column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" a 215 c 218 g 154 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:5039044"
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Pred. No. 2.2e-59;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1328 ttgcgactgcacacgtacacggggccatctataaacaaagggggttgcttacctcagcag 1387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 CGAGGCCCCTGCACATAAGTGTGAAGAAATACTGGCAGAAGAGACTGGAATCCGGCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0067 row: L column: 03
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                             High quality sequence stop: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          אסט עט טיט DNA GSS 29-SEP-2000 1M0067L03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0067L03 R, DNA sequence. A2337037
                                                                                                                                                    Class: plasmid ends
                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                  308,
                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                         /organism="Mus musculus"
/strain="C57BL/6J"
                      /db_xref="taxon:10090"
                                                                                                           Location/Qualifiers
/clone="UUGC1M0067L03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 aaaaaaggggattctcctgggctcctgagcaccagaaggcatttgatgctatcaaaaagg
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gatggatgaccaacgcccgcatgacccactatcaaagcctgcttctcacagagagggtca
                                                                                                                                                             agaatataactgtaatagccccccatgcattggagaacatcgttcggcagcccccagacc
                                                                                                                                                                                                                                                                             TAAAGGCCGTTGCTACAGTAGCCCTACTCGTTAAGGATGCTGACAAATTAACTCTGGGAC
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                                                                                                                   AGCAAATAACTGTGGTAGCCCCCCACTCTTGAAAGCATTATCTGTCATCCCCCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggatgagcgtaagggagtagcccgaggagttttaaccccaaaccctaggaccatggagga 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA
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                                                                                                                                                                           503;
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_GSSs: RPCI-24-352A17.TJB
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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/cell_type="Spleen/Brain"
/note="Wector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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/clone="RPCI-24-352A17"
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  Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse EAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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Other_GSSs: RPCI-24-155A1.TV
                                                                                                                                                                                                  Department of Eukaryotic Genomics
                                                                                                                                                                                                                       Contact: Shaying Zhao
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                                                                                                                                                                            Institute for Genomic Research
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                                                                         TAAAGACATTAAAAACAAAGAAGAAATTCTGGCCCTGTTGGAAGCCATACATGCACCTAA
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector_at the
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/strain="C57BL/6J"
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/clone="RPCI-24-155A1"
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                                                                                                                                                                 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_GSSs: RPCI-24-154N5.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ715272 755 bp DNA GSS 24-JAN-2001 RPCI-24-154N5.TJ RPCI-24 Mus musculus genomic clone RPCI-24-154N5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 154 row: N column: 5
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/RPCI-24 Mouse BAC Library produced by Pieter de Jong The
library was cloned in the pTARBAC1 cloning vector at the
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/clone="RPCI-24-154N5"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
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                                                                                                                                                                     Unpublished (1999)
Other_GSSs: RPCI-24-293G13.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH083773 653 bp DNA GSS 18-JUL-2001
RPCI-24-293G13.TV RPCI-24 Mus musculus genomic clone RPCI-24-293G13
                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                            Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                        BH083773.1 GI:14903370
library availability, please contact Pieter de Jong
                   Clones are derived from the mouse BAC library RPCI-24. For BAC
                                   Email: szhao@tigr.org
                                                                                                                                                                                                             Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                              Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                  house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence.
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                                                       301 838 0200
301 838 0208
                                                                                               Medical Center Dr.,
                                                                                                 Rockville,
                                                                                                                                                                                                                                                                    Shatsman, S., Akinret, B.,
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                                                                                                 20850, USA
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                                                                                   CTGATCAAAGATGCTGACAAATTGACAATGGGACAACAGGTGACTGGTGTAGCCCCTCAT
                                                                                                                    ctggtcaaggacgctgaccaaattgactttgggacagaatataactgtaatagccccccat
                                                                                                                                                                                              cttgatcctgtagccagtggttggcccgtatgtctgaaggctatcgcagctgtgggccata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-293G13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-24"
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CAGGTACGTGAGTTTCTGGGGGACTGCTGGCTTTTGTAGACTCTGGATTCCAGGCTTTGCA

Matches

455;

Similarity

10.1%;

Score 335; DB 13; Pred. No. 1.3e-56; 0; Mismatches 200;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 700 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0104 row: E column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center University of Utah
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                           polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicilin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomedical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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RPCI-24-173A19.TV RPCI-24 Mus musculus genomic clone RPCI-24-173A19
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 173 row: A column: 19
                                                                                                                                                                                                                                                                       Unpublished (1999)
Other_GSSs: RPCI-24-173A19.TJ
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 689)
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                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                               Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                        Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agaaccattaaagagacccttaccaaattgaccacagagactggcattaatgattggatg
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                                                                                                                                                                                                                                                                                                                                                       ccctatgaattgctctacgggggaccccccccgttggcagaaattg-----cctttgca 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                   gctctcctgccctttgtgctttttagggtgaggaacacccctggacagtttgggctgacc
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                     gagactcggtggaagggaccttatctcg 2614
                                                                                                                                                                                           gtgaggcagcgagcgtggaagcagctccgggaggcctactcaggaggagacttgcaagtt 2526
                                                                                                                                                                                                                                                                                                                     CCTTTTGAAGTTCTGTATGGAGGACCTCCCCCCTTAATGGAAGCTGGTAGAACATTAGTT 209
                                                                                                                                                                                                                                                                                                                                                                                                   GAGCCACGGTGGAAGGGACCCTATTTGG
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                                                                                                               ccacatcgcttccaagttggagattcagtctatgttagacgccaccgtgcaggaaacctc 2586
                                                                                                                                                         ATTAGAACCCAGATTTGGGACCAACTGAAAGCAGCCTATACCCCCAGGGACCACCGCAGTA 89
                                                                                                                                                                                                                                          TCCGACTCTGACCCTGTCTTACCCTCCTCTTTGCTTATTCAAATAAAGGCCCTAGAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-173A19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-24"
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/note="Vector: pTARBAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                        1 CAGTAGCCCTGTTGATTAAAGATGCTGACAAATTGACAATGGGACAACAGGTGACTGTTG 60
gccatcaactattgattgaggagactggggtccgcaaggaccttacagacataccgctga 1108
                                            CCATCCTCAACCCAGCTACCCTTCTCCCTCTAACAAATGATTCCGTCCCAGTACATCAAT
                                                                       ccgctctcaaccctgccactcttctgcctgaagagactgattgaaccagtgactcatgatt 1048
                                                                                                                                  CCCGAATGCCACACTATCAGAGCCTGCTGAAATGAGCGTGTAACCTTTGCGCCCCCTG
                                                                                                                                                               cccgcatgacccactatcaaagcctgcttctcacagagagggtcactttcgctccaccag 988
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 155 row: I column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-155I1.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao, S., Nierman, W., Malek, J., Shatsman, S., Ak
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 817)
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RPCI-24-15511.TJ RPCI-24 Mus musculus genomic clone RPCI-24-15511,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="$pleen/Brain" | Site_2: BamH1; Note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BaC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-24-15511"
/clone_lib="RPCI-24"
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                                                                                                                                                                                                                                                                                                              High quality sequence stop: 692.
Location/Qualifiers
                                                                                Insert Length: 10000 Std Error: Plate: 0570 row: J column: 04 Seg primer: CACACAGGAAACAGCTATGACC
                                                                  Class: plasmid ends
                                                                                                                               Email: ddunn@genetics.utah.edu
                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                          University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                              plasmid inserts
                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Matches 452; Conservative
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                                                                                                                                                                                                                                            2225 ggatgaatagaaccattaaagagacccttaccaaattgaccacagagactggcattaatg 2284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 CCAACCTGAAGTCAGTGGCTCAAAAGATTATAGACTCCTGCAAACCATGTGCATTCACTA 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      691 TCACCCATCTGGGAGTTGAAAAAATGATGAGACTAATTAAAATTCCCCGATACCAAGTCC 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTTGTAGACACCTTTTCAGGATGGGTTGAGGCGTTTCCCCACTAAAACTGAGACTGCCC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      actgggaagtggacttcactgaggtaaagccggctaaatacggaaacaaatatctattgg 1984
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attggatggctctcctgccctttgtgctttttagggtgaggaacacccctggacagtttg 2344
                                                                                                                                                                                                                                                                                                                                               TGGGCATCGATTGGAAATTACACTGTGCTTACCACCCTCAAAGCTCAGGACAGGTAGAGA 212
                                                                             ACTGGGTGGCTCTCCTCTTTGCGCTCTTCCGAGCCCGAAACACCCCTGGACATTTCA
                                                                                                                                                                                                            GGATGAATAGGACCTTAAAAGAGACCTTGACTAAATTAGCCATTGAGACCTGCGGGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0570J04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                           Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
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Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
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Department of Eukaryotic Genomics
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
Site_2: BamH1; Site_2: BamH1; Site_3: BamH1; BamH1; Site_3: BamH1; Site_3: BamH1; BamH1; Site_3: BamH1; Site_3: BamH1; BamH1; Site_3: BamH1; Bam
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                                                                                                High quality sequence stop: 610
                                                                                                                   Class: plasmid ends
                                                                                                                                   Email: ddunn@genetics.utah.edu
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Plate: 0218 row: E column: 17
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Fax: 801 585 7177
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                     2585 togagacto-ggtggaagggacottatotogtacttttgaccacacca 2631
                                                                                                              2525 ttccacatcgcttccaagttggagattcagtctatgttagacgccaccgtgcaggaaacc
                                                                                                                                                                                                                                        2468
                                                                                                                                                                                                                                                                                                                                2408
                                                                                                                                                                                                                                                                                                                                                                                       2350 accccctatgaattgctctac--gggggaccccccccgttggcagaaattgcctttgcac 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2290 atggctctcctgccctttgtgctttttagggttgaggaacacccctggacagtttgggctg
479 TTGAGACTCTGTTGGAAAGGCCCTTATCTTGTACTCTTAACCACCCTA 526
                                                                                      419 CCCCACATCGCTTCCAAGTTAGAGATTCGTTCTACATTAGACGTCTCCACGCAGAAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2110 tcagacaatggtccagctttcgttgcccaggtaagtcagggactggccaagatattgggg 2169
                                                                                                                                                                                                                                                                                        299
                                                                                                                                                                                                                                                                                                                                                             240 A-CCCCTATAAATCACTCTACGGGGGGGGGGGGGGCTCCACTGGTAAAAATAGCCTCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 ATAGCTCTCCTACCCTTTGTGCTCTTCAGGGTTAAAAAACACCCCTGGACAGTTTGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AACAGAACCATT-AAGAGACCCCTTACCAAATTGACAGCAGAGACTGGCGCGCTAATGATTGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATTGATTAGAAGTTACATTGTGCATACAGGCCCCAAAGCTCAGGACAGGTAGAGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCAATAACAGACCTGCATTTGTTGCCCAGGTAAATCAGGGACTGGCCAAGATATTGGGG 60
                                                                                                                                                                              TGAGACAGCAAGCGAAGAAGTAGCTCCAGAAGGCCTACTCAAGAGAAAAAAGACCTGCAAG
                                                                                                                                                                                                         tgaggcagcgagcgtggaagcagctccgggaggcctactcaggag---gagacttgcaag
                                                                                                                                                                                                                                                                       ATAGTGCTGACATGCTTTCCACGCCTTTCTTCTTCTAGGCTCGAGGTGCTCAAGTGGG
                                                                                                                                                                                                                                                                                               atagtgctgatgtgctgctttcccagcctttgttctctaggctccaaggcgctcgagtggg 2467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aatagaaccattaaagagacccttaccaaattgaccacagagactggcattaatgattgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified the shared adaptors to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGCIM0218E17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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                                                           February 23, 2002, 23:36:01; Search time 6550.43 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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	14	80.		729	13	8	AZ318021	1M003600
υ	15	73.		673	13	36	AZ329067	1M0053G10
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	18			646	13	A2967275	67275	2M0238G10
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Ö	21	55.		685	13	AZ636636	36	1M0495002
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	24	35		376	11	BF441469	6	257863 MA
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	27	48.		705	13	A2337037	~	1M0067L03
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	30	41.		842	13	BH106844	4	RPCI-24-3
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	32	0		975	11	BF784826	9	602111174
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Ü	35	£ .	4.1	617	13	AZ420279	AZ420279	1M0198K05
	36	36.		653	13	BH083773	m	RPCI-24-2
	37			632	10	AL134888	8	DKFZp762K
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	33	36.		813	11	528	6	602918048
υ	40	36.		682	13	ഥ	9	2M0257006
	41	33		700	13	275	4	2M0104E02
O	42	33.		689	13	8979	37994	RPCI-24-1
	43	÷		817	13	AZ717731	17731	RPCI-24-1
O	44	30.		692	13	9692	9626	1M0570J04
٥	45			688		A2912534	12521	,

ALIGNMENTS

RESULT 1 AK014027	
rocus	AK014027 2085 bp mRNA HTC 05-JUL-2001
DEFINITION	lus 13 days embryo head cDNA, RIKEN full-
1	
ACCESSION	
VERSION	AK014027.1 GI:12851651
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) 13 days embryo head cDNA to mRNA,
	clone_lib:RIKEN full-length enriched mouse cDNA library
	clone:3110009E22.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 2085)
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Methods in enzymology. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 (bases 1 to 2085)
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Suqahara, Y., Shibata, K.,
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to
	prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome research. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3 (bases 1 to 2085)
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
	Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
	Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
	roneda, I., Isnikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

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                                                                                                                                                                                                                                                                                         Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hondani,K., Ishii,Y., Ttoh,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,K., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [5' GAGAGAGAGAAGATCCAACAACTCTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGGTVTTPLSLTLDHWSEIRSRAHNLSVEIKKGPWRTFCASEWP
TFDVGWPPEGTFDLTVIFEVKAIVFQDGPGSHPDQOPYITVWQDLVONSPPWIKPWIP
KRRGSRALARRPKYKRDKDPPEKEPLFGPSALDKIYPEIEGPPEWPEPPPYFLPPP
ASTPPQLPEPGFGAGGGTVGGPAGTGSRSAQSLSADGVPDTMSAFPLCAVGPAADLH
SLQTLQYWPFSSADITWMSCYFRKSWTNQPGGVINVISSAHLG"
504 c 573 g 464 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (6SC), RIKEN Yokohama, Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                4 (bases 1 to 2085)
The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp/) for
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 2085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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356. .1147
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/db_xref="MGD:MGI:1920342"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="3110009E22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="head"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative"
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                                                                                                                                                                                                          FANTOM Consortium.
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                                                                                                                              11076861
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REFERENCE
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                                                                                                                                                   REFERENCE
                                                                                                                                                                                AUTHORS
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                                                                              JOURNAL
                                                                                                                              PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                            TITLE
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Length 2085;

DB 12;

Score 600;

7.38;

Query Match

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1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 962 -------gagccctcttcctcgtatctaccccgagatcgaggagccgccgac 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1232 cttttettetgeagatetetataattggaaaactaaceateeeettteteggaggatee 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ttctgagtgtctgttttcggtgatgcgctttcggtttgcagctgtcctctcagaccgt 310
                                                                                                                                                                                                                                                                                                                                               371 ggacgccccggggaggtggggagagccagggacgcctggtggtgtctcctactgtcggtcaga 430
                                                                                                                                                                                                                                                                                                                                                                                                           148 GGATGCCTCGGAGCAAGGGAAGGACTCTAGG---AGTCCGACTGGGACGGGAGTAAAGA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggaccgagttctgttgttgaagcgaaagcttccccctccgcggccgtccgactctttgc 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 ctgcttgtggaagacgcggacgggtcgcgtgtgtctggatctgttggtttctgtctcgtg 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                731 tggatggccatcagaggggacctttaattctgaaattatcctggctgttaaggcaatcat 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791 ttttcagactggacccggctctcatcctgatcaggagccctatatccttacgtggcaaga 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 tececgaatectggetettgg-----agaagaaaaacaaacacteggeegaaaagt 961
                                            Gaps
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                                                                                                                                                              31 TICAAACITICGGITIGCGGICGCAACAICICACGICICACGGGAGACAGAGACCCGAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 CTCGGTAGTCTTCCTGGATTGGAAGAACTACTCACCAGCCCGACCTTCTGCATCTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 TGTCTGTTTTGTGT----TTTTTGTCACCTGGACGATGGGACAGACTGTGACGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611 ccttagtttgactctcgaccattggactgaagttagatccagggctcataatttgtcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 GGAGATCAAGAAGGGACCTTGGCGGACTTTTTGTGCTTCTGAGTGGCCAACATTTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 GGGCTGGCCACCAGAGGGGACTTTGACCTGACTGTGAACTTAAAGCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559 CTTTCAGGATGGACCTGGGTCCCACCCAGACCAGCAACCTTACATAACTGTGTGGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  916 AAGCCGGAGGCCACAGAGTCTCTCCGCAGATGGGGTTCCTGACACCATGTCTGCCTTTCC
                                         81;
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.. wismatches 740; Indels
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               60.6%;
               Best Local Similarity 60.6
Matches 1265; Conservative
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1087	1351	1411	1471	1531 1327	1591	1651	1711	1771	1831 1623	1891	1951	2011	2062	2122	2182 1978	2241	
AGCTGATCTCTATAACTGGAAATCCTACTTTTTCAGAAATCC	pacggggttggtggagtccttatgttctctcaccagcctacttgggatga 	cagctgctgcagacactcttcacaaccgagagcgagagaga	tagaaaaaatgttcctggggccgacgggggacccacgcagttgcaaaatgagattga 1 	atgggatttccttgactcgcccggttgggactacaacacggctgaaggtagggagg 1 	gaaaatctatogocagottctggtggcggtctccggggcgcctcaagacggccac 1 	aatttggctaaggtaagagaggtgatgcagggaccgaacgaa	catggaagcettcaggegttcaccettttgatectacetcagaggecea 	aagoctcagtggccttgattgggcagtcggctctggatatcaggaagaaact 1 	tcagagactggaagggttacaggaggctgagttacgtgatctagtgagagaggcagagaa 1 	cagaagggagacagaagaggaaaggaacagagaaaaggaaaaggagaga 	agacgtgatagacggcaagagaagtttgactaagatcttggccgc 1 		cctagacagtcagggaacctgggcaataggacccactcgacaaggacca 2/ 				ataccggagcggagcattcagtgctgctacaaccattaggaaaact 2287
TTC	ccaacgcct(AGCTGGACT	ttgtcaac TTGCCAAC	ggctagaa GGCTCAGA	catgggat CGTGGGGT	cttgaaaa GTTGACAG	taatttgg 	tgagagget AGAGAGATT	gaaageet ACAAGEEG	tcagagac ACAGAGAC	ggtgtatte AGTGTTTAC	agaaagggaggaa AAGAAAGAAAAT	agtggttg AGTAGTAG	caacaggg	gtgtgcgt ATATGCAT	aggaccga TGCCCCTA	cctccccg 	ataccgga ATACCGGG
03	1292	1352	1412	1472	1532	1592 1388	1652	1712 1508	1772	1832	1892	1952	2012	2063	2123 8	2183 (2242 6
op .	ογ Op	Oy Dp	Qy Db	Qy	Qy Db	Oy Dp	Oy Dp	oy Oy	Qy Db	Qy Db	Oy Dp	Oy Db	Qy Db	Qy	Qy Dp	Qy	Qy Dp

RESULT BI184013

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/ub_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco R; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-E2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996.
                                                                                                                                                                                                                                                                                                                                     Contact: Pomp, D. D. Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 5362
Email: dpomp@unl.edu
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="University of Nebraska, Lincoln Swine Selection Lines"
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Generation and sequence characterization of a normalized cDNA
Unbrary from swine ovarian follicles
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 agaccgettetegtgagtgatttggggtgtegectetteegageceggaegagggggtt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AGACCGCTTCTCGTGAGTGATTTGGGGTGTCGCCTCTTCCGAGTCCGGACGAGGGGGATT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 cggcgtctctgttctgagtgtctgttttcggtgatgcgcgctttcggtttgcagctgtcc 299
         10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 tggtgtacgactgtgggccccagcgcgcttggaataaaaatcctcttgctgtttgcatca 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI184013 857 bp mRNA EST 10-JUL-
UNL-P-FN-cf-b-12-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-cf-b-12-0-UNL 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UNL-P-FN-cf-b-12-0-UNL" /clone_lib="UNL-P-FN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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1 217 c 248 g
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                                                                                          BI184013.1 GI:14658422
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Best Local Similarity
                                                                                                                                                                Sus scrofa
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                           DEFINITION
                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                 AUTHORS
TITLE
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                                                                     ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                            REFERENCE
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konoo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                773 ggctgttaaggcaatcatttttcagactggacccggctctcatcctgatcaggagcccta 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       833 tatccttacgtggcaagatttggcagaagatcctccgccatgggttaaaccatggctaaa 892
252 CGGCGTCTCTGTTTTTGTGTTTTCTGGGATGCGCGCTTTCGGTTTGCAGCTGTCC 311
                                                                 totcagaccgtaaggactggaggactgtgatcagcagacgtgctaggaggatcacaggct 359
                                                                                                                                                         360 gecacectgggggacgececggggaggtggggagagecagggacgeetggtggtetectae 419
                                                                                                                                                                                                   372 GCCGCCCTGGGGGACGCCCCGGGAGGTGGGGAGAGCCAGG--TGCCTGGTGGTGTTCCTTC 429
                                                                                                                                                                                                                                             tgtcggtcagaggaccgagttctgttgttgaagcgaaagcttccccctccgcggccgtcc 479
                                                                                                                                                                                                                                                                     653 ggctcataatttgtcagttcaggttaagaagggaccttggcagactttctgtgcctctga 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785 TATCCTTACATGGCAAGATTGG----CAGAGATCCTCNGCATGGATTAAACCATGGCTAAT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus 10 days embryo CDNA, RIKEN full-length enriched library, clone:2610305J24, full insert sequence. AK011989 GI:12848454
                                                                                                                                                                                                                                                                                                                                       550 TCTGTTTCGTGTGTCTTTGTCTTATGCGTCCTTGTC-CCAGTTTTAATATGGGACAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 gtgacta-----cccccttagttttgactctcgacca-ttggactgaagttagatccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 TCCCAGACCGTAAGGACTGGGGGACTGTGATCAGTAGACGTGCTAGGAGGATCACAGGCT
                                                                                                                                                                                                                                                                                                                                                                                    490 GACTCTTTTGCCTGCTTGTGGAAGGCGCGGACGGGTCGCGTGTGTCTGGATCTGTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    609 GTGACGACCCCCCCCCCTTAGTTTGACTCTCAACCATTTGGACTGAAGTTAAATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 atggccaacattcgatgttggatggccatcagaggggacctttaattctgaaattatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GGGACCTTTAATTCTGAGATTATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mF
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:2610305J24.
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 GCCTCATAATTTGTCAGTTCAGGTTAAGAA-----
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Nature 409, 685-690 (2001)

S Adachi, J. Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haraya, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatau, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Kondo, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Okido, T., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Tapima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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PLRPGTKILAIOENGEKEKPKPPLGRDDDRSTPVTKPPKIYSEIEEPPEWPDTPQPPP
YAPOPOPSABGSPLPQAPAGGGGPSTGTRSRRGVTPEGPADSTVALEPLRAIGAPPADP
NSLQPLQYWPPSSSDLYMKAHPPPFSENPAGLTGLVESLMYSHQTWDDCQOLLQTL
ETTEREREILLEARKWRDEAGRPVQTPAETDEGFPLTRPRWDYNTAGSREBLSNYRR
VLVAGLRGAARQPTNLAKVREVWQGATEPPSVFLERLMEAYRRYTPFDPTSEGQRASV
IMAFIGGSARDIRKKLQTIEGLQDYTIRDVVREAEKVYHRRFTEDKKLEREKREEKREE
                                                                                      Shibata, T. Itoh, M. Alzawa, K., Nggaoka, S., Sasaki, N., Carninci, P., Shibata, K., Itoh, M., Alzawa, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGQTVSTPLSLTKDHWTDVRARGONLSVKVKKKPWMTFCSSEWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute
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Genome research. 10 (10), 1617-1630 (2000)
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/db_xref="MGD:MGI:1905349"
/db_xref="MGD:MGI:1919770"
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/db_xref="G1:12848455"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FANTOM Consortium.
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Length 2096;

DB 12;

Score 552.4; DB 12 Pred. No. 1.1e-101;

6.78;

Query Match Best Local Similarity

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2; Constitution
ctacccccttagtttgactctcgaccattggactgaagttagatccagggctcataatt
tgrcagticaggitaagaagggaccttggcagactttctgtgcctctgaatggcca
atgttggatggccatcagagggacctttaattctgaaattatcctggctgttaag.
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ctgttagaggctagaaaaatgttcctggggccgacggcgacccacgcagttgcaaaa
tgagattgacatgggatttcctttgactcgcccggttgggactacaacacggctgaagg

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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS
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1 (bases 1 to 549, W.W., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
1703 agaggeceagaaageeteagtggeettggeetteattgggeagteggetetggatateag 1762
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                                                                                                                                                                          1782 AGTCTTCCTTGAAAGGCTCATGGAGGCTTATAGGAGATATACCCCATTCGACCCCACGTC 1841
                                                                                                                                                                                                                                gaagaaacttcagagactggaagggttacaggaagctgagttacgtgatctagtgagaga 1822
                                                                                                                                                                                                                                                                                                                1902 GAAGAAGTIACAGCGAATIGAGGGCTIGCAGGATIACACCAIAAGGGAIGTIAGAGA 1961
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110922 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW657531.1 GI:7423429
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DOBOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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Seq primer: ATTTAGGTGACACTATAG.
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BACKWARD: GTTTTCCCAGTCACGACG
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2935)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
                                                                /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

144 c 121 q 139 t
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                                                                                                                                                                                                                                                                                                                                                                362 CAATACTGGGTTAACTCCCTGTGTTTCTACCACGTCTTTAACCAATCCAAAGATTTCTG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 TGTCATGGTCCAGCTCGTCCCTGGGTACACTACCATCCTGAGGAAGTAGTCATCGATGA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AGGGCCTCCTTATTATGAGGGAATGGCTAGAGAAGGGAAATTCAATGTGACCAAAGAGCA 181
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Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA, clone_lib.RIKEN full-length enriched mouse cDNA library clone:1300007C21.
                                                                                                                                                                                                  DB 10; Length 549;
                                                                                                                                                                                                                                    39; Indels
                                                                                                                                                                                                5.8%; Score 473.6; DB 1092.7%; Pred. No. 1.1e-85; Live 0; Mismatches 39
           /clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/db xref="taxon:9913"
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FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 (bases 1 to 2935)

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Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                   Shibata, K. Itoh, M. Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwaqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiwaqi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKE Integrated sequence analysis (RISA) system-384-format Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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Methods in enzymology. 303, 19-44 (1999)
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/db_xref="MGD:MGI:1897042"
/db_xref="MGD:MGI:1914777"
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/tissue_type="liver"
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/clone_lib="RIKEN full-length enriched mouse cDNA library" 11; 1316 gtcccttatgttctctcaccagcctacttgggatgattgtcaacagctgctgcagacact 1375 1376 cttcacaaccgaggaggagagagaattctgttagaggctagaaaaaatgttcctggggc 1435 aaagtegageeetetteetegtatetaeeeegagategaggageegeegaettggeegga 1016 cctcctggagctccggtggtggagggacctgctgccgggactcggagccggagggggcg 1136 accccggagcggacagacgagatcgcgatattaccgctgcgcacctatggccctcccatg 1196 ACTGCGGGGAAGGAAGCACCTCCCGCAGCGGACTCCACCTCCTCCCAGGCATTCCCACT 1245 1356 GTCCGTCCTCATCACCCACCAGCCCACCTGGGACGACTGTCAGCAGTTGTTGGGGACCTT 1415 950 GGTCCTTCTGCGCAACCTCCGTCCCGATCTGCCCTTTACCCCGCCCTTACCCCCTCTATA 1009 1010 AAGCCCAAACCTCCTAAGCCCCAGGTTCTCCCTGATAGCGGCGGACCTCTCAT---TGA 1065 CCTTCTCACAGAGGACCCCCGGCGGTACGGAGCACAACCTTCCTCCTCTGCCAGAGGGA 1125 485 ttttgcctgcttgtggaagacgcggacgggtcgcgtgtgtctggatctgttggtttctgt 544 545 ctcgtgtgtctttgtcttgtgcgtccttgtctacagtttt...--aatatgggacagac 598 777 650 CGTAACTACCCCCCCTGAGTCTAACCTTGCAGCACTGGGGAGATGTCCAGCGCATTGCAT 709 ataatttgtcagttcaggttaaggagggaccttggcagactttctgtgcctctgaatggc 717 1017 accccaacctgttcccccaccccttatccagcacagggtgctgtgaggggacctctgcc ttaaggcaatcatttttcagactggacccggctctcatcctgatcaggagccctatatcc ccagggggccaattgcagcc-cctccagtattggcccttttcttctgcagatctctataa 1256 ttggaaaactaaccatcccctttctcggaggatccccaacgcctcacggggttggtgga 710 CCAATCAGTCTGTGGATGTCAGGAAGAGGCGCTGGGTTACTTTCTGTTCCGCCGAATGGC TCAAGTCTAGAGTGTTTTGTCCTGGTCCCCACGGACACCCGGATCAGGTCCCATATATCG CGATGAAAAAGAGGGGGCGCCACCTCCGAGGTTCCCCCCCTTCTCCCATGGTGTCTCG CCGTATGGGGGGGAGATGGCCAGCTTCAGTACTGGCCGTTTTCCTCCTCTGACTT---agtgacta-cccccttagtttgactctcgaccattggactgaagttagatccagggctc caacattcgatgttggatggccatcagaggggacctttaattctgaaattatcctggctg 530 TITIGCTTTCGGTTTTACGCCGAAACCGCGCGCGCGCGTCTGATTTGTTGTTGTTGTTGT 590 TCTTTTGTTCTTCGTTAGTTTTCTCCTGTCTTTAAGTGTTTTCGAGATCATGGACAGAC 47; Length 2935; Indels Score 472; DB 12; 1 Pred. No. 2e-85; 0; Mismatches 965; ب 633 /dev_stage="adult" 860 c 773 g Query Match 5.7%; Best Local Similarity 54.4%; Matches 1208; Conservative 1126 1186 1197 1246 BASE COUNT 1077 1137 599 929 718 778 830 838 890 897

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2446 2266 2306 2366 2426 gatgggagetcaaatttettttga---acaaggaagaceagaagtgtetgtgaataacaa 2503 aaggaactgccccaagaag----ggaaacaaaggaccgaaggtcc---tagctctaga 2146 gctacaaccattaggaaaactaaaaagaaaaaaatcctgggtgatgggtgccacagggca 2326 ggtggcgggtctccggggcgctcaagacgcccactaatttggctaaggtaagaggt 1615 gatgcagggaccgaacgaacctccctcggtatttcttgagaggctcatggaagccttcag 1675 1656 AACCCAGGGACCTAATGAGTCTCCCTCAGCCTTTTTAGAGAGACTCAAGGAGGCATATCG 1715 geggiteaccettitigateetaceteagaggeecagaaageeteagiggeeetiggeeti 1735 1716 caggracacrectrargacecregagacecaggecaaagaaacaargrerargrear 1775 cattgggcagtcggctctggatatcaggaagaaacttcagagactggaagggttacagga 1795 1776 CATCTGGCAGTCTGCCCCGGATATCGGGCGAAAGTTAGAGCGGTTAAAAGATTTAAAGAG 1835 ggctgagttacgtgatctagtgagagaggcagagaggtgtgtattacagaagggagacaga 1855 CAAGACCTTAGGAGACTGAGGAAGCTGAAAAGATCTTTAATAAGGAGAAACCC 1895 1896 GGAAGAAAGAAGGAACGTATCAGGAGAAACAGGAAAAGGAAAAGGAAGAACGCCGTAGGGC 1955 1916 acggcaagagaagtttgactaagatcttggccgcagtggttgaagggaagagcagcag 1975 1956 AGAGGATGAGCAGAGAGAAAGAAAGGACGGAGGAGACATAGAGAGATGAGAAGCT 2015 1596 CTTAGCGGGTCTCCAAAACGCGGGCAGAAGCCCCACCAATTTGGCCAAGGTAAAAGGGAT 1655 CTCTTTCCTCCATGTACCAGACTGCCCTATCCTCTGCTAGGAAGAGACTTGCTGACTAA 2487 ACTCAAAGCCCAGATCCACTTCGAGGGATCAGGAGGACTAGGTTGTGGGACCAATGGGACA caataggaccccactcgacaaggaccagtgtgcgtattgtaaagaaaaggacactggggc 2147 agaagataaagattaggggagacggggttcggacccccccgagcccagggtaactt 2247 CAAAGTCGGGGGGCAACCCGTCACCTTCCTGGTAGATACTGGGGCCCAACACTCCGTGCT ctcgtttctggtcatccctgagtgcccagtaccccttctaggtagagacttactgaccaa ggagagagagagattttaggaaaattaggtcaggccctagacagtcagggaacctggg 2016 CTTGGCCACTGTAGTTAGTGGACAGAGACAGGGTAGACAG------GGGGGAGAGCG 2207 gaaggtggagggggaaccagttgagttcctggttgataccggagcggagcattcagtgct 2307 GACCCAAAATCCTGGACCCCTAAGTGACAAGTCTGCCTGGGTCCAAGGGGCTACTGGAGG acggcagtatccatggactacccgaagaaccgttgacttgggagtgggacgggtaaccca 1476 TGATGGACGCCCCACTCAGTTGCCTAATGAAGTCAATGCTGCTTTTTCCCCTTGAACGCCC cgacgggcgacccacgcagttgcaaaatgagattgacatgggatttcccttgactcgccc cggttgggactacaacacggctgaaggtagggagagcttgaaaatctatcgccaggctct 2096 2387 2427 2036 2187 2267 2327 2447 1496 1556 1616 1676 1736 1796 1976 1436 q qq Ob οy a δ g ò q QΥ qq δλ g ŏ g ŏ g QΥ Dp δ q δλ q q Д qq $_{\rm Q}$ δy δ qq δy αq Ω δ

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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1 (bases 1 to 467)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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2564 aaagcctgatcaagatatacagt---cctggttggagcagtttccccaagcctgggcaga 2620
                                                                                                   2621 aaccgcagggatgggtttggcaaagcaagttcccccacaggttattcaactgaaggccag 2680
                                                                                                                                                                                      2667 AACTGGGGGCATGGGAGTTCGCCAAGCGCCTCTGATTATACCTCTGAAGGCAAG 2726
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                                                                                                                                                                                                                                                                                                         BF441465 467 bp mRNA EST 0
257856 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4360
Fax: 402 762 4390
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/clone_lib="MARC 2PIG"
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Plate: 86 row: C column: 8
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 466)

1 Therenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries for ST discovery in swine Unpulshed (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithdemail.marc.usda.gov
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                                                                                                            1659 ctcatggaagcettcaggeggttcaccettttgatectaceteagaggeecagaaagee 1718
121 AAAAATGTTCCTGGGGCGACGGGGGGCACCCACGCAGTTGCAAAATGAGATTGACATGGGA 180
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Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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FORWARD: AGGAAACAGCTATGACCAT
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Best Local Similarity 94.2<sup>o</sup>
Matches 436; Conservative
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Sus scrofa
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us-09-171-553b-3.feb22std.rst

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Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
University of Iowa Clone distribution: clones will be available
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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tttcccttgactcgccccggttgggactacaacacgggtgaaggtagggaggcttgaaa 1538
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Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
                 1 CTCACGGCGTTAGTGGAGTCCCTTATGTTCTCTCACCAGCCTACTTGGGATGATTGTCAG
                                                                         cagetgetgeagacaetetteacaacegaggagegagagagaattetgttagaggetaga
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/db_xref="taxon:9823"
/clone="M1-P-AY1-nrp-a-02-0-UI"
/clone="M1-P-AY1"
/lab_host="DH10B (Life Technologies)"
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
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97044477
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/organism="Sus scrofa"
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Sus scrofa
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AYI library is normalized library derived from the MI-P-AYO library, ultimately derived from placenta tissue. For a detailed description of the library from which this clone was derived, please visit our web site at this clone this: /pigase, genome.lastate.edu/. The procedure used to this: library has been previously described (Bonaldo, Lenno and Soares, Genome Research 6: 791-806, 1996)

TAG_SEQ=None found 106 t
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other, GSSs: RPCI-24-370H8 .TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPCI-24-370H8.TJ RPCI-24 Mus musculus genomic clone RPCI-24-370H8, DNA sequence.
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//ocll_type="Spleen/Brain"
//ocle="Vector: pTARBAG1; Site_1: BamH1; Site_2: BamH1;
//ocle="Wector: pTARBAG1; Site_1: BamH1; Site_2 Site_1 Site_1 Site_2 Site_1 Site_2                                                                                                                                                                                                                                              end
                                                                                                                                                              library availability, please contact Pieter and the particular of pdejongemail. Tho. Org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.chori.org/bac_ends/mouse/bac_end_intro.html. Plate: 370 row: H column: 8 Seq primer: SP6 class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1230 ccctttcttctgcagatctctataattggaaaactaaccatcccctttctcggaggat 1289
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                                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GATTGTCAGCAGCTTTTGCAGGTTCTTTTCACCACAGAAGAAGAAGAAGAATCCTGATG 179
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Pred. No. 1.3e-71;
0; Mismatches 228; Indels
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/clone="RPCI-24-370H8"
/clone_lib="RPCI-24"
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 to 452)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
    aaggtgtattacagaagggagacagaagaggagaagaaggaacagagaaaaggaaaaggagaa 1889
                                                                                      1890 gaagaaagggaggaagacgtgatagacggcaagagaagaatttgactaagatcttggcc 1949
                                                                                                                                                                            1299 ctcacggggttggtggagtcccttatgttctctcaccagcctacttggggatgattgtcaa 1358
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                                                                                                                                                                                                                   720 GCAGTIGIGAATGATAGACAGTCAGGGAAAGGTAAAACAGGACTICTGGGCAACAGGGCA 779
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257857 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF441466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ASS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sus scrofa"/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 86 row: C column: 9 Seq primer: ATTTAGGTGACACTATAG.
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library was cloned in the pTARBACI cloning vector at the BanHI sites using MboI partially digested male C57BL/6J
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 564)
                                                                                                                                                                                                                  5040 ggaatacctaaggtaatagggtcagacaatggtccagctttcgttgcccaggtaagtcag 5099
                                                                                                                                                                                                                                                                                                                                                                      5160 tcaggacaggtagagaggatgaatagaaccattaaagagccettaccaaattgaccaca 5219
                                                                                                                                                                                                                                                                                               ggactggccaagatattggggattgattggaaactgcattgtgcatacagaccccaaagc 5159
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                                                                                                                                                                                                                                                                                                                                                                                                          121 TCAGGACAGGTAGAGGATGAATAAAACCATAAAAGAGACCCTTACCAAATTG-CTGCT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized cDNA
                                                                                                                                                                                                                                           5400 ctcaaggcgctcgagtgggtgaggcagcgagcgtggaagcagctccgggaggcctactca
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UNL-P-FN-br-h-08-0-UNL.sl UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-br-h-08-0-UNL 3', mRNA sequence.
                                                                                                                                            Score 385; DB 13; Length 576;
Pred. No. 1e-67;
0; Mismatches 95; Indels
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Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
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Other GSSS: RPCI-24-149D1.TV
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/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ730616 576 bp DNA GSS 25-JAN-2001
RPCI-24-149D1.TJ RPCI-24 Mus musculus genomic clone RPCI-24-149D1,
                                                       1419 aaaaatgttcctggggccgacgggcgacccacgcagttgcaaaatgagattgacatggga 1478
                                                                                                                                  1479 tttcccttgactcgccccggttgggactacaacacggctgaaggtagggagagcttgaaa 1538
                                                                                                                                                                                                              1539 atctatcgccaggctctggtggcgggtctccgggggcgcctcaagacggcccactaatttg 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (Pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Seg primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                         ctcatggaagcettcaggggggttcaccettttgatectacetcagagggeccagaaagec 1718
120 AAAAATGTTCCTGGGGCCGACGGGCGACCCACGCAGTTGCAAAATGAGATTGACATGGGA 179
                                                                                                                                                        Contact: Shaying zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                           1719 tcagtggccctggccttcattgggcagtcggc 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 TCAGTGGCTTTGGCCTTTATAGGACAGTCAGC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-149D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-24"
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AZ730616.1 GI:12491859
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5399

8122 ccctgcgtggtgtacgactgtgggccccagcgcgcttggaataaaaatcctcttgctgtt 8181

144 CTTTGTTGTGAACCCCATAAAAGCTGTCCCGACTCCGCACACGCCGCCGCAGTCCTTAC 85

DP OY OY

8182 tgcatcaaaaaaaaaaaaaaa 8205

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/clone_lib="UNL-P-FN"
/clone_lib="UNL-P-FN"
/clone_lib="UNL-P-FN"
/dev_stage="ADULT"
/lab_host="DHIDB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pt7T3D-Pac (Pharma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 mucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="University of Nebraska, Lincoln Swine Selection
                                                                                                         The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NoLI site and the oligo-dT track served to verify it as a clone from the normalized porcine ovarian follicles library
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TAG_TISSUE=porcine ovarian follicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
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                                                                                   dpomp@unl.edu
                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 -29 POLYA=Yes.
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Matches 477; Conservative
rel: 402 472 6416
                                       Fax: 402 472 6362
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                                                                                                                                             BH056750 864 bp DNA GSS 18-JUL-2001
RPCI-24-94C16.TVB RPCI-24 Mus musculus genomic clone RPCI-24-94C16,
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Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Upublished (1999)
Other GSSs: RPCI-24-94C16.TJ RPCI-24-94C16.TV
Contact: Shaying Tale and Cenomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fex: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 94 row. C column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
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/db_xref="taxon:10090"
/clone="RPCI-24-94C16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TTAGCGGCACCTCTGTACCCACTCACTAAAGAAAAGTCCCGTTCACCTGGACAGAAGAA 120
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                          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                           AZ318021 729 bp DNA GSS 29-SEP-ZUUU 1M0036004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                      Mammalia; Eutheria; Colordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 729)
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1515 gctgaaggtagggagagcttgaaaatctatcgccaggctctggtggcgggtctccggggc 1574
                                                                                       1455 ttgcaaaatgagattgacatgggatttcccttgactcgccccggttgggactacaacacg
                                                                                                                                                                         1395 gagagaattotgttagaggotagaaaaaatgttootggggoogaoggggggacocaogcag
                                                                305 CTCCCTAACCTCGTGGACGAGGCTTTCCCCCTTGAACCGCCCCAACTGGGACTACAACACC
                                                                                                                                                     245 GAAAGAATCCTGATGGAGGCGAGAAAAAATGTTCTAGGAGGAGGACGACACCCCACTGCC
                                                                                                                                                                                                                                     185 CAACCCACTTGGGATGATTGTCAGCAGCTTTTTGCAGGTTCTTTTCACCACAGAAGAAGA 244
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BASE COUNT
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                                                                                                                                     1215 cccctccagtattggcccttttcttctgcagatctctataattggaaaactaaccatccc 1274
                                              1275 cctttctcggaggatccccaacgcctcacggggttggtggagtcccttatgttctctcac 1334
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                                                                                                        65 CCTTTACAATACTGGCCTTTTTCCTCTTCTGATTTATATAATTGGAAAACTAACCACCCT 124
CCCTTCTCAGAGAACCCCTCTGGGCTTACTGGGCTCCTTGAGTCACTTATGTTCTCCCAT 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 10000 Std Error: Plate: 0036 row: O column: 04
Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                                                                                                                                                                                                                 with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="UUGC1M0036004"
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73.48;
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                                                                                                                                                                                                                                                 Score 380.4; DB Pred. No. 8.5e-67
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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1M0053G10F Mouse 10kb plasmid UUGCIM library Mus musculus
clone UUGC1M0053G10 F, DNA sequence.
                                                                                                                                                                                                                                                          High quality sequence stop: 673
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Plate: 0053 row: G column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0053 row: G column: 11
                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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1 (bases 1 to 673)
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                    musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0053G10"
                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                             1. .673
(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                       /sex="Male"
                                                               /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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BASE COUNT
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Best Local Similarity
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                                                                                       5443 tccgggaggcctactcaggag--gagacttgcaagttccacatcgcttccaagttggaga 5500
                                                                                                                                                                                                         5387 tttgttctctaggctcaaggcgctcgagtgggtgaggcagcga----gcgtggaagcagc 5442
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5501 ttcagt 5506
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                                                                                                                                                                                                                                                                                          205 GGGGGCTCCACTGGTAAAAATAGCCTCTGTACATAGTGCTGACATGCTGCTTTCCCAGCC
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                                                                                                                                                                        acccccccgttggcagaaattgcctttgcacatagtgctgatgtgctgctttcccagcc
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                                                      TCCAGAAGGCCTACTCAAGAGAAGAGCCTGCAAGCCCCACATCTCTTACAAGTTAGAGA
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Search completed: February 23, 2002, 23:37:03 Job time: 9424 sec

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gb_gss:BH121259
gb_gss:AZ967275
gb_gss:BH124013
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Database length: 1077921985
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Query: US-09-171-553B-4
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gb_gss:BH112876
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                     gb_est2:BF659611
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H121259 RPC1-24-374G11.TV RPC1
A2967275 2M0238G10F Mouse 10kb
B124013 RPC1-24-230P16.TV RPC1
A2420279 1M0198K05F Mouse 10kb
A2986580 2M0268P18R Mouse 10kb
A2862103 2M0169D03R Mouse 10kb
BC089942 mab8806.xl NC1_CGAP_S
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A262638 1M0520120R Mouse 10kb
A2708792 RPC1-23-238P4.TJ RPC1-BE283558 601102758F1 NC1_CGAP_I
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AZ786922
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3 2M0057L01F Mouse 10kb
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4 2M0257D10F Mouse 10kb
7 up04h01.x1 NCI_CGAP_Lu
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             257857 MARC 2PIG Sus s
uz88f01.x1 NCI_CGAP_Lu
uy32b01.x1 NCI_CGAP_Lu
602825515F1 NCI_CGAP_N
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257856 MARC 2PIG Sus
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             Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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gb_gss:AZ959168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer genome research. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                  5 (bases 1 to 2096)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Adachi,J., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Hori,F.,
Haranagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J.,
Imotani,K., Ishii,Y., Itoh,M., Koya,S., Kurihara,C., Matsuyama,T.,
Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T.,
Koya,S., Kurihara,C., Matsuyama,T.,
Koya,S., Kurihara,C., Matsuyama,T.,
Koya,S., Kurihara,C., Matsuyama,T.,
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.GlyGluLysAsnLys	115 . 1035 T
LeuAsnLysProArgLysProGlyProArgIleLeuAlaLeu 114	101 L 988 C
euThrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrp 100 :::: ::: :: TGGTATGGGAGGACTTGGCCACGCTACCCACCCCCGTGGGTTCGCCCATTC 987	84 e : 938 T
eIlePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84 :::	67 e 888 T
ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl 67 ::: CAGCAGAAGGAACTTTTTACTTACCCACCATAAGGGCTGTGAAGGCCAT 887	51 F 838 C
roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50 ::: :::	34 r 788 C
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YAPQPOPSAPSĞPLPQAPAGGGGPSTGTTRSRRCYTPEGPADSTYALPLRA IĞA FAÇ NSLQPLQYWPSSSDLYNWKAHHPPESSURAÇLTGLYUSLMYSHQPTWDDCQQLLQTL FTTEERERILLEARKUNVDEAGARPYQTPAELDEGFPLTRPRWDY YHASGRERLSNYRR VLYAGLRGAARQPTNLAKVREYMQGATEPPSVFLERLMEAYRRYTPFDPTSEGQRASV IMAFIĞQSAPDIRKKLQRIEĞLQDYTIRDVVREAEKVYHRRETEDKKLEREKREKREE EDRRDRRQEKVLTRLIAAVG" 500 a 527 c 577 g 492 t	BASE COUNT
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133	7 yrTyrArgArgGluThrGluGluGluLysGluGlnArgLysGluLysGlu 4	41
417 1975	00 yLeuGlnGluAlaGluLeuArgAspLeuValArgGluAlaGluLysValT 4 	40 192
400 1925	34 IleGlyGlnSeralaLeuAspIleArgLysLysLeuGlnArgLeuGluGl 4 	38,
383 1875	57 roPheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlaPhe : 	36 182
367 1825	0 OPTOSETValPheLeuGluArgLeuMetGluAlaPheArgArgPheThrP 	35 177
350 1775	34 ProThrAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGluPr :	33 172
333 1725	17 yslleTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgArg :	31 167
317 1675	0 uThrargProGlyTrpAspTyrAsnThralaGluGlyArgGluSerLeuL 	30 162
300 1625	4 AspGlyArgProThrGlnLeuGlnAsnGluIleAspMetGlyPheProLe	28 157
283 1575	7 luGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGlyAla 	26 152
267 1525	0 nProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLeuPheThrThrG 	25 147
250 1475	34 AspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerHisGl:::	23 142
233 142	17 erSerAlaAspLeuTyrAsnTrpLysThrAsnHisProProPheSerGlu ::: 6 CCTCTTCTGACCTTTACAACTGGAAAGCTCATCACCCCCCTTTTTCAGAA	21 137
217 137!	01 .ProProMetProGlyGlyGlnLeuGlnProLeuGlnTyrTrpProPheS :::::	20 132
200 132	.86 GluArgThrAspGluIleAlaIleLeuProLeuArgThrTyrGly 	18 127
185 127	.69 alValGluGlyProAlaAlaGlyThrArgSerArgArgGlyAlaThrPro	10 12:
169 123	.52 uSerSerThrGlyCysCysGluGlyThrSerAlaProProGlyAlaProV	112
152 118	36 ArgGlyAlaAlaAspLeuAlaGlyThrProThrCysSerProThrProLe	11:
113	::: ::::: ::: ::: ::: GCACACCAGTGACGAAACCCCCCAAGATCTATTCAGAGATTGAAGAACCC	10

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REFERENCE
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
library, clone:3110009E22, full insert sequence.
AK014027
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Eutheria; Rodentia;
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US-09-171-553B-4 x AK014027
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                                                                                                                                                                                                                                                                                                                                                  356 ATGGGACAGACTGTGACGACCCCCTAAGTTTGACCTTAGATCACTGGTC 405
                                                                                                                                                                            34 roTrpGlnThrPheCysAlaSerGluTrpProThrPheAspValGlyTrp 50
                                                                                                                                                                                                                                                                                              17 rGluValArgSerArgAlaHisAsnLeuSerValGlnValLysLysGlyP
                                                                                                                                                                                                                                                                                                                                                                          eIlePheGlnThrGlyProGlySerHisProAspGlnGluProTyrIleL 84
                                                                                                                                               CTTGGCGGACTTTTTGTGCTTCTGAGTGGCCAACATTTGATGTGGGCTGG
                                                 CCACCAGAGGGGACTTTTGACCTGACTGTGATCTTTGAAGTTAAAGCCAT 555
                                                                                             ProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValLysAlaIl 67
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       further details.
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75.315
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/db_xref="GI:12851652"
/translation="MGQTVTTPLSLTLDHWSEIRSRAHNLSVEIKKGPWRTFCASEWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="MGD:MGI:1906029"
/db_xref="MGD:MGI:1920342"
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356. .1147
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/db_xref="taxon:10090"
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                                                                                                                aSerArgArgProThrAsnLeuAlaLysValArgGluValMetGlnGlyP 347
                                                                                                                                                                                                          GluSerLeuLysIleTyrArgGlnAlaLeuValAlaGlyLeuArgGlyAl 330
                                                                                                                                                                                                                                                                                                     lyPheProLeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArg 313
CAGCTGAAACCCCGTCTGTTTTCTAGAGAGATTAATGGAGGCTTACGGA 1472
                                        {\tt roAsnGluProProSerValPheLeuGluArgLeuMetGluAlaPheArg}
                                                                                     GGCAAGATGCCCCTCCAATCTGGCAAAGGTAAGAGAAGCTATGCAGGGGC 1422
                                                                                                                                                                                   GAGAGGTTGACAGTTTACTGCCGGGCTCTAGTGGCAGGTCTCAAGGGAGC 1372
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            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                Mus musculus (strain:C57BL/6J) adult male liver clone_lib:RIKEN full-length enriched mouse cDNA clone:1300007C21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK004927 2935 bp mRNA HTC 05-:
Mus musculus adult male liver cDNA, RIKEN full-length
library, clone:1300007C21, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                           CAP trapper.
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Akahira,S., Akimura,T., Aono,H., Arai,A., Adachi,J., Aizawa,K., Akahira,S., Fukunishi,Y., Furuno,M., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Rishi,Y., Haraka,M., Kato,H., Kawai,J., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,K., Kurihara,C., Matsuyama,T., Kojima,Y., Konno,H., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Miyazaki,A., Nishi,X., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Miyazaki,A., Nishi,X., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,Y., Shibata,Y., Shinagawa,A., Shiraki,T., Sasaki,D., Shibata,K., Shibata,Y., Tagawa,A., Takahashi,F., Tanaka,T., Tagima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Quality: 1223.50
Ratio: 3.245
milarity: 66.963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                     /dev_stage="adult"
860 c 773 g
                                                                                                                                                                                                                                                                /tissue_type="liver"
/clone_lib="RIKEN_full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                          /clone="1300007C21"
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/db_xref="MGD:MGI:1914777"
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                                                                        CCTCCTCTGACTT.....AAAAATAATAACCCTTCCTTTCTGAA 1326
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                                                                                                                                                                                                              CCCGCAGCGGACTCCACCTCCCCAGGCATTCCCACTCCGTATG..... 1252
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                                                                                                                                                                                                                                                                                                                  215 ProPheSerSerAlaAspLeuTyrAsnTrpLysThrAsnHisProProPh
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                                                                            100 CCCATCAACCCACTTGGGATGATTGTCAGCAGCTTTTGCAGGTTCTTTTC
                                                                                                                           248 erHisGlnProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLeuPhe
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                                                                                                                                                                                 50 CTCAGAGAACCCCTCTGGGCTTACTGGGCTCCTTGAGTCACTTATGTTCT
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Quality:
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPCI-24-370H8.TJ RPCI-24 Mus musculus genomic clone RPCI-24-370H8,
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Class: BAC ends.
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Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
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The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Other_GSSs: RPCI-24-370H8.TV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                    AZ318021 729 bp DNA GSS 29-SEP-2000 1M0036004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0036004 R, DNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 729)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Welss,R.
                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                        house mouse.
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                         194 LeuProLeuArgThrTyr...GlyProProMetProGly...GlyGlnLe
161 CTTGAGTCACTTATGTTCTCCCATCAACCCACTTGGGATGATTGTCAGCA
                                                                                                       111 AAACTAACCACCCTCCCTTCTCAGAGAACCCCTCTGGGCTTACTGGGCTC
                                                                                                                                                                                                                                                                208 uGlnProLeuGlnTyrTrpProPheSerSerAlaAspLeuTyrAsnTrpL 225
                                                                                                                                                                                                              61 CATTCCTTTACAATACTGGCCTTTTTCCTCTTCTGATTTATATAATTGGA 110
                                                                                                                                                                                                                                                                                                                     11 CTTGCCCTTAGAGCACATGTGGGAGGGCCAGCGCCCAGGACCTAATGATCT
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Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNAv2 (gil4732114 jgb)AF129072 l), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicifin resistance."
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4.359
90.795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UUGC1M0036004"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
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LOCUS BH121259
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                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGCAGGAGAGAGAG
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                                                                                                          Unpublished (1999)
Other.GSSs: RPCI-24-374G11.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                  Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                        BH121259 679 bp DNA GSS 19-JUL-2001 RPCI-24-374G11.TV RPCI-24 Mus musculus genomic clone RPCI-24-374G11
                                                     9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
Clones are derived from the mouse BAC library RPCI-24. For library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 679)
                                                                                                                                                                                                                                                                                                                                                                                            BH121259.1 GI:14964771
                                      Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence.
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                                                                                                  ProAsnGluProProSerValPheLeuGluArgLeuMetGluAlaPheAr
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GAGATACACCCCTTTTGACCCCTTGTCAGAGGGGGCAGAGAGCCGCTGTAG
                                                                                                                                                         CCGCTAGACGGCCCACCAATTTGGCTAAGGTAAGAGAGGTCTTGCAAGGG
                                                                                                                                                                                                                                       GGGACGCCTCCTTGTCTATCGCCGGACTCTAGTGGCAGGTCTCAGAGGAG
                                                                                                                                                                                                                                                           GCTTTTCCCTTGAACCACCCCAACTGGGACTACAACACCGCGGAAGGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTCTCAGAGAACCCCTCTGGACTTACTGGGCTCCTTGAGTCACTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/rdb/bac_ends/mouse/bac_end_intro.html plate: 374 row: G column: 11
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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/db_xref="taxon:10090"
/clone="RPCI-24-374G11"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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397

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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 ysGluLysGluArgGluGluArgGlu 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 CCATGGCCTTCATTGGTCAGTCCGCTCCCGACATTAAGAAAAAGCTACAA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aGluLysValTyrTyrArgArgGluThrGluGluGluLysGluGlnArgL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgLeuGluGlyLeuGlnGluAlaGluLeuArgAspLeuValArgGluAl 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAGAAAGAAATAGAGGAGAGGGAA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGAAAGTCTATCATAAGAGGGAAACAGAAGAAGAGAGGCTGGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laIeuAlaPheIleGlyGlnSerAlaIeuAspIleArgLysLysIeuGln 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCTGGAGGGGCTCCAAGATCATACGCTCCAAGATTTAGTAAAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2M0238G10F mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0238G10 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ967275.1 GI:13838502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CGTTGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ967275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                       /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UUGC2M0238G10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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ORIGIN
        seq_name: gb_gss:BH124013
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COMMENT

TITLE

REFERENCE

AUTHORS

SOURCE KEYWORDS VERSION ACCESSION

FEATURES

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alignment_block:
US-09-171-553B-4 x AZ967275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 GlyPheProLeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyAr 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 uPheThrThrGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 PheSerHisGlnProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CAGACTGAACCACCCTCAGTCTTCCTTGAGCGTCTCATGGAGGCATATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 laSerArgArgProThrAsnLeuAlaLysValArgGluValMetGlnGly 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 alProGlyAlaAspGlyArgProThrGlnLeuGlnAsnGluIleAspMet 296
                                                      447 LysAsnLeuThrLysIleLeuAlaAlaValValGluGlyLys 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TTTCACCACAGAAGAAAGAAAGAATCCTGATGGAGGCGAGAAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTCTCCCATCAACCCACTTGGGATGATTGTCAGCAGCTTTTGCAGGTTCT
                                                                                                                                                                                                                                                          aGluLysValTyrTyrArgArgGluThrGluGluLysGluGlnArgL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gArgPheThrProPheAspProThrSerGluAlaGlnLysAlaSerValA
||||:::|||||||||:::||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProAsnGluProProSerValPheLeuGluArgLeuMetGluAlaPheAr 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCTAGACGGCCCACCAATTTGGCTAAGGTAAGAGAGGTCTTGCAGGGG
                                                                                                            ysGluLysGluArgGluGluArgGluGluArgArgAspArgArgGlnGlu 446
                                                                                                                                                                                                                                                                                                                                              AGGCTGGAGGGGCTCCAAGATCATACGCTCCAAGATTTAGTAAAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATGGCCTTCATTGGTCAGTCCGCTCCCGACATTAAGAAAAAGCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGTACACCCCTTTTGACCCCCTCGTCAGAGGGGCAGAAAGCCGCTGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTAGGAGAGGACGGCACACCCACTGCCCTCCCTAATCTCGTGGACGAG
AGAAATTTGAGTAAAATTTTGGCCGCAGTTGTAAATGATAGA 642
                                                                                                                                                                                                                               AGAGAAAGTCTATCATAAGAGGGAAACAGAAGAAGAGAGGCAGGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                    ArgLeuGluGlyLeuGlnGluAlaGluLeuArgAspLeuValArgGluAl 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laLeuAlaPheIleGlyGlnSerAlaLeuAspIleArgLysLysLeuGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. The stratage of the selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861.00
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Percent Identity: 76.636
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alignment_block:
US-09-171-553B-4 x BH124013
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                      Align seg 1/1 to: BH124013
                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
  103
                                              256
                                                                                                                                                                                                                     223 AsnTrpLysThrAsnHisProProPheSerGluAspProGlnArgLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                           53
                                                                                                                                                                             3 AATTGGAAAACTAACCACCCTCCCTTCTCAGAGAACCCCTCTGGACTTAC
                  ysGlnGlnLeuLeuGlnThrLeuPheThrThrGluGluArgGluArgIle
rGlyLeuValGluSerLeuMetPheSerHisGlnProThrTrpAspAspC
                                                                                    TGGGCTCCTTGAGTCACTTATGTTCTCCCATCAACCCACTTGGGATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 230 row: P column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Other_GSSs: RPCI-24-230P16.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao,S., Nierman,W., Malek,J., Shatsman,S., A. Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH124013 644 bp DNA GSS 19-JUL-2001 RPCI-24-230P16.TV RPCI-24 Mus musculus genomic clone RPCI-24-230P16
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Spleen/Brain" /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA.
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/clone="RPCI-24-230P16"
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                                                                                                                                                                                                                                                                                      Contact: Robert B. W. University of Utah Gountersity of Utah Rm. 308, Biomedical F. Contact Co
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0198 row: K column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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genomic

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alignment_block: US-09-171-553B-4 \times AZ420279/rev
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335 rAsnLeuAlaLysValArgGluValMetGlnGlyProAsnGluProProS 352
                                                                 315 TATCGCCGGACTCTAGTGGCGGGTCTCAAAGGGGCCTGCACGACGGCCCAC 266
                                                                                                                              319 TyrArgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgArgProTh 335
                                                                                                                                                                                                                               302 rgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSerLeuLysIle 318
                                                                                                                                                                                                                                                                                                                           415 GACTCCCACCAACCTTCCTAACCTTATTGATGAAGCTTTTCCTTTGACCC
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptored vector DNA, and transformed into chemically competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."

158 c 155 g 166 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
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89.623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     845.50
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Gaps:
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_gss:AZ986580
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 ArgArgGluThrGluGluGluLysGluGlnArgLys 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 lnGluAlaGluLeuArgAspLeuValArgGluAlaGluLysValTyrTyr 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 GATCCTTCATCGGAGGGCAGCAAGCAGCTGTTGCTATGGCTTTCATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 CGGTCTTTCTAGAACGGCTAATGGAGGCCTATAGGAGGTATACCCCGTTC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 erValPheLeuGluArgLeuMetGluAlaPheArgArgPheThrProPhe 368
                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGTCAGCTCCCGATATAAAAAAGAAGCTGCAAAGACTCGAGGGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGluGlyLeuG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlaPheIleGl 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGA.....GAGAGACGGAAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ986580 677 bp DNA GSS 27-APR-2001
2M0268P18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
Clone UUGC2M0268P18 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0268 row: P column: 18
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ986580
                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
High quality sequence stop: 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                    musculus C57BL/6J (female) was obtained Laboratory Mouse DNA Resource
was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                       /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                              /clone="UUGC2M0268P18"
                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            . 677
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alignment_block:
US-09-171-553B-4 x AZ986580
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506 AAGAGAGGTCTTGCAGGGGCAGACTGAACCACCCTCAGTCTTCCTTGAGC
                                                                                                                                                                 340 lArgGluValMetGlnGlyProAsnGluProProSerValPheLeuGluA 357
                                                                                                                                                                                                                                                           324 ValAlaGlyLeuArgGlyAlaSerArgArgProThrAsnLeuAlaLysVa
                                                                                                                                                                                                                                                                                                                                                                                                 307 yrAsnThrAlaGluGlyArgGluSerLeuLysIleTyrArgGlnAlaLeu 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 uGlnAsnGluIleAspMetGlyPheProLeuThrArgProGlyTrpAspT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 LeuGluAlaArgLysAsnValProGlyAlaAspGlyArgProThrGlnLe 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 lnGlnLeuLeuGlnThrLeuPheThrThrGluGluArgGluArgIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 alleLeuProLeuArgThrTyr...GlyProProMetProGly...GlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 SerArgArgGlyAlaThrProGluArg.....ThrAspGluIleAl 192
                                                     rgLeuMetGluAlaPheArgArgPheThrProPheAspProThrSerGlu 373
                                                                                                                                                                                                                             GTGGCAGGTCTCAGAGGAGCCGCTAGACAGCCCAACCAATTTGGCTAAGGT 505
                                                                                                                                                                                                                                                                                                                                              ACAACACCACGGAAGGTAGGGGACGCCTCCTTGTCTATCGCCGGACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTAACCTCGTTGACGAGGCTTTCCCCCTTGAACCGCCCCAACTGGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGAGGCGAGAAAAAATGTTCTGGGAGAGGACGGCACACCCACTGCCCT 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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87.054
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 AlaGlnLysAlaSerValAlaLeuAlaPheIleGlyGlnSerAlaLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 GGGCAGAGAGCCGCTGTAGCCATGGCCTTCATTGGTCAGTCCGCTCCCAA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ862103 677 bp DNA GSS 21-FEB-2001 2M0169D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic close UUGC2M0169D03 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 10000 Std E
Plate: 0169 row: D column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308,
               10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb[AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                       adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                      polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="UUGC2M0169D03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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DEFINITION
                                          seq_documentation_block:
                                                                               seq_name: gb_est2:BG089942
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                                                                                                                                                                                                                                                                       roThrSerGluAlaGlnLysAlaSerValAlaLeuAlaPheIleGlyGln
|||:::||||||:::||||||||||
|CTCGTCAGAGGGGCAGAAAGCTGCTGTAGCCATGGCCTTCATTGGTCAG
                                                                                                                                                                                                                SerAlaLeuAspIleArgLysLysLeuGlnArgLeuGluGlyLeuGlnGl 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgGlnAlaLeuValAlaGlyLeuArgGlyAlaSerArgArgProThrAsn 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spLeuTyrAsnTrpLysThrAsnHisProProPheSerGluAspProGln
                                                                                                                   TCATACGCTCCAAGATTTA 11
                                                                                                                                                        uAlaGluLeuArgAspLeu 409
                                                                                                                                                                                              TCCGCTCCCGACATTAAGAAAAAGCTGCAAAGGCTGGAGGGGCTCCAAGA
                                                                                                                                                                                                                                                                                                                                                    CTTCCTTGAGCGTCTCATGGAGGCATATAGGAGGTACACCCCTTTTGACC 130
                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCTAAGGTAAGAGGGCTCTTGCAGGGGGCAGACTGAACCACCCTCAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGGACTCTAGTGGCAGGTCTCAGAGGGGC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgLeuThrGlyLeuValGluSerLeuMetPheSerHisGlnProThrTr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTATATAATTGGAAAACTAACCACCCTCCCTTCTCAGAGAACCCCTCT 511
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BG089942 645 bp m
mab88d06.x1 NCI_CGAP_SP2
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4.241
87.444
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  mRNA
2 Mus
  musculus cDNA clone
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IMAGE:3977506
                    26-JAN-2001
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alignment_block:
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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445 CGAGGCTGGGCCCCTGTCCAAACTCCAGCTGAGATAGATGAAGGATTTC
                                                                                                 495 ACCGAGGAGAGAGAGGATTCTCCTCGAGGCTCGGAAAAATGTCCGAGA 446
                                                                                                                        266 ThrGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGl
                                                                                                                                                                                                  545 ACCAGCCGACTTGGGATGACTGCCAGCAGCTTCTGCAGACTCTATTCACA
                                                                                                                                                                                                                       249 isGlnProThrTrpAspAspCysGlnGlnLeuLeuGlnThrLeuPheThr 265
                                                                                                                                                                                                                                                                                                   595 CAGAAAACTGCAAGGACTCACTGGGTTGGATCATTAATGTATTCAC
                                                                                                                                                                                                                                                                                                                                                  232 rGluAspProGlnArgLeuThrGlyLeuValGluSerLeuMetPheSerH 249
                                                                                                                                                                                                                                                                                                                                                                                                 642 TTTTTCTTCTGTGACCTTTACAANTGAAAGGTC...ATCCCCCCCTTTTT 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 PheSerSerAlaAspLeuTyrAsnTrpLysThrAsnHisProProPheSe
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                          Tissue Procurement: David Segal Ph.D., Herbert Morse M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Cente Clone distribution: NCI-CGAP clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 645) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other_ESTs: mab88d06.yl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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BG089942.1 GI:12572505
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87.442
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/tissue_type="NK cells (flow-sorted)"
/lab_host="DH10B (T1-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roLeuThrArgProGlyTrpAspTyrAsnThrAlaGluGlyArgGluSer 315
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                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8545 row: g column: 15 High quality sequence stop: 598.
                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institutes of Health, Mammalian Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; S:
1 (bases 1 to 598)
NIH-MGC http://mgc.nci.nih.gov/
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                                                           /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1:
Site_2: NotI; Cloned unidirectionally. Primer: C
                                                                                                   /clone="IMAGE:3495206"
/clone_lib="NCI_CGAP_Lu29"
                                                                                                                                         /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
                                                                                                                                                                                                                         Location/Qualifiers
                                            /lab_host="DH10B"
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                                                                                                                                                                                                                       TTGGCCAGTCAGCTCCTGACATTAGGAAG
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                                                                                                                                                                         gb_gss:AZ650638
                                                             1M0520L20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0520L20 R, DNA sequence.
AZ650638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                        to: AZ650638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

147 c 169 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|sF129072 1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                          800.00
4.372
91.960
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/strain="C57BL/6J"
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Percent Identity: 76.382
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 AsnGluProProSerValPheLeuGluArgLeuMetGluAlaPheArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 TAGGAGAGGACGCCACCCACTGCCCTAATCTCGTGGACGAGGCT
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Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                          Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                        9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                            Other_GSSs: RPCI-23-238P4.TV
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M.,
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AZ708792.1 GI:12438716
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RPCI-23-238P4.TJ RPCI-23
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DE RPCI-23-238P4,
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alignment_block:
US-09-171-553B-4 x AZ708792
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451 GAGAAAAAAGAGGCAGAAGAACAGGGAATCGACGGGACCGTCGACAGGA
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                                                                                                                                                                     CAGAGAAAGTGTTTCATAAGAGAGAGACGGAAGATGAAAAAAAGGAAAGA
                                                                                                                                                                                                            laGluLysValTyrTyrArgArgGluThrGluGluGluLysGluGlnArg 429
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/organism="Mus musculus"
/strain="C57BL/6J"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-238P4"
/clone_lib="RPCI-23"
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//lab_host="PH10B"
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Gaps: 5
Percent Identity: 65.217
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446 501 462 4551 551 479	ULYSASNLEUTHYLYSIIELEUAIBAIBVBILVBIGlUGIYLYSSETS 462 ::: :::
462	erArgGluArgGluArgAspPheArgLysIleArgSerGlyProArgGl
551	GGAGAGATAGG
479	SerGlyAsnLeuGlyAsnArgThrP
562	TCAGGGAACCTGGGCAACTGGCGAGAAGCCAGGATTGCAGACCCCAACCC
487	oLeuAspLysAspGlnCysAlaTyrCysLysGluLysGlyHisTrpAl
612	CAGTTGGAAAAGGACCAGTGTGCGTATTGCAAAGAAAGGGGGACATTGGGT 661
503	aArgAsnCysProLysLysGlyAsnLysGlyProLysValLeuAlaLeuG
662	TCGGGAATGCCCAAAGAGAGAGCCAAGGTGCTGGCCCTCG
520	luGluAsp 522
702	ATCAAGAT 709

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gb_htc:AK004796
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gb_gss:BH083773
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gb_gss:AZ827524
gb_gss:AZ982997
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gb_gss:BH042410
gb_gss:AZ337037
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Database length: 1077921985
Search time (sec): 3515.700000
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Query: US-09-171-553B-5
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gb_gss:AZ717731
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                              gb_est2:BI408111
gb_est2:BF162779
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gb_gss:BH041228
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-Q=/cgn2_1/USPTO_spool/US09171553/runat_22022002_122825_11137/app_query.fasta_1.3312
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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                                                                                                      gb_gss:BH034484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Results were produced by the GenCore software, version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyright (c) 1993-2000 Compugen Ltd.
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 Documentation
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BH090616
BI107577
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BI152889
AZ6177566
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AZ974419
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BI143830
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AZ353894
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BH056750 RPCI-24-94C16.TVB RPC
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                                                                                                                                                                  AZ825369 2M0100I04R Mouse 10kb
AZ962118 2M0230N14R Mouse 10kb
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AZ643009 1M0506J17F Mouse 10kb
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AK004571 Mus musculus adult ma
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14 RPCI-24-352A17.TVB RPCI
72 RPCI-24-154N5.TJ RPCI
72 RPCI-24-154N5.TJ RPCI
74 2M0104E02F Mouse 10kb
77 2M0264E02F Mouse 10kb
                   0 602907110F1 NCI_CGAP_K
B RPCI -24-329L23.TJB RPC
1 602918919F1 NCI_CGAP_I
'9 601769243F1 NCI_CGAP_I
6 RPCI -24-331M11.TVB RPC
                                                                                                                                                                                                   0 RPCI-24-301E24.TJ RPCI
7 1M0067L03R Mouse 10kb
8 1M0450C07F Mouse 10kb
8 RPCI-24-356P6.TJ RPCI-
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RPCI-24-155A1.TJ RPCI
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602918048F1 NCI_CGAP_1
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2M0249C06F Mouse 10kb
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RPCI-24-230J18.TJ RPC
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gb_est2:BI414234
gb_gss:AZ660560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                           ORIGIN
                                                                             BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308,
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                                                                                                                                                   purified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
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.8e-65

RPCI-24-247H6.TV RPCI

alignment_scores:

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gb_gss:AZ897994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ636636 685 bp DNA GSS 13-DEC-2000
1M0495002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 685
Location/Qualifiers
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Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 685)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone UUGC1M0495002 R, DNA sequence
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Str and selected for ampicillin resistance."
                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) gblaF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and the property of the insert adaptors.
                                                                                                                                                                                                                                                 was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5
                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UUGC1M0495002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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1325.96
1320.90
1317.04
1314.57
                                                                                    The sheared, adaptored mouse DNA was annealed to
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1.1e-64
2.1e-64
3.4e-64
4.7e-64
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| AZ403060 1M05170L07R Mouse
| AZ758880 1M051809F mouse
| BI414234 602986684F1 NCI_C
| AZ660560 1M0538P10R Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 S. 2030 E.,
                    (Stratagene) cells
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                                                                                                                                                                                                                                                    429 gLeuTrpIleProGlyPheAlaThrLeuAlaAla 440
                                                                                                                                                                                                                                                                                                                        413 ThrThrAlaLysGlnValArgGluPheLeuGlyThrAlaGlyPheCysAr 429
                                                                                                                                                                                                                                                                                                                                                                                             135 GATGGCTCACAGAGGCCCGGAAGAAGACTGTTATGATGATCCCATCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 CTGTCAAACTGAGGTAACCTACCTGGGGTATACCCTCCGAGGGGGGTAAAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 GCAGAACTGAGTGACTTGGGGTATCGAGTTTCGGCTAAAAAGGCACAAAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 LeuGluLeuSerAspLeuGlyTyrArgAlaSerAlaLysLysAlaGlnI1 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 TrpTyrThrValLeuAspLeuLysAspAlaPhePheCysLeuArgLeuHi 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 oValGlnAspLeuArgGluValAsnLysArgValGlnAspIleHisBroT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685 AATACACCACTTCTGCCGGTTCGAAAACCAGGGACCAATGACTATCGCCC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 ASnThrProLeuLeuProValArgLysProGlyThrAsnAspTyrArgPr 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eCysArgArgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlyGlnA 396
                                                                                                                                                                                                          ACTCTGGATTCCAGGCTTTGCAACCCTAGCAGCA 2
                                                                                                                                                                                                                                                                                                  ACTACCCCACGGCAGGTACGTGAGTTTCTGGGGGACTGCTGGCTTTTGTAG
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                                                        RPCI-24-356L4.TU RPCI-24 Mus musculus genomic clone RPCI-24-356L4,
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                          DNA sequence.
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Gaps: 0
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                                                182 rProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArgL 199
                                                                                                172 GTTTTTGTGGGACTGAAGACAGATGCAACCCCTATAGGAGTGCGCCAATA
                                                                                                                                 166 GlnValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnTy 182
                                                                                                                                                                                                                 122
                                                                                                                                                                                                                                                    149 lnAlaTrpAlaGluThrAlaGlyMetGlyLeuAlaLysGlnValProPro 165
                                                                                                                                                                                                                                                                                                                                        118 ValLeuThrLeuGlnLeuAspAspGluTyrArgLeuTyrSerProGlnVa 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                           25 GTCTTAGCCCTGCAGCTTGAGGAAGAATACCGATTGCATGAA...GGCAT 71
TCCAATGAGCCGTGAAGCAAGAGATGGAATCAGGCCACATATTCAGAGAC
                                                                                                                                                                                                      AAAGCAAACAGAGGTGCTAGACCTAAAAGACTGGTTGACTGCTTTCCCTA 121
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Ratio: 4.341
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are darilability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC opage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 356 row: L column: 4
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
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1 (bases 1 to 791)
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_2: BamH1; Sites using MboI partially digested male C57BL/6JDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-356L4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       672 CTCCCAGGTAACCCTGCTCCAATATGTTGATGACTTGCTCCTTGCTGC.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 laThrLysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 CCAGCCCATATTCGCCTTTGAGTGGAGAGATCCTGACACTGGACAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 rGlnProLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGAGTTGGGTTACCGGGCC 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lyGlnLeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est2:BI107577
          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1107 row: n column: 05
                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BI107577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602894023F1 NCI_CGAP_Lu29
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 799)
                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                        EST
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  quality
sequence stop:
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                                                                                                                     Consortium (LLNL)
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alignment_block:
US-09-171-553B-5 x BI107577
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690 LeuAlaGluGlyLysSerIleAsnIleTyrThrAspSerArgTyrAlaPh 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 spAlaAspLysLeuThrLeuGlyGlnAsnIleThrValIleAlaProHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 yTrpProValCysLeuLysAlaIleAlaAlaValAlaIleLeuValLysA 540
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                                                                               lyThrSerAlaGlnLysAlaGluLeuMetAlaLeuThrGlnAlaLeuArg
                                                                                                                                                                               AlaValValAspGlyThr.ArgThrIleTrpAlaSerSerLeuProGluG
                                                                                                                                                                                                                                                                                    heThrAspGlySerSerTyrValValGluGlyLysArgMetAlaGlyAla
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                                                  GTACATCAGCTCAAAAAGCGGAACTAATCGCATTAATTCAAGCCTTAAGG
                                                                                                                                                       GCAGTAGTGGATGGAACAGGCTGTCATATGGGCCAGCAGTCTGCCGGAGG
                                                                                                                                                                                                                                                         TCACGGACGGAAGCATTTGTGGTAGAAGGTAAGCGGAAGGCTGGGGCT
                                                                                                                                                                                                                                                                                                                                                         CCGGCCAGACCTCACAGACCAACCTTGGCCAGGG...GCGATGACTTGGT
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Ratio: 4.236
nilarity: 90.114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

215 c 218 g 154 t 1 others
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Stem cell origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="CZECH II (feral)"
/db_xref="taxon:10090"
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70.508

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KEYWORDS
SOURCE
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                                                BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hrSerAlaGlyArgGluIleLysAsn.LysGluGluIleLeuSerLeuLe 739
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 94 row: C column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhaò,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Other_GSSs: RPCI-24-94C16.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medical Center Dr., Rockville, MD 20850, USA
                                                                                                     DNA.
                                                                                                              /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The Library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="RPCI-24-94C16"
                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                       /cell_type="Spleen/Brain"
                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 yPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGluLysGlyG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 ValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpIleProGl 434
                      662 ThrArgThrIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLy
                                                                                                                                    645 erTyrValValGluGlyLysArgMetAlaGlyAlaAlaValValAspGly 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 lAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGlnAsnIleT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 AGACTCTGGGGCCGTGGAAGAGGCTAGTGGCCTACCTGTCTAAAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 AlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrLysProPh 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 CGTTCACCTGGACAGAAGAACACCAAAAAGACTTTAACAGCATAAAGGCT
                                                                                                                                                                                                                                                                                                                            601 GATGAAGAAACTGGATCGAGAAAGGATCTGACTGAC.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 rGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrLeuL 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551 hrValIleAlaProHisAlaLeuGluAsnIleValArgGlnProProAsp
730 AAACATGTAATTTGGGCAAGTTAACTTCCAGAAGGAACTTCCGCTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GTCCACAATGTTAGCGGCACCTCTGTACCCACTCACTAAAGAAAAAGTCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTACGTGAGTTTCTGGGAACGGCAGGCTTTTGTAGACTCTGAATACCAGG
                                                                                                                                                                                                                                                                                                                                                         IleGluGluThrGlyValArgLysAspLeuThrAspIleProLeuThrGl 634
||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTGGATGACAAATGCCCGGATGACCCACTACCAGAGCCTGTTGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTAATCACTCCCCATGCGTTAAAGAGTATTGTATGACAGCCCCCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCCAGTTGCCAGTGAATGGCCCTCCTGCCTAAAAGCCATCGCTGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGACCGAGTGACTTTTGCCCTACCTGCCATCCACAATCCTACCACCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCCCTACTTGTTAAAGATACTGGCAAGCTTACTCTAGGTCAGCATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspProValAlaSerGlyTrpProValCysLeuLysAlaIleAlaAlaVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLysLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCATATACGTTGATGAGCCAGCTGGAGTAGCCCGCAGAGTCCTGACTC
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                                                                                                                                                                                                              .....CAAACTTGGCCAGGTGTGCCTGACAGGTACACAGATGGTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCCAAGACGGATGACTCTACCTGGGTACACCAATGTGCTGATATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euProGluGluThrAspGluProValThrHisAspCysHisGlnLeuLeu
                                                                                                        GCTTTGTGGTGGAGGGGAAAATAAGAGCAGGAGAGGCAGTGGTTGACAGA
                                                                                                                                                                                                                                                                 yGluValLeuThrTrp......PheThrAspGlySerS
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83.390
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alignment_scores

779

679 645 636 600

550

500 584 450

400

534 300

350

250 501 200

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGAGCTCCTGACGCTAACTAAAGCTCTGCCGCTGGCAAAAGGTAGGC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sAlaGluLeuMetAlaLeuThrGlnAlaLeuArgLeuAlaGluGlyLysS 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_gss:AZ980516
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2M0257006R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0257006 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0257 row: O column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ980516.1 GI:13851743
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              143
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Location/Qualifiers
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801 585 7177
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              Ø
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. The sheared application of the sheared application of the sheared selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UUGC2M0257006"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
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alignment_block:
US-09-171-553B-5 x AZ980516/rev
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                   395 lnArgTrpLeuThrGluAlaArgLysLys 404
                                                                                                                                                                    131
                                                                                                                                                                                                              362
                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 AsnSerProThrIlePheAspGluAlaLeuHisArgAspLeuAlaAsnPh 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 GCGGACAGACTGGTCAACTAACCTGGACTAGGCTACCACAGGGGTTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 ACATGGTATACAGTCCTGGACTTAAAAGATGCCTTCTTTTGCCTGCGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 gProValGlnAspLeuArgGluValAsnLysArgValGlnAspIleHisP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 TrpAsnThrProLeuLeuProValArgLysProGlyThrAsnAspTyrAr 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 ATATCCAGAGGTTGCTAGACCAAGGAGTTTTAGTGGCCTGTCAATCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 isValGlnArgLeuIleGlnGlnGlyIleLeuValProValGlnSerPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 GTAAGACAATACCCCCATGAGCAAGGAAGCTAGGGAGGGCATCCGGCCTC 632
31
                                                                                  81
                                                                                  AATTTGTCAAACTGAGGTAACCTACCTGGGGTATACCCTCCGAGGGGGGTA
                                                                                                        CTCACAGAACTGAGTGACTTGGGGTATCGAGTTTCGGCTAAAAAGGCACA
                                                                                                                                                                                                            LeuLeuGluLeuSerAspLeuGlyTyrArgAlaSerAlaLysLysAlaGl 378
                                                                                                                                                                                                                                                                                                                                                                 eArgIleGlnHisProGlnValThrLeuLeuGlnTyrValAspAspLeuL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTCGCGGCAGCCTCGAAGGAGCTGTGTCACCAGGGAACTGAGAGGCTC
                                                                                                                                                                                                                                                                                            euLeuAlaGlyAlaThrLysGlnAspCysLeuGluGlyThrLysAlaLeu 361
                                                                                                                                                                                                                                                                                                                                                                                                                        AATTCCCCCACCCTGTTTGACGAGGACCTCCATCGGGATCTCGCGCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACCCTAAGAGTCAGCTCCTGTTTGCCTTTGAATGGAGGAACCCAGAGG
AAAGATGGCTCACAGAAGCCCCGGAAGAAG
                                                                                                                                                                                                                                                                                                                                        TCGCGCTCGAAACCCTCAGCTTACCCTACTACAGTATGTGGATGATCTCT
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seq_documentation_block:
LOCUS BI152889

mRNA sequence.

DEFINITION 602918048F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5068643 5',

mRNA

05-JUL-2001

813 bp

seq_name:

gb_est2:BI152889

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alignment_block:
US-09-171-553B-5 x BI152889
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TITLE
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                        233 LeuArgGluValAsnLysArgValGlnAspIleHisProThrValProAs 249
                                                                                                                                              216 euLeuProValArgLysProGlyThrAsnAspTyrArgProValGlnAsp
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                                                                                                     201 TACTTCCAGTAAAAAAACCAGGGACCAGGGACTATCGTCCAGTACAGGAC
                                                                                                                                                                                                         151 GCTCCAACAAGGGATTTTGGTCCCATGCAAATCCCCTTGGAACACTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 nValIleGlnLeuLysAlaSerAlaThrProValSerValArgGlnTyrP 183
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                                                                                                                                                                                                                                                                                                                                                                                                                  51 GGTGATTGAACTTAAGTCCGGGGCCCACCCCTATAGGGGGTCCGACAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GCGTGGGCAGAGACGGGAGGGAGTGGGGATGGCAAAGTG.GTCCCCCCTGT 50
CTTAGAGAAGTCAACAAGAGAGTTCAGGACATACACCCCACGGTGCCAAA
                                                                                                                                                                                                                                                           uIleGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrProL 216
                                                                                                                                                                                                                                                                                                              CCATGAGCAGAAGCTCAAGAGGGTATACGCCCTCCAAATCAACAAACT
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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1 (bases 1 to 813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
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4.208
90.421
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/clone="IMAGE:5068643"
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                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0469 row: L column: 20
                                                                                                                                                                                        University of Utah Genome Center University of Utah
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Unpublished (2000)
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Plate: 0469
Seq primer:
                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 IleHisProThrValProAsnProTyrAsnLeuLeuSerAlaLeuProPr 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yPheLysAsnSerProThrIlePheAspGluAlaLeuHisArgAspLeuA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euArgLeuHisProThrSerGlnProLeuPheAlaPheGluTrpArgAsp
salaLeuLeuGluLeuSeraspLeuGlyTyrargalaSeralaLysL 376
                                                                                            GATCTGCTCCTAGCTGCAGAAACACGCGAGGACTGTGAAATTGGGACCCA
                                                                                                                                                                                   AspLeuLeuLeuAlaGlyAlaThrLysGlnAspCysLeuGluGlyThrLy 359
                                                                                                                                                                                                                                                                                    LaAsnPheArgIleGlnHisProGlnValThrLeuLeuGlnTyrValAsp 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGAGAGTGGACAAGCCGGACAGCTCACATGGACGAGGCTGCCTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGGTTACACCCCAACAGCCAGCCCTTGTTCGCTTTCGAATGGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTCGGACATGGTACACAGTCCTGGATCTCAAAGATGCTTTTTTCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATACACCCCACAGTGCCAAATCCTTATAACCTCCTCAGCACCTTGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCAAGAACTCGCCCACTTTGTTCGATGAAGCCCTACACCGAGATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class:
High qu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|473214|gb|AF1290721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the insert adaptors and polynomial to the complementary to the co
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C5/BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 988.00
4.682
92.544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
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/clone="UUGC1M0469L20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1 to:
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COMMENT
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                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lyPheCysArgLeuTrpIleProGlyPheAlaThrLeuAlaAlaProLeu
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                                                                                                                                                                                                                                                                                           Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 155 row: I column: 1
                                                                                                                                                                                                                                                        Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other_GSSs: RPCI-24-15511.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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AZ717731
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 817)
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                         /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1;
                                                                      /sex="Male"
                                                                                                /clone_lib="RPCI-24"
                                                                                                                  /db_xref="taxon:10090"
/clone="RPCI-24-15511"
                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                              Location/Qualifiers
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BASE COUNT
ORIGIN
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US-09-171-553B-5 x AZ717731
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650
                                                                                              600
                                                                                                                    734 GluIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArgLeuAlaIl 750
                                                                                                                                                                                                                717 ysGlnArgGlyLeuLeuThrSerAlaGlyArgGluIleLysAsnLysGlu 733
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                                                                                                                                                                                       550 GGCAGCAAGGGCTATTGACCTCGGCTGGTAAAGACATTAAAAACAAAGAA
                                                                                                                                                                                                                                                                                   500 TGACAGCCGCTATGCTTTGCTACAGCACACATCCATGGGGCCCATCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           667 laSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluLeuMetAla 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 AAAGCGAAAGGCTGGAGCTGCGGTGGTAGATGGGAAAAAGGTAATTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650 yLysArgMetAlaGlyAlaAlaValValAspGlyThrArgThrIleTrpA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 GlyGluValLeuThrTrpPheThrAspGlySerSerTyrValValGluGl 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TCGCTGAAGAAACTGGGACCAGAAGTGACCTGACCAACCCTGGCCT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 TCTCCCTCTAACAAATGATTCCGTCCCAGTACATCAATGTATGGACATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 AATGAGCGTGTAACCTTTGCGCCCCCCTGCCATCCTCAACCCAGCTACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 spArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 eThrValIleAlaProHisAlaLeuGluAsnIleValArgGlnProProA 567
                                          750 eIleHisCysProGlyHisGlnLysAlaLysAspLeuIleSerArgGlyA 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
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                                                                                                                                                                                                                                                                                                               rAspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAlaIleTyrL 717
                                                                                                                                                                                                                                                                                                                                                                                  CTTATTCAAGCCCTCCGAGAGGCTAAAGGTAAGATCATTAACATCTACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTGTTGTGGCCCCTCATGCCTTAGAAAGTATCGCGCGTCAGCCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                        LeuThrGlnAlaLeuArgLeuAlaGluGlyLysSerIleAsnIleTyrTh
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CATCCACTGCCCCGGCCACCAAAGAGGGGAGAAGACTTGGTGGCCAGGGGCA
                                                                                           GAAATTCTGGCCCTGTTGGAAGCCATACATGCACCTAAGAAGGTAGCCAT
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alignment_block: US-09-171-553B-5 x AZ715956

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VERSION
KEYWORDS
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    Percent Similarity:
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC opage: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 155 row: A column: 1
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Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 789)
                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_GSSs: RPCI-24-155A1.TV
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RPCI-24-155A1.TJ F
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                            Ratio:
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                                                                                                                                                                                                               /cell_type="Spleen/Brain"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: Bam
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: Bam
/note="Vector pTARBAC1 cloning vector
library was cloned in the pTARBAC1 cloning vector
972.50
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                                                                                                                                                                                                      BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-155A1"
/clone_lib="RPCI-24"
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to: AZ715956

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                                                                                                                                                                                                                                                                                                                                   760 ysAspLeuIleSerArgGlyAsnGlnMetAlaAspArgValAlaLysGln 776 ::||||||:::::::::|||:::
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                                                                                                                                                                                                                                                                                                         702 AAGACTTGGTGGGCCAGGGCCAACCGAATGCAGACTCAGTAGCAAAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 MetGlyLeuAlaLysGlnValProProGlnValIleGlnLeuLysAlaSe 173
                                                                                                                                                                                                                                                                                                                                                                                                        190 luGlyI1eTrpProHisValGlnArgLeuI1eGlnGlnGlyI1eLeuVal 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                          240 alGlnAspIleHisProThrValProAsnProTyrAsnLeuLeuSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 rAlaThrProValSerValArgGlnTyrProLeuSerArgGluAlaArgG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 GGCCACCCCTATAGGGGTCCGACAATATCCCCATGAGCAGAGAAGCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GTGGGGATGGCAAAACTGGTCCCCCCCGTGGTGATTGAACTTAAGTCCGG
LeuProProGluArgAsnTrpTyrThrValLeuAspLeuLysAspAlaPh
                                                                           TTCAGGACATACACCCCACGGTGCCAAATCCTTATAACCTCCTCAGCACC
                                                                                                                                                                                                                           yThrAsnAspTyrArgProValGlnAspLeuArgGluValAsnLysArgV 240
                                                                                                                                                                                                                                                                                                                                                                                   AGGGTATACGCCCCCAAATTAACAAACTGCTCCAACAAGGGATTTTGGTC
                                                                                                                                                                               GGACCAGGACTACCGTCCAGTACAAGACCTTAGAGAAGTCAACAAGAGAG
                                                                                                                                                                                                                                                                             ProValGlnSerProTrpAsnThrProLeuLeuProValArgLysProGl 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9852 row: c column: 20 High quality sequence stop: 701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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3.748
73.926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (T1 phage resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 281 c 252 g 185 t
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/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE: 4239307"
/clone_lib="NCI_CGAP_Kid14"
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                               273
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REFERENCE
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                                                                                                                                                                                                                                                                                                   seq_name: gb_gss:BH106844
                                                                                                            SOURCE
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                                                                                                                                                                           ACCESSION
      AUTHORS
                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 AlaProLeuTyrProLeuThrLysGluLysGlyGlyPheSerTrpAlaPr 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 lyThrAlaGlyPheCysArgLeuTrpIleProGlyPheAlaThrLeuAla 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 lValGlnIleProAlaProThrThrAlaLysGlnValArgGluPheLeuG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 TCTTGCGAGCATGGGCCACGGTGG.....TCCCAGAAGCAGAAAAAACAGG 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 erLeuArgGly.GlyGlnArgTrpLeuThrGluAlaArgLysLysThrVa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 rAlaLysLysAlaGlnIleCysArgArgGluValThrTyrLeuGlyTyrS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 yrValAspAspLeuLeuAlaGlyAlaThrLysGlnAspCysLeuGlu 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 gAspLeuAlaAsnPheArgIleGlnHisProGlnValThrLeuLeuGlnT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 GGGACCCAAAACTCCTGGGCGAGTTAGGTAAAGCTGGGGTATCGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AGATCTTGCCTCTTTTCCGAGCCAATAACCCACAGGTGACTCTTCTGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 rpArgAspProGlyThrGlyArgThrGlyGlnLeuThrTrpThrArgLeu 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 TTTCTGTTTGAGGTTACACCCCAACAGCCAGCCCTTGTTCGCTTTCGAAT 402
                                                                                                                                                                                                                                                                                                                                                                                     GluArgLysGlyValAlaArgGlyValLeuThrGlnThrLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roAlaLeuAlaLeuProAspValThrLysProPheThrLeuTyrValAsp 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCGCCGGGT...TGCGACCTG................
                                                                                                                                                                                                                                                                                                                                             CGGGAAAGAGGGGCCACCGCGGACGAGCGACACAAAAAAGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGGGCCCGGGCCCA...GTAACCTCCCCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTTCCCTACCAAGAAGGGATCCGCGCCAAGAACACTGCTTGAACCAAA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oGluHisGlnLysAlaPheAspAlaIleLysLysAlaLeuLeuSerAlaP 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTGCAGATCCCGAGCCCACAATGTCGCCAGTA.....GAAGTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTAA.AAGGCTCAGTTATGCCAGATAGAAGTGACCTACCTAGGATATG
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                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 842)
                                                                                                                                                                                          RPCI-24-352A17.TVB RPCI-24 Mus musculus RPCI-24-352A17, DNA sequence.
  Zhao,S.,
                                                                                                                                                                                                                                         BH106844
                                                                                    Mus musculus
                                                                                                                                                    BH106844.1 GI:14937281
                                                                                                                                                                           BH106844
                                                                                                          house mouse.
    Nierman, W.,
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  Malek,J.,
                                                                                                                                                                                                                                       DNA
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                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
  Shatsman, S.,
                                                                                                                                                                                                              genomic
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Akinret, B.,
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                                          Murinae; Mus
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US-09-171-553B-5 x BH106844
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                                                                                                                                                                                                                                                                                                118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other_GSSs: RPCI-24-352A17.TJB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA.
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4.221
85.768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-352A17"
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423 GlyThrAlaGlyPheCysArgLeuTrpIleProGlyPheAlaThrLeuAl 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 rSerLeuArgGlyGlyGlnArgTrpLeuThrGluAlaArgLysLysThrV 406
                                                                                                                 roGluHisGlnLysAlaPheAspAlaIleLysLysAlaLeuLeuSerAla 472
                                                                                                                                                                                                                                                                               aAlaProLeuTyrProLeuThrLysGluLysGlyGlyPheSerTrpAlaP 456
ProAlaLeuAlaLeuProAspValThrLysProPheThrLeuTyrValAs 489
                                                                         AGGAACACCAAAAAGCCTTTAACAGCATAAAGGCTGCTCTGCTTGCAGCC
                                                                                                                                                                                                                 GGCACCTCTGTACCCACTCACTAAAGAAAAGTCCCGTTCACCTGGACAG 267
                                                                                                                                                                                                                                                                                                                                                            GGAACGGCAGGCTTTTGTAGACTCTGAATACCAGGGTCCACAATGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCCTCCGAGAAGGAAAGCAGTGGTTCACCGAAGCTCGAAAGAAGACTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATGCAGATCCCAACCCCCACCACTCTGTGACAAGTACGTGAGTTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Spleen/Brain" /cell_type="Spleen/Brain" /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /note="Vector at the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6JDNA."
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seq_name: gb_gss:A2715272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 isAlaLeuGluAsnIleValArgGlnProProAspArgTrpMetThrAsn 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 ATGCGTTAAAGAGTATTGTATGACAGCCCCCTGACCATTGGATGACAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 GlyTrpProValCysLeuLysAlaIleAlaAlaValAlaIleLeuValLy 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 spGluProValThrHisAspCysHisGlnLeuLeuIleGluGluThrGly 622
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                                                                                                 Unpublished (1999)
Other_GSSs: RPCI-24-154N5.TV
Other_GSSs: RPCI-24-154N5.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ715272 755 bp DNA GSS 24-JAN-2001
RPCI-24-154N5.TJ RPCI-24 Mus musculus genomic clone RPCI-24-154N5
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
                                                                                                                                                                                                                                                                                                     Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                               Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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AZ715272.1 GI:12451823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia;
1 (bases 1 to 755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 TGCCTCAGGGATTCAAGAACTCGCCCACTTTGTTCGATGAAGCCCTACAC
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                                                                                                           406 alvalGlnIleProAlaProThrThrAlaLysGlnValArgGluPheLeu
                                                                                                                                                                                                                                                                      252 TTGGGACCCAAAACCTCCTGGGCGAGTTAGGTAAGCTGGGGTATCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                        356 luGlyThrLysAlaLeuLeuLeuGluLeuSerAspLeuGlyTyrArgAla
452 GGGACCGCCGGGTTTTGCAGACTCTGGATTCCCGGATTTGCCACACTAGC 501
                       423 GlyThrAlaGlyPheCysArgLeuTrpIleProGlyPheAlaThrLeuAl 439
                                                                                                                                                                              352 TGTCTTGAGAGATGGACAACGGTGGCTCACAAAAACCAGAAAACAAGCTG
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                                                                                                                                                                                                 rSerLeuArgGlyGlyGlnArgTrpLeuThrGluAlaArgLysLySThrV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                    nTyrValAspAspLeuLeuAlaGlyAlaThrLysGlnAspCysLeuG
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                                                                                                                                                                                                                                                                                           SerAlaLysLysAlaGlnIleCysArgArgGluValThrTyrLeuGlyTy 389
                                                                                        TTATGCAGATCCCGACCCCAACCACTGCTCGCCAGGTAAGAGAGTTCCTG
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4.271
88.933
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/clone="RPCI-24-154N5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
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439

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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ827524 700 bp DNA GSS 20-FEB-2001 2M0104E02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0104E02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ827524.1 GI:12997432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C5/BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                         /clone="UUGC2M0104E02"
                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                        . 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Std Error: 0.00
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Ø 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

182 c 175 g 165 t was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

ORIGIN BASE COUNT

alignment_block: alignment_scores: Align seg 1/1 to: AZ827524 from: 1 to: US-09-171-553B-5 x AZ827524 Percent Similarity: 455 582 uLeuThrGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaT 599 405 549 snileThrValIleAlaProHisAlaLeuGluAsnIleValArgGlnPro 516 LysLeuAspProValAlaSerGlyTrpProValCysLeuLysAlaIleAl 532 532 aAlaValAlaIleLeuValLysAspAlaAspLysLeuThrLeuGlyGlnA 305 255 499 205 482 155 466 105 449 ysGlyGlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAlaIle 465 432 eProGlyPheAlaThrLeuAlaAlaProLeuTyrProLeuThrLysGluL 449 416 LysGlnValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpII 432 55 TCCAGGCTTTGCAACCCTAGCAGCACCTCTATATCCTTTGACTAAGGAAG 104 5 CGGCAGGTACGTGAGTTTCTGGGGACTGCTGGCTTTTGTAGACTCTGGAT ProAspArgTrpMetThrAsnAlaArgMetThrHisTyrGlnSerLeuLe hrLeuLeuProGluGluThrAspGluProValThrHisAspCysHisGln GCTAAATGAGCGTGTAACCTTTGCGCCCCCTGCCATCCTCAACCCAGCTA CCTGACAGATGGATGACAAATGCCCGAATGACACACTATCAGAGCCTGCT AGGTGACTGTTGTGGCCCCTCATGCCTTAGAAAGTATCGTGCGGCAGCCA 454 AGCAGTAGCCCTGTTGATCAAAGATGCTGACAAATTGACAATGGGACAAC AAATTAGATCCTGTTGCTAGTGGATGGCCCACATGTCTGAAAGCTATTGC TGACACAAGCACTGGGACCCTGGAAGAGACCTGTAGCCTATTTGTCAAAA euThrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLys 515 GCCTTTCGTCCTATATGTGGACGAGAGAGCGGGTGTAGCCAGGGGAGTGT SProPheThrLeuTyrValAspGluArgLySGlyValAlaArgGlyValL 499 AAGTCGTCTCTAATGACTGCCCCCCCCCCTAGCATTACCAGACTTGACTAA LysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValThrLy 482 GGGTTCCTTTCGAGTGGAAAGAAGAACACCAGAGAGCTTTTGAGGCTATC Quality: Ratio: 91.845 960.50 4.488 Percent Identity: 76.824 233 615 504 565 404 354 304 254 154 54

83.019

to:

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DEFINITION
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LOCUS AZ982997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CGTTGTAAAAACGACGGCCAGTClass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: E column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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2M0264E02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0264E02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
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         148
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                     was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and the complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

163 c 188 g 169 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UUGC2M0264E02"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                           DEFINITION
                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                        seq_name:
                                 ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AsnLeuLeuSerAlaLeuProProGluArgAsnTrpTyrThrValLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 AAGTTAACAAAAGGGTCCTGGACATTCACCCCACAGTCCCGAACCCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              615 AGTTCGAAAACCAGGGACCAATGACTATCGCCCGGTGCAAGACCTCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                   115 CCTACCTGGGGTATACCCTCCGAGGGGGTAAAAGATGGCTCACAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                              385 hrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeuThrGluAla 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 GAGCTGTGTCACCAGGGAACTGAGAGGCTCCTCACAGAACTGAGTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 GlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLeuSerAspLe 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 alThrLeuLeuGlnTyrValAspAspLeuLeuLeuAlaGlyAlaThrLys 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 ACCTGGACTAGGCTACCACAGGGGTTCAAAAATTCCCCCCACCCTGTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 euPheAlaPheGluTrpArgAspProGlyThrGlyArgThrGlyGlnLeu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 AATTTATTAAGCTCTCCCCACCCGAGAGAACATGGTATACAGTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 luValAsnLysArgValGlnAspIleHisProThrValProAsnProTyr
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                                                                                                                                                                                                                                                                                                                   402 ArgLysLysThrValValGlnIleProAlaProThr 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGGCCCTCCATCGGGATCTCGCGCCTTTTCGCGCTCGAAACCCTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTAAAAGATGCCTTCTTTTGCCTGCGCTTGCACCCTAAGAGTCAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pGluAlaLeuHisArgAspLeuAlaAsnPheArgIleGlnHisProGlnV
                                                                                                                                                                                                                                                                  CGGAAGAAGACTGTTATGATGATCCCATCGCCAACG 30
                                                                                                                                                                                                     gb_htc:AK004796
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   library, clone:1200015M12, AK004796 AK004796.1 GI:12836246
                                                                                        Mus musculus adult
                                                                                                                      AK004796
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                     3234 bp III.... adult male lung cDNA, Ringa ...
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                                                                                           cDNA, RIKEN full-length enriched
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FEATURES

REFERENCE

AUTHORS

TITLE

JOURNAL

SOURCE KEYWORDS

ORGANISM

VERSION ACCESSION

BASE COUNT

66

266 335 316

166

366

416

285

466 268 251

516

235

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COMMENT
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RS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukudi, Shi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirakaka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sayabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission
              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
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Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 3234)
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US-09-171-553B-5 x AK004796
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703 TACTCTGAATGAGAAATATCTAGAGGAAGAACCAGTCGATCCGAGTCAGA 752
                                                                                                                                                                                                                                                                       272 AlaPhePheCysLeuArgLeuHisProThrSerGlnProLeuPheAlaPh 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 erAlaLeuProProGluArgAsnTrpTyrThrValLeuAspLeuLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 gGluGlyIleTrpProHisValGlnArgLeu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sArgValGlnAspIleHisProThrValProAsnProTyrAsnLeuLeuS 255
                                                                                                            ACTCAGGAGAATAGATGACAGTGGCAAATAGAGAGGTTAACAGTAAAGA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AGGAGGAGAAACAAAAGAAGGATAGAGGTCTGCAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAGTGCAG...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGAGAAGGACAGGGTAAGTTGGTAAGAAAGTTAGTGTAAGTAGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACTAGAAAGTCCCAACAATCTGACCAAGGTAACAGGAAGTTACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCACCTGTGAGTCTAACTGCCAGGCTCTGATGGGGGGTCTCATCTCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCAGTTAGGGAGGCATCTGCCCACTTGGGGCTTCTGTCCAAGGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTGCACTCCCTTCTCTGCTCTAAAGTTCCCTCTTCTCAGAAGG.....
                                                 ......ThrGlyArgThrGly......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....IleGlnGlnGlyIleLeuValProValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....TGGCACCACCTGAGTTGCTGGCAGTGAGTCTGTTCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                 .....ArgAspProGly.....
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/tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
/dev_stage="adult" 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="MGD:MGI:1904372"
/db_xref="MGD:MGI:1918989"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="1200015M12"
                                                                                                                                                                                                                                                                                                                                     ....AGCTCAAAGCAAATCTTCAGCAG
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Gaps: 58
Percent Identity: 33.028
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527

477

327 199

602

290

299

576

569 1499	AlaLeuGluAsnIleValArg.GlnProProAspArgT ::::: :::	557 1450
556 1449	yGlnAsnIleThrVallle.AlaProHis :::::: ::::::	547 1400
547 1399	leAlaAlaValAla.IleLeuValLysAspAlaAspLysLeuThrLeuGl :::::::::::	531 1358
531 1357	rLysLysLeuAspProValAlaSerGlyTrpProValCysLeuLysAlaI :: 	514 1313
51 4 1312	euGlyProTrpArgArgProValAlaTyr.LeuSe 	498 1265
498 1264	rLysProPheThrLeuTyrValAspGluArgLysGlyValAlaArgGlyV 	481 1239
481 1238	IleLysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspValTh	465 1189
464 1188	lyGlyPheSerTrpAlaProGluHisGlnLysAlaPheAspAla	450 1139
450 1138	AlaAlaProLeuTyrPro	433 1113
433 1112	GlnValArgGluPheLeuGlyThrAlaGlyPheCysArgLeuTrpIlePr ::::::::	417 1063
416 1062	alValGlnIleProAlaPro ::: TGTTTCATACTCCTCCACCG	400 1013
400 1012	LeuGlyTyrSerLeu CTG	383 993
383 992	AspLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleCysArgArgGl	367 970
366 969	ysGlnAspCysLeuGluGlyThrLysAlaLeuLeuLeuGluLeuSer::::::: :::	351 926
351 925	rValAspAspLeuLeuLeuAlaGlyAlaThrL:::	340 885
340 884	ASPLeuAlaAsnPheArgIleGlnHisProGlnValThrLeuLeuGlnTy ::::::::::::::::::::::::::::::::::::	324 835
323 834	lnGlyPheLysAsnSerProThrIlePheAspGluAlaLeuHisArg :::::: :::	308 793
308 792	CGAGAAAAAGAGTTCAGAAAACATGAGGCTGACCAAGACC	300 753

882	rqLeuProGlyVal	865
2015	::: ::: AGACTGGTAAAAGAAACCCT	1984
865	${\tt yThrLysHisLeuGlnGlnLeuValArgThrSerProTyrHisVal}$	849
1983		1983
848	$ys { t GluGlyLeuGluTyrValGlnGlnIleHisArgLeuThrHisLe}$	832
1983		1983
832	TyrGlyLysGluIleLeuPro	815
815 1983	LysIleAspGlnPheSer ::: AAATTA	799 1950
1949		1946
99	euProIleIleGluThrProLysAlaProGluProArgArgGl	782
782 1945	.snGlnMetAlaAspA ::: ATCAGATGGCAAATC	766 1896
1895	оттентосурктоступта	o 4
n co		1867
49	:luIleLeuSerLeuLeuGluAlaLeuHisLeuProLysArgLeu	w
1867	CAGACAAAGAGAGCTGTTGACATCTGC	1839
732	lnArgGlyLeuLeuThrSerAlaGlyArgGluIleL	716
1838		1831
716	laPheAlaThrAlaHisValHisGlyAla.Il	700
699 1830	uGlyLys 	683 1817
683 1816	PAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaGluLeuMetA :::	666 1767
666 1766	SARGMETALAGIYAlaAlaValValAspGlyThrArgThrIleTr	651 1717
651 1716	GluValLeuThrTrpPheThrAspGlySerSerTyrValValGluGlyLy	635 1667
634 1666	ValArgLysAspLeuTh ::: ::: aCTCGAAATGATCTGAA	619 1617
618 1616	ProValThrHisAspCysHis	602 1576
602 1575	hrPheAlaPr CCTTCGCTCC	586 1532
585 1531	AlaAr	569 1500

2016	AGAAACTGAAGGGAACACGAATATAGTCCTCTCA	04
882	lnLeuValAsnAlaAsnProSerArgIleProProGlyLysArgLeuArg 8	361
2050	TGA 2	0.5
899 2053	GlySerHisProGlyAlaHisTrpGluValAspPheThrGluValLysPr 9 :::::: ::: :::::	11.5
915 2103	OAlaLysTyrGlyAsnLysTyrLeuLeuValPheValAspThrPheSerG 9 :::	14
932 2141	lyTrpValGluAlaTyrProThrLysLysGluThrSerThrValValAla 9	19
949 2191	LysLysIleLeuGluGluIlePheProArgPheGlyIleProLysValII 9	23 6
965 2238	eGlySerAspAsnGlyProAlaPheValAlaGlnValSerGlnGlyLeuA 9	22 00
982 2288	laLysileLeuGlyileAspTrpLys.LeuHisCysAlaTyrArgProGl 9	32
998 2329	nSerSerGlyGlnValGluArgMetAsnArgThrIleLysGluThrLeuT 1 ::: ::: ::::::: :::	01
1015 2378	hrLysLeuThrThrGluThrGlyIleAsnAsp.TrpMetAlaLeuLeuPr 1	03
1031 2425	oPheValLeuPheArgValArgAsnThrProGlyGlnPheGlyLeuThrP 1 : :::	04
1048 2475	roTyrGluLeuLeuTyrGlyGlyProProProLeuAlaGluIleAlaPhe 1 :::::::::::::	52
1065 2525	AlaHisSeralaaspValLeuLeu.SerGlnProLeuPheSerargLeu. 1 ::: :::	08 57
1081 2572	LysalaLeuGluTrpValArgGlnArgAla\TrpLysGln.L 1	62
109 4 2622	euArgGluAlaTyrSerGlyGlyAspLeuGlnValProHisArgPheGln 1 :::	11 66
1111 2666	ValGlyAspSerValTyrValArgArgHisArgAlaGlyAsnLeuGluTh 1	12
1127 2710	rArgTrpLysGlyProTyrLeuValLeuLeuThrThrPro 1140 ::: ::: TCACTAGAAGGGTCCCTGCCTAGTTCTGTTTACTAATCCG 2749	

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gb_est2:B1109841
gb_gss:AZ417785
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gb_gss:AZ836232
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gb_gss:AZ989131
gb_est2:B1082444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences: 11351937
Database length: 1077921985
Search time (sec): 3515.700000
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Database: EST:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: Feb 24, 2002 8:31 AM
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gb_gss:AZ739547
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gb_gss:AZ642336
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gb_gss:AZ336017
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gb_est2:BF159914
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gb_gss:AZ327473
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gb_gss:AZ376517
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-Q2/C9n2_1/USPT0_spool/US09171553/runat_22022002_122825_11137/app_query.fasta_1.3312
-Q2/C9n2_1/USPT0_spool/US09171553/runat_22022002_122825_11137/app_query.fasta_1.3312
-DB=EST -OFMT=fastap -SUFFIX=feb22std.rst -GAPOP=12.000
-GAPEXT=4.000 -MINARCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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-THR_MAX=100 -FHR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=PfS
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=20000000
-USER=US09171553_eCGN1_1_9008 -NCPU=6 -ICPU=3 -LONGLOG
-USUMER-US09171553_eCGN1_1_9008 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                         gb_gss:AZ349077
                                                                                                                                                        gb_gss: AZ647666
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уb_gss:вн059027
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5.3e-48
3.0e-47
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1.2e-44
2.1e-44
9.0e-44
1.3e-43
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5.8e-47
1.5e-46
2.4e-46
3.7e-46
6.5e-46
                                                                                                                                                                                                   1.2e-42
1.5e-42
2.0e-42
1.2e-41
1.3e-41
1.2e-41
1.1e-41
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BI158931
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AZ970955 2M0244H16F Mouse
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2M0244H16F Mouse 10kb
RPCI-24-326G3.TJ RPCI
                                                                   2M0272E22F Mouse 10kb
602877669F1 NCI_CGAP_I
                                                                                                               602893174F1 NCI_CGAP_N
602921838F1 NIH_CGAP_N
                                                1M0085K21R Mouse
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gb_est2:BF786434
gb_gss:AZ887402
gb_gss:BH055839
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                                                                                                                                                                                                           alignment_block:
US-09-171-553B-6 x AW657531
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Quality:
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                          305 nGlyAlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerC 322
    EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW657531.1 GI:7423429
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3 TCCCCCGGTGTTCCTGTTAAGACAGGACAGAGACTCTTCAGTCTCATCCA
                       SerProGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleG1 305
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21180013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110922 MARC 1BOV Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG Plate: 94 row: E column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te: 94 row: E column: 12 primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                       /not="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
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BF786434 602112966F1 NCI_CC
AZ887402 RPCI-24-176N10.TJ
BH055839 RPCI-24-93P16.TVB
AZ018624 RPCI-23-382C22.TV
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_gss:AZ970955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 TATGAGCAGGCCTTAGAAAATCAGTATTTAGTACCTGGTTATAACTGATG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 TyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTr 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 TAGGAAAAGCTCCCCCATCCCACCAACACCTTTGCAATAGTACTATGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 leGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValVal 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 GTCCCGAAATAAGCTCACCCTCACTGAAGTTTCCGGGAAGGGGACATGCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 ySerArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gProLysArgGluProValSer.LeuThrLeuAlaValMetLeuGly 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCATCCTGAGGAAGTAGTCATCGATGAGTATGACTATCGGCCTACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrHisProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnAr 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAAAAAGAGAGCCCGTGACCCCTTAACCCCTAGCCGTTATACTAGGA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluArgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGl 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAGCTTTCCAAGCCATCAACTCCACCGACCCCGATGCCAGTTCTTCTT 102
High quality sequence stop: 754.
Location/Qualifiers
                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0244 row: H column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 754)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                  Class: plasmid ends
                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                        University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ970955 754 bp DNA GSS
2M0244H16F Mouse 10kb plasmid UUGC2M library Mus
close UUGC2M0244H16 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                             USA
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FEATURES

COMMENT

TITLE

SOURCE

VERSION

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alignment_block:
US-09-171-553B-6 x AZ970955/rev
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                      522 erLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPhe 538
                                                                                                                                                                                                                                                                489 ln.GlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAs 505
                                                                                                                                                                                                                                                                                                                     466
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                                                                                                                                                                                                                                                                                                                                                                                                                                   604 TGGAGAAGAGCCCCATTACCTTAACTTTGACAGTTCTATTAGGATTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 TAGTTCCAAAGATTTCTGCATTTTGGTTCAGCCTATTCCTAGACTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 nGlnSerLysAspPheCysValMetValGlnIleValProArgValTyrT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 TrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAs 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         751 TGGGCTTGCAATACCGGTCTCATTCCTTGTGTGTCTATGTCTGATTTTAA
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CCCTGTCCGAAGTGGTGCTACAGAATAGAAGGGGATTAGACTTATTATTC
                                                                                                                                                        pLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrS 522
                                                                                                           TCTTAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTT
                                                                                                                                                                                                                   AATACTAATGAA......GAACTACGTGCAGCTATGGATGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yrHisProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnArg 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCATGATGATAGCTCCTTTTTAGACAAATTTGAGCATCGGGTC...CGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114/gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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4.025
89.754
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0244H16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
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seq_documentation_block:
LOCUS BH059027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     639 MetValLeuArgGlnGlnTyrGlnGlyLeu 648
                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_GSSs: RPCI-24-326G3.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS
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RPCI-24-326G3.TJ RPCI-24 Mus
                                                                                                                                                                                                                                                                                            library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
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                                                                                                                                                                                                                                                    primer: SP6
                                                                                                                                                                                                                                   BAC ends
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                                                                    /db_xref="taxon:10090"
/clone="RPCI-24-326G3"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                           row: G column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 CTCCCTACTCTGAAGGGGTTGCTTTTAATGAAGATTTTAATAAAACAAGT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 roProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnValThrLys 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 rThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 GlyGlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSe
                                                                                                                                                                                                                                                                                                                                                            461 alSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyVal 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 uAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCysAsnThrG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 AGTCATGCC...TTATGCTCATGGGGAACAGGAAAGAAATTAACCCTGTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 GluHisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeu...
633 AATCTGTTGATGCATTAGAGAAATCCTTGACGTCCCTGTCAGAAGTAGTA
                                                511 luSerValSerAsnLeuGluGluSerLeuThrSerLeuSerGluValVal 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 lValLeuAspGluTyrAspTyrArgTyrAsnArgProLysArgGluProV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 CAACTATTACCTTGTGCCATATCCAGTTGGTTGGTGGGCCTGTAACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 CTGAAGTGTCAGGAGCAGCCCTTGTCTCTGTACAGGGACACCTCCTCCTG
                                                                                                      592 CTTAAGAGAA......GCTATAAATGAAGATTTAAGCATGCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 CTCGGATCCAGATGCCACTACATACTGCTGGTTATTCCTATCATCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGGCAAAGACTGTTCAACCTGATTAGAGGAGCCTTTTATGCCCCTTAACAG
                                                                                                                                                                                                                                        GlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLySGl 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCACCAACACCTATGTGGTCGGACTTAATTCTGTATCCAGGACAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....ThrGluValSerGlyLysGlyThrCysIleGlyLysAlaProProS 378
                                                                                                                                                       yLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysG
                                                                                                                                                                                                             GGAATGGGTTTAGCAGCCTTGGTTGAGGGTAGACAAGGAATTCACACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGAAGATGAATATATCAGTAAG.....AAGTTGAAAAGAGATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTATCATGGTTCATCTTCTATCTCGCATGTATTATTCCTGCCTCCCG 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erHisGlnHisLeuCysTyrSerThr.ValValTyrGluGlnAlaSerGl 394
                                                                                                                                                                                                                                                                                                                 TCTCCATTACTCTAGCTATGTTAATGGGGGTCGGTCTTACAGA.GGAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865.50
3.652
76.699
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Gaps: 6
Percent Identity: 58.252
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ORIGIN
                     BASE COUNT
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                           source
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:::|||||||||:::
TAGTCAGAGATTCTATGCAGAAATTGAGGGAAAGACTGGAAAGGGAA... 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLe 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTACAAAACAGAAGAGGTTTAGATTTATTGTTTTTAAGGGAAGGTGGACT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCATGGATGACCACTTTACTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 288 row: p column: 13
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorg Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC Mode Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Other_GSSs: RPCI-24-288P13.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 774)
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                     221
                                             BamHl sites using MboI partially digested male C57BL/6J DNA."
                                                                                  /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                  /clone_lib="RPCI-24"
/sex="Male"
                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="RPCI-24-288P13"
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                     162 c
                172 g
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                  219 t
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alignment_block:
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                                                                                                                                                                              587
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                    heGluGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAla
                                                                                                                                                                                                     PheTyrValAspHisSerGlyAlaIleArgAspSerMetAsnLysLeuAr 570
                                                                                                                                                                                                                                                                                     euPheLeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCys 553
                                                                                                                                                                                                                                                                                                                                                                               uThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLe
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                                                                                                                                                                         TTTTATGTTGACCATTCATGAGTAATCAAAGATTCTATGGCCAAACTTAG
                                                                                                                                                                                                                                                              TATTCCTTAAAGAACGAGGACTCTGTGCTGCCCTAAAAGAAGAATGTTGA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThr
                                                                                    AGAACGCCTAGATATACGTGAAAGAAAATAGAAAGCCAACAAGGATGGT
                                                                                                                              gLysLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyTrpP 587
                                                                                                                                                                                                                                                                                                                                                   AACTTCCCTGTCCGAAGTGGTGCTACAAAATAGAAGGGGATTAGACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGATCTTAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGTATCATGATGATAGCGCCTTTTTAGACAAATTTGAGCATCGGGTC
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85.878
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604 LeuThrGlyProLeuValValLeuLeuLeuLeuLeu

ATAGCAGGACCTTTGATTACTCTTATGCTTTTGCTT 772

alignment_block: $us-09-171-553B-6 \times Az351242/rev$

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COMMENT
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LOCUS AZ351242
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  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ351242 701 bp DNA GSS 29-SEP-: 1M0089L09F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0089L09 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 0089 row: L column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid inserts
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1 (bases 1 to 701)
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                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308,
                                                                                                                                                                                 211
                                                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UUGC1M0089L09"
820.00
3.923
89.316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Percent Identity:
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                                                   Length:
                             Gaps:
     67.949
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SOURCE
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                                                                                                                                                                                                                                                seq_name: gb_est2:BI151181
                                                                   KEYWORDS
                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AZ351242 from: 1 to:
                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 HisAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValSerAs 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 yrAspTyrArgTyrAsnArgProLysArgGluProValSer.LeuThrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 nIleValProArgValTyrTyrHisProGluGluValValLeuAspGluT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 ValSerThrSerValPheAsnGlnSerLysAspPheCysValMetValGl 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 GGCAGTTCTATTAGGATTGGGAGTAGCGGTTGGAGTAGGTACAGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 TTGAGCATCGGGTC...CGCTGGAGAAGAGAACCCGTTACCCTTAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700 GTGTCTATGTCTGTTTTAATAGTTCCAAAGATTTCTGCATTTTGGTTCA 651
                                                                                                                                                                                                                                                                                                                                                                                                                 615 uThrValGlyProCysLeuIleAsnArgPheValAlaPheValArgGluA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 rMetAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArgGluA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 AAAGAAGAGTGTTTTTTATGTTGACCATTCAGGAGTAATCAAAGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 LysGluGluCysCysPheTyrValAspHisSerGlyAlaIleArgAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 GGGGATTAGACTTATTATTCCTTAAA...GGAGGACTCTGTGCTGCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 nLeuGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnArgA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 laAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeu 498
                                                                                                                                                                                                                                                                                                                             632 rgValSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             599 ThrLeuLeuSerAlaLeuThrGlyProLeuValValLeuLeuLeuLeuLe 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 TATGGCCAAACTTAGAGAACGCCTAGATATACGTAAAAGAGAAAAGAGAAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laAspGlnGlyTrpPheGluGlyTrpPheAsnArgSerProTrpMetThr 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAACAAGGATGGTTCGAAAGCTGGTTTAATAAGTCCCCTTGGCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                         CGTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTATAACCAA 416
                                                                                                                                                                                                                                                                                                ACTCTCCTCCACCATAGCAGGACCTTTAATTACACTTATGCTTTTGCT
                                                                                                                                             mRNA SOUTH
Mus musculus
Eukaryota; M
                                                                     EST
                                                                                           BI151181.1 GI:14611182
                                                                                                                BI15118:
                                                                                                                                    mRNA sequence.
                                                house mouse.
  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                      mRNA
                                                                                                                                                                Mus
                                                                                                                                                                musculus
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                                                                                                                                                              clone IMAGE:5067273 5',
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alignment_block:
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TITLE
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422 nGlnSerLysAspPheCysValMetValGlnIleValProArgValTyrT 439
                                                                         406 TrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAs 422
                                                                                                                                                                                                                                                                                                         372
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                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ATTTCAACAGAACCAGCAGCCAT...ACTTCCTGCTCTTGGGGTACAGGA 148
                                                                                                                                                                                                                                                                                                                                                                          341 ysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySerArg 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 uCysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluArgL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 PheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTrpLe 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ATGCCTGTCCTTGGGTCCGCCTTATTATGAAGGAATCGCCTTCAATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TTTTATGCCCTTAACAGAACTGATCCAAGCGCTACTGAGGACTGCTGCT
                                                                                                                                             TGTCCAGAACGGAAGCTAATTACTATCTTGTACCTTCCCCGGTTGGATGG 298
                                             TGGGCTTGCAATACAGGACTTACTCCCTGTGTATCAACTAAGGTTTTTAA 348
                                                                                                                                                                                       yrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrp 405
                                                                                                                                                                                                                                            AGGTACCCCACCTTCCACTCACAAACACCTATGCGGACAAATTCAGTCCG
                                                                                                                                                                                                                                                                                          eGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValValT
                                                                                                                                                                                                                                                                                                                                            CAAAAACTGACCCTGACTGAAGTATCCGCGAGGAATCCAGGTCTCTGTAT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI1181 row: f column: 10
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1_ (bases 1 to 845)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
188 c 216 g 215 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               787.00
3.422
79.861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="spontaneous tumor, metastatic
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:5067273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Lu29"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580 CTAGCGGCAATAGAGAAGTCCATTGACGCTTTAGAAAAATCTTTGACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489 lnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAsp
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                          University of Utah Genome Center University of Utah
                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS
  Email: ddunn@genetics.utah.
Insert Length: 10000 std
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FEATURES
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US-09-171-553B-6 x AZ850764/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 TTGAGCATCGGGTC...CGCTGGAGAAGAGAACCCGTTACCTTAACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 GCTTATTCCTAGACTCCTGTATCATGATGATGATGCTCCTTTTTAGACAAAT 540
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                                                                                                                                                                                                                                                                                                             482 aAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuH 499
                                                                                                                                                                                                                                                                                                                                                                                                                                   466 AlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrGlyThrAl 482
                                                       516 LeuGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnArgAr 532
                                                                                                                         404 GTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTATAACCAAA 355
354 TTAGAAGAATCTTTAACTTCCCTGTCCGAAGTGTTGCTACAGAATAGAAG
                                                                                                                                                                                                                                                                                                                                                                        TGCCTTAATTAAGACCCCCCAATACTATGAA......GAACTAC 405
                                                                                                                                                                                isAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValSerAsn 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMRM2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                776.50
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89.450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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/clone="UUGC2M0152C18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ813042 625 bp DNA GSS 20-FEB-2001
2M0080E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0080E11 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 625)
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                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0080 row: E column: 1
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                                                                                                                                                                                                                                                 Class: plasmid ends
High quality sequence stop: 625
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                                                                                                                                                                                                                                                                                                    Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                /sex="Male"
                                                                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                /clone="UUGC2M0080E11"
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             599
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-171-553B-6 x AZ813042/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
573 uGluArgArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyT 590
                                                                                 557 AspHisSerGlyAlaIleArgAspSerMetAsnLysLeuArgLysLysLe 573
                                                                                                                                                                                                                                                                                               523 uSerGluVallValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                         507 ArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 ACTATGAA.....GAACTACGTGCAGCTATGGATATTGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 lnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeu 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 rAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyProGinG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 LysArgGluProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyTh 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 nSerLysAspPheCysValMetValGlnIleValProArgValTyrTyrH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557 TTCTAAAGATTTCTGCATTTTGGTTCAGCTTATTCCCAGACTCTTGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           607 GCTTGCAATAACGGTCTCACTCCTTGTGTGTCTATGTCTGTTTTTAATAG
                                                AAGAAGGAGGACTCTGTGCTGCCTTAAAAGAAGAATGTTGTTTTTATGTT 173
                                                                                                                                                                                     rgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrVal 556
                                                                                                                                                                                                                                                              GTCTGAAGTGGTGCCAAAATAGAAGGGGATTAGACTTATTATTCCTTA
                                                                                                                                                                                                                                                                                                                                                                        AGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCAGCTGGAGTAGGTACAGGAACCGCTGCCTTAATTAAGACCCCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnArgPro 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAsnGl 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGATGATAGCTCTTTTTTAGATAAATTTGAACATCGGGTC...CGCTGG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: AZ813042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi[4732]14[gb]AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
a 128 c 120 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 2
Percent Identity: 69.565
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440

ORIGIN BASE COUNT

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alignment_block:
US-09-171-553B-6 x BI106669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                         Align seg 1/1 to: BI106669
                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est2:BI106669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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314 rAspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyProP 331
                                                                                        298 GlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSerTh 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607 ProLeuValValLeuLeuLeu 613
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                                                 4 CAGAGGATGTTTAACCTAGTGAGAGGAGCCTTTTATGCCCTTAACAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTTAATTACACTTATGCTT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTTAATAAGTCCCCTTGGCTCACCACTCTCCTCCCACTATAGCAGGA 23
                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11105 row: p column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 921)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602893272F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5038336 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI106669.1 GI:14557562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BI106669
                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:5038336"
/clone_lib="NCI_CGAP_Lu29"
                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo (Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

211 c 229 g 232 t
                                                                                                                                                                                                                                                    763.00
3.206
78.289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .921
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54.276
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683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 GAAGACAGCTATGCGGGCCGG.....CGGTCAAAAAGAGAACCAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 LeuAspGluTyrAspTyrAsgTyrAsnArgProLysArgGluProValSe 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 HisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeuThrGl 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 rLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyT 479
                                                                                                                                                           577 .ArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPheAsnA 593
                                                                                                                                                                                                                    783 TAGTTAGAGACTCCTATGCAGAACCTGGACAGAACGATTTCAAGCGAAGG
                                                                                                                                                                                                                                                                     561 laIleArgAspSer.MetAsnLysLeuArgLysLysLeuGluArgArg.. 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATCCAAGCGCTACTGAGGACTGCTGGCTATGCCTGTCCTCGGGTCCGC
                                                                                                          AACACGGGAACCGGATGCCCAACGGGGTAGCTGAGTCGGGTTTGAATCCA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysGlu 511
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GA 884
                                                                                                                                                                                                                                                                                                                            GTGCTGCCCTTAAAGAAGAGTGCTGCTTCTATTGCAGATCATACAGGAAT 782
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGAACAGGAGAGGTCTTGATTCGTCGTCCTAAAGACAGGAGGACTGTT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATTGACGCTTTAGAAAAATCTTTGACCTCCCTGTCTGAGGTAGTTTT 682
                                                rg 593
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seq_name: gb_gss:AZ356870
seq_documentation_block:

Align seg 1/1 to reverse of: AZ356870

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COMMENT
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alignment_block:
US-09-171-553B-6 x AZ356870/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0098F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0098F09 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS
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                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
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Plate: 0098 row: F column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah (
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                              Ratio:
                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 644
                                                                                                                                                                                                                                         purified. The sheared, adaptored mouse DNA was anneased to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi14732114|gb|AFR1290721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="uuGC1M0098F09"
                                                                         3.897
88.372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                         Percent Identity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AAAGAAGGAGGACTCTGTGCTGCCCTAAAAGAAGAATGTTGTTTTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 ArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrVa 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 TAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  506 uArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrSerL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 TACTATGAAAAA......CTACGTGCAGCTATGGATGTTGATCT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 oLysArgGluProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyT 473 :::||||||||||||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639 CACTCTAGTAAAAGTGGTCAGTATCTAGTGCCCCCCTCAGACACAGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTCCAAAAATTTCTGCATTTTGGTTCAGCTTATTCCTAGACTCCTGTAT 490
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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 610)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                               AZ376517 610 bp DNA GSS 1M0130J20F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0130J20 F, DNA sequence.
Unpublished (2000)
                           plasmid inserts
                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                            AZ376517
                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                                               and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                          house mouse.
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alignment_block:
US-09-171-553B-6 x AZ376517/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                 497 uLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValS
                                                                                   461
                                                                                                                        481 ThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGl 497
                                                                                                                                                                                                                 464 hrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrGly 480
                                                                                                                                                                                                                                                                                                                                                                                                            608 GTTCAGCTTATTCCTAGACTCCTGTATCATGATGATAGCTCCTTTTTAGA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 ValGlnIleValProArgValTyrTyrHisProGluGluValValLeuAs 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                          ACCGCTGCCTTAATTAAGACCCCCCAATACTATGAA......GA
                                                                                                                                                                                                                                                                                                    CAGATTTGAGCATCGGGTC...CGCTGGAGAAGAGAGCCCCGTTACCTTAA 512
                                                                                                                                                                                                                                                                                                                                                pGluTyrAspTyrArgTyrAsnArgProLysArgGluProValSerLeuT 464
                                                                                                                                                                                       CTTTGGCAGTTCTATTAGGATTAGGAGTAGCGGCTGGAGTAGGTACAGGA
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0130 row: J column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt-end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubmic (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730.50
3.970
90.196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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/clone="UUGC1M0130J20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 c
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                                                                                424
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_gss:AZ430249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               614 euLeuThrValGlyProCysLeuIleAsnArgPheValAlaPheValArg 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581 GluAlaAspGlnGlyTrpPheGluGlyTrpPheAsnArgSerProTrpMe 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 spSerMetAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArg 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 CCAAATTAGAAGAATCTTTAACTTCCCTGTCCGAAGTGGTGCTACAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631 GluArgValSer 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 GAAAGCCAACAAGGATGGTTCGAAAGCTGGTTTAATAAGTCCCCCTTGGCT 124
                                                                                  source
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AZ430249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0214 row: G column: 11
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                             University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                    Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                      308,
                                                                                                                                     quality sequence stop: 591
                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inserts
                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg.,
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                           Location/Qualifiers
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alignment_block:
US-09-171-553B-6 x AZ430249/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 uGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyP 488
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                                                                                                                                                              571 sLysLeuGluArgArgArgArgGluAlaArgGluAlaAspGlnGlyTrpPheG 588
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                                                                                                                                                                                                                                                            300 TATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCTAAACTTAAAGA
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200 AAAGCTGGTTTAATAAGTCCCCTTGGCTCACCACTCTCCTCTCCACTATA
                                                                                                                               250 ACGCCTAGATATACGTAAAAGAGAAAGAGAAAGCCCACAAGGATGGTTTG
                                                                                                                                                                                                                                                                                                                                                                                     TCCTTAAAGAAGGAGGACTCTGTGCTCCCTTAAAAGAAGAATGTTGTTTT
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125 c 115 g 186 t
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATGGTACTAAGGCAACAATATCGGGTCCTT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rm. 30
84112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., Mongo, M., Wongo, Mand Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 673,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 10000 Std E. Plate: 0068 row: F column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus bases 1 to 673)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ddunn@genetics.utah.edu
                  10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                          polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from M musculus C57BL/6J (male) was obtained from the Jackson
chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UUGC1M0068F24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .673
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                  seq_name: gb_gss:AZ642336
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COMMENT

TITLE

VERSION

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alignment_block:
US-09-171-553B-6 x AZ337993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 yrAsnArgProLysArgGluProValSerLeuThrLeuAlaValMetLeu 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GGAATAGGTATGGCAGTAGGAGTGGGGACGGGAGTGTCAGCTTTGATAGA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 gValTyrTyrHisProGluGluValValLeuAspGluTyrAspTyrArgT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 ValPheAsnGlnSerLysAspPheCysValMetValGlnIleValProAr 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 GCCGGCGGTCAAAAAGAGAACCAATTACTTTAACCCTGGCTGCATTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CGTATATTATCACCCTGCATCCAGTTTA....GAAGAAAGCTATGCTG
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                                                                                     CCTTGTATAAATAAATAGAGGAATGGCTTTCATCCAGAGTAAAATTGATAC
AGTAAAACTCATGGTTCTTCAAAGGCAATATCAA
                                        aValGlnIleMetValLeuArgGlnGlnTyrGln 646
                                                                                                                                   ProCysLeuIleAsnArgPheValAlaPheValArgGluArgValSerAl 635
                                                                                                                                                                                                                           erAlaLeuThrGlyProLeuValValLeuLeuLeuLeuLeuThrValGly 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTTCTATGCAGATCATACAGGAATAGTTAGAGACTCTATGCAGAAACTG
                                                                                                                                                                              CCGCTGTAGCCGGACCAATCCTTATGATATGCTTAGCTNTAGTTTTCGGC
                                                                                                                                                                                                                                                                           GTTTGAGTCGTGGTTTGAATCACAACCATCTTGGATAACTTCTTTAATTT
                                                                                                                                                                                                                                                                                                                                                                 AGAGAAAGATTAGAGCAAAGGAAACGGGAACGGGATGCTCAACGGGGGTG
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1 120 c 167 g 188 t 1 others
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alignment_scores:
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US-09-171-553B-6 x AZ642336
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Align seg 1/1
                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0505 row: M column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ642336.1 GI:11768843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 624)
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                                                                                                                                                                                                                                                                                           203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 624
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801 585 7177
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     AZ642336
                                                                                                                                                                                                                                                                            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb)AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                    721.50
3.964
92.386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0505M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
  from:
                                                                                                                    Percent Identity: 70.051
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reilly
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LOCUS AZ741412
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                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643 lnGlnTyrGlnGlyLeuLeuSerGlnGlyGluThrAspLeu 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 AGCTTTTATTAGAGAAAGGATAAACGCAGTCCAAGTTATGGTCCTAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 ACACTTATGCTTTGCTTACTTTTGGCCCATGCATCCTTAATAAGTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 ValLeuLeuLeuLeuThrValGlyProCysLeuIleAsnArgPheVa 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593 rgSerProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLeuVal 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 TAAAAGAGAAAGAGAAAGCCAACAAGGATGGTTTGAAAGCTGGTTTAATA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            560 GlyAlaIleArgAspSerMetAsnLysLeuArgLysLysLeuGluArgAr 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 lyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHisSer 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 LysGluSerValSerAsnLeuGluGluSerLeuThrSerLeuSerGluVa 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 ProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValG1 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 GGTGCTGCAAAATAGAAGGGGATTAGACTTATTATTCCTTAAAGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 lValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 GAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCCTGTCCGAAGT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 ysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeu 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 yValGlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluL 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_gss:AZ741412
                                                                                                             Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M. Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-74Cl3.TV
                                                     Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 659)
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RPCI-24-74C13.TJ RPCI-24
9712 Medical Center Dr., Rockville,
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                            Institute for Genomic Research
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MD 20850, USA
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alignment_block:
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                       488
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                                                                                                                                                                                                                                                                                           438 yrTyrHisProGluGluValValLeuAspGluTyrAspTyrArgTyrAsn 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 alTyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArg 404
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roGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGlu
                                                              uGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATCCAGTCTAGCAAAAGTGGTCAGTATCTAGTGCCCCCCTCTAGACACA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGGGCCGGGTACCTCAGGTTAAAGGGCACCTCTGTAATCAGACCCAGA 109
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Ratio:
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 74 row: C column: 13
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Fax: 301 838 0208
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/clone="RPCI-24"74C13"
/clone_lib="RPCI-24"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector of the pTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
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3.868
84.545
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/strain="C57BL/6J"
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Gaps: 2
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645 ACGCCTAGAT 654
                                           571 sLysLeuGlu 574
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                                                                                                                                                                                                                                                  heLeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPhe
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                                                                                                                                                                                                                  TCCTTAAAGAAGGAGGACTCTGTGCTGCCCTAAAAGAAGAATGTTGTTTT 594
                                                                                                                                                                                                                                                                                                                           TTCCCTGTCCGAAGTGGTGCTACAGAATAGAAGGGGATTAGACTTATTAT 544
                                                                                                         TATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCCAAACTTAGAGA 644
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Sequence:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13	. <u>μ</u>	13	13	13	13	13	11	13	11	11	10	DB
AZ3490//	AZ850764	AZ642336	AZ814037	AZ430249	вн122287	AZ351242	BI182742	AZ970955	BF712162	BI182930	AW657531	ID
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AZ597961 AZ336017 AZ416306	B1328061 AZ327473 BF702741	AZ54/666 AZ727116 AZ406003	BH051865 AL120896 BH058168	BF703671 .	BH040768 BF703805	BH124666 AZ417785	BH059027 AZ730616	BE569478 AZ406484	AZ987182	AZ375836	AZ439189 BI185535	AZ356870	AZ499035	83623	AZ813042	AZ620796
AZ597961 1M0412K22 AZ336017 1M0066P05 AZ416306 1M0191D01	B1328061 6029/9695 AZ327473 1M0050K14 BF702741 MI-P-E3-a	AZ64/666 1M0514J12 AZ727116 RPCI-24-1 AZ406003 1M0175N06	BH051865 RPC1-24-2 AL120896 DKFZp762N BH058168 RPC1-24-3	MI-P-E4-	BH040768 RPCI-24-2 BF703805 MI-P-02-a	RPC1-24 1M0193E	BH059027 RPCI-24-3 AZ730616 RPCI-24-1		2M026		AZ439189 1M0229N10 BI185535 UNL-P-FN-			AZ836232 2M0131E01	2M00	AZ620796 1M0453I12

ALIGNMENTS

	JOURNAL MEDLINE COMMENT	TITLE	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AW657531 LOCUS DEFINITION ACCESSION
USDA, AKS, US MEAT ANIMAL RESEATCH CENTER PO BOX 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR PRImers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCCCAGTCACGACG Plate: 94 row: E column: 12	Genome Res. 11 (4), 626-630 (2001) 21180013 Contact: Smith TPL	Keele, J.W. Sequence evaluation of four pooled-tissue normalized bovine cDNA Libraries and construction of a gene index for cattle	Bovidae; Bovinae; Bos. 1 (bases 1 to 549) Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett ,G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and	AW05/331.1 G1:/423429 EST. COW. Bos taurus Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	()

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VERSION
KEYWORDS
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 564)
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BI182930.1 GI:14657339
EST.
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                                                                                Sus scrofa
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Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
144 c 121 g 139 t
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
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Pred. No. 1.7e-91;
0; Mismatches 40
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TITLE
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                                                                                                aatgattggtccacggagcgcgggctctcgatattttaaaatgattggtccatggagcgc 2766
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Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                       AACTGACTGGCACCATAGAAGAACTGATTACACATTGACAGCCCTAGTGACCTATCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized porcine ovarian follicles library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 -29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and sequence characterization of a normalized cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYA=Yes.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described constructed construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_TISSUE=porcine ovarian follicles
TAG_SEQ=CACACT"
129 c 143 g 151 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB=UNL-P-FN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UNL-P-FN-br-h-08-0-UNL"
/clone_lib="UNL-P-FN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="ADULT"
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Pred. No. 1.8
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564; 78;

Gaps

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Missouri-Columbia, 65211 Clone distr
available through Research Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                Seq prime
POLYA=Yes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iowa State University
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                                  /Clone_lib="MI-P-E6"
/lab_host="pH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E6 library is derived from fetus at gestational day 20. a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.lastate.edu/.
TAC_LIB-MI-P-E6
                 TAG_TISSUE=fetus at gestational day
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1 to 602)
TAG_SEQ=AGGAA"
                                                                                                                                                                                                                                                   /clone="MI-P-E6-acx-e-11-1-UM"
                                                                                                                                                                                                                                                                              /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                               strain="crossbreed"
                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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SOURCE

ORGANISM

Mus musculus house mouse. AZ970955.1 AZ970955

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

KEYWORDS VERSION

GSS.

RESULT 4 AZ970955/c

DEFINITION

AZ970955

clone UUGC2M0244H16 F,

2M0244H16F Mouse 10kb plasmid UUGC2M library Mus musculus

27-APR-2001

genomic

DNA sequence

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Best Local :
                                                                                                                                                 2726 gcgggctctcgatattttaaaatgattggtccatggagcgcggggctctcgatattttaaa
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                                                                                                                                                                                                2606 agaattgattacacattgacagccctagtgacctatctccaactgcaatctgtcactctgc
                                                                                                                                                                                                                                                                                                                                                                                   2366 aacaagacaagaagtggggaatgaaaggatgaaaatgcaacctaaccctcccagaaccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2246 cctttgttagagaacgagtgagtgcagtccagatcatggtacttaggcaacagtaccaag
                                             104 CACTCGGGGCCGCAGTCCTCTACCCCTGCGTGGCGTACGACTGTGGGCCCCCAGCGCGCTT
                                                                                          164 ATGATTGGTTTGCGAAGCGCGGGCTTTGTTGTGAACCCCATAAAAGCTGTCCCGATTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                    422 CACAAGACAAGAAGTGGGGAATGAAAGGATGAAAATGCAGCCTAACCCTCCAAGACCCCA
                                                                                                                                                                                    284 CCAGGAGCCCGCGCAAATGCGGAACCTCCGGAACTGTAGAAAAACGATTGGTCCACGGAGT
                                                                                                                                                                                                                                                                                                                                                                       362 AGAAGGTAGTGAAGAGCCCTAACTCCAGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 CCTNTGTTAGAGAATGAGTGAGTGCAGTCCAGATCATGGTACTTAGGCAACAGTACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
cactcggggccgcagtcctctacccctgcgtggtgtacgactgtgggccccagcgcgctt
                                                                                                                                      GCGGGCTCTCGATGTTTTAAAATGATTGGTCCACGGAGCACGGGCTCTCGATGTTTTAAA
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72.9%;
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Pred. No. 4.4e-67;
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                           1762 gctgtaatgctcggattagggacggccgttggcgttaggaacagggacagctgccctgatc 1821
                                                                                                                                                                                                                                                              1642 gatttgtgtgtcatggtccaaatcgtcccccgagtgtactaccatcctgaggaagtggtc 1701
                                                                                                                                              1702 cttgatgaatatgactatcggtataaccgaccaaaaagagaacccgtatcccttacccta 1763
                                                                                                                                                                                                                                                                                                                                                                           1582 tgggcatgcaatactgggttaaccccctgtgttttccacctcagtcttcaaccaatccaaa 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
574 ACAGTTCTATTAGGATTAGGAGTAGCGGCTGGAGTAGGTACAGGAACCGCTGCCTTAATT 515
                                                                                                                                                                                                                 691 GATTTCTGCATTTTGGTTCAGCTTATTCCTAGACTCCTGTATCATGATGATGATAGCTCCTTT
                                                                                                                                                                                                                                                                                                                            751 TGGGCTTGCAATACCGGTCTCATTCCTTGTGTGTCTATGTCTGATTTTAATAGTTCCAAA 692
                                                                                                       TTAGACAAATTTGAGCATCGG----GTCCGCTGGAGAAGAGAGCCCCATTACCTTAACTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0244 row: H column: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: PWD42nv; Rurified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 293.6; DB 13;
Pred. No. 4.2e-53;
0; Mismatches 244;
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                                                                                                                                                    Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI182742 494 bp mRNA EST 10-JUL UNL-P-FN-bo-e-05-0-UNL.S1 UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-bo-e-05-0-UNL 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   library from swine ovarian follicles Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pig.
Sus scrofa
                                                                                                              normalized porcine ovarian follicles library Seq primer: M13 -29
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Pomp,
                                                                                         POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and sequence characterization of a normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caetano, A.R.,
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 494)
                                               1. .494
/strain="University of Nebraska, Lincoln Swine Selection
                       /organism="Sus scrofa":
                                                                 Location/Qualifiers
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Sim hes 391;
                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                             tgtacgactgtgggccccagcgcgcttggaataaaaatcctcttgctgtttgcatcaaaa 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCCCATAAAAGCTGTCCCAATTCCGCACTTGGGGCCGCAGTCCTCTACCCCTGCGTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggagcgcggggctctcgatattttaaaatgattggtttgtgacgcacaggctttgttgtg 2818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tattttaaaatgattggtccacggagcgcgggctctcgatattttaaaatgattggtcca 2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcctgctatcctggcctaagtaagataacaggaaatgagttgactaatcgcttatctgga 2578
                                                                                                                                                                                                                                                                                                                                                                                      CCTACGAC -- TGGGCCCCAGCGCGCTTGGAATAAAAATCCTCTTGCTGTTTGCATCAAGA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaccccataaaagctgtcccgattccgcactcggggccgcagtcctctacccctgcgtgg 2878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTAGAAAAATGATTGGTCCAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATCTCAACTGCAATCTGTCACTCCGCCCAGGAGCCCGCGCAAATGCGGGACCTCCGCAAC 214
                                                                                                                                                                                                                                                                            AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GGAGTGCCGGCTCTCGATGTTTTAAAATGATTGGTTTGCGAAGCGCGGGCTTTGTTGTG 133
                         AZ351242
AZ351242.1 GI:10430479
                                                                                AZ351242 701 bp DNA GSS 29-SEP-2000 1M0089L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0089L09 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_LIB-UNL-P-FN
TAG_TISSUE=porcine ovarian follicles
TAG_SEQ=CACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UNL-P-FN-bo-e-05-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="ADULT"
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79.1%;
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1731 accaaaaagagaacccgtatcccttacccta-gctgtaatgctcggattagggacggccg 1789

TAGACTCCTGTATCATGATGATAGCTCCTTTTTAGACANATTTGAGCATCGGGT----CCG

585

584 CTGGAGAAGAGAACCCGTTACCCTTAACTTTGGCAGTTCTATTAGGATTGGGAGTAGCGG

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FEATURES
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                                                                                                                                                                       Matches 455;
                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                         1611 tgtttccacctcagtcttcaaccaatccaaagatttgtgtgtctatggtccaaaatcgtccc 1670
1671 ccgagtgtactaccatcctgaggaagtggtccttgatgaatatgactatcggtataaccg 1730
                                                            {\tt TGTGTCTATGTCTGTTTTTAATAGTTCCAAAGATTTCTGCATTTTGGTTCAACTTATTCC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0089 row: L column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Utah University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                    purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. a 149 c 134 g 206 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil47321419 gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/clone="UUGC1M0089L09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCCAAACTTAGAGAACGCCTAGATA
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                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 288 row: P column: 13
                                                         Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Other_GSSs: RPCI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeor-Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RPCI-24-288P13.TJ RPCI-24 Mus
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                                         BAC ends.
                Location/Qualifiers
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CACCACTCTTCTCCCACCATAGCAGGACCTTTGATTACTCTTATGCTTTTGCTTAC
                             CCATTCATGAGTAATCAAAGATTCTATGGCCAAACTTAGAGAACGCCTAGATATACGTGA 657
                                                                                                                                                                                                                                                             gtttctaagagaaggtgggttatgtgcagccttaaaagaagaatgttgcttctatgtaga
                                                                            AAGAGAAATAGAAAGCCAACAAGGATGGTTCGAAAGCTGGGTTAATAAGTCCCCTTGGCT
                                                                                                       aagggaaagagaggctgaccaggggtggtttgaaggatggttcaacaggtctccttggat 2156
                                                                                                                                                                              tcactcaggagccatcagagactccatgaacaagcttagaaaaaagttagagaggcgtcg
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                                                                                                                                                                                                                                        ATTCCTTAAAGAACGAGGACTCTGTGCTGCCCTAAAAGAAGAATGTTGATTTTATGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGTATCATGATGATAGCGCCTTTTTAGACAAATTTGAGCATCGG----GTCCGCTGGAG 309
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                                                                                                                                                                                                                                                                                                                     AGAATCTTTAACTTCCCTGTCCGAAGTGGTGCTACAAATAGAAGGGGATTAGACTTATT
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/Cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; The Indian Condition of the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="RPCI-24-288P13"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
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                          1728 ccgaccaaaaagagaaacccgtatcccttaccctagctgtaatgctcggattagggacggc 1787
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589 CCGCTGGAAAAGAGACCCGTTACCTTAACTTTGGCAGTTTTATTAGGATTGGGAGTAGC 530
                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0214 row: G column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center 
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                               Similarity
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801 585 7177
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                               adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance. The sheared and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomedical Polymers Research Bldg., 20 S.
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/clone="UUGC1M0214G11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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/strain="C57BL/6J"
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                                                                                                                                  8.6%;
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                                                                                                        Score 254.4; DB 13;
Pred. No. 1.2e-44;
0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00
                                                                                                                                                               Length 591;
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                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CCCTTGGCTCACCACTCTCCTCCCACTATAGCAGGACCTTTAATTACACTTATGCTTTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATACGTAAAAGAGAAAGAAAGCCCCACAAGGATGGTTTGAAAGCTGGTTTAATAAGTC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCTAAACTTAAAGAACGCCTAGA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agatctgctgtttctaagagaaggtgggttatgtgcagccttaaaagaagaatgttgctt 2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caacctagaagagtcoctgacttctttgtctgaagtggttctacagaaccggaggggatt 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acttggtgagctacatgcggccatgacagaagatctccggagccttaaaggagtctgttag 1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgttggcgtaggaacagggacagctgccctgatcacaggaccacagcagctagagaaagg 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTACTTTTGGCCCATGCATCCTTAATAAGTTAGTAGCTTTATTAGAGAAAAGGATAAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acttacagttgggccttgcttaattaataggtttgttgcctttgttagagaacgagtgag 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           teettggatgaeeaceetgetttetgetetgaeggggeeectagtagteetgeteetgtt 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctatgtagatcactcaggagccatcagagactccatgaacaagcttagaaaaagttaga 2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATTAGAAGAATCTTTAACTTCCCTATCCGAAGTGGTGCTGCAAAATAGAAGGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GAGCTACGTGCAGCTATGGATGTTGATCTTAGAACCATAGAACAGTCTATAAC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTGGAGTAGGTACAGGAACCGCTGCCTTAATTAACACCCCCCAATACTATGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCAGTCCAAGTTATGGTACTAAGGCAACAATATCGGGTCCTTCAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACTTATTATTCCTTAAAGAAGGAGGACTCTGTGCTCCCTTAAAAGAAGAATGTTGTTT
                                          High quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                     University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 632)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ814037 632 bp DNA GSS 20-FEB-2001
2M0081N06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                            Plate: 0081 row: N column: 06
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0081 row: N column: 00
                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ814037.1 GI:12983945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone UUGC2M0081N06 R,
                                                                                       Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ814037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nouse mouse
                                                                                                                                                                                                                                                     USA
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                              Weiss
                                                                                                                                                         Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence.
                                                                                                                                                                                                                                                                            20 S. 2030 E.,
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1977 gtttctaagagaaggtgggttatgtgcagccttaaaagaagaatgttgcttctatgtaga 2036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1737 aagagaacccgtatcccttaccctagctgtaatgctcggattagggacggcggttggcgt 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAGAGAACCCGTTACCTTAACTTTGGCAGTTCTATTAGGATTGGGAGTAGTGGCTGGAGT
                                                                                                                                                                                                                                               CACCACTCTCCTCCACCATAGCAGGACCTTTAATTACACTTATGCTTTTGCTTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcactcaggagccatcagagactccatgaacaagcttagaaaaaagttagagaggcgtcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gctacatgcggccatgacagaagatctccgagccttaaaggagtctgttagcaacctaga 1916
   GGTTATGGTACTAAGGCAACAATATCGGGTCCTTC
                                          gatcatggtacttaggcaacagtaccaaggccttc 2311
                                                                                                                                                             AAGAGAAAGGAAAGCCAACAAGGATGGTTCGAAAGCTGGTTTAATAAGTCCCCTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                aagggaaagagaggctgaccaggggtggtttgaaggatggttcaacaggtctccttggat 2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATTCAGGAGTAATCAAAGATTCTATGGCCAAACTTAGAGAACGCCTAGATATACGTAA 349
                                                                                                                         TGGCTCCTGCATCCTTAATAAGTTAGTCGCTTTTATTAGAGAAAAGGATAAATGCAGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCCTTAAAGAAGGAGGACTCTGTGCTGCCCTAAAAGAAGGATGTTGTTTTTATGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -CTACGTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTATAACCAAATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTACAGGAACTGCTGCCTTAATTAAGACCCCCCAATACTATGAAGAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggaacagggacagctgccctgatcacaggaccaccagcagctagagaaaggacttggtga 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAATCTTTAACTTCCCTGTCCGAAGTGGTGCTACAGAATAGAAGGGGATTAGACTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UUGC2M0081N06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 253; DB 13;
Pred. No. 2.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWD42nv; Purified genomic DNA from M.
564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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1857

62

170

ORIGIN BASE COUNT

Matches

Вb Qy В Qy В Qy DЪ Qy 밁 Qy 밁 Qy В Qy В

410

530

밁 QΥ

1742 aaccogtatcccttaccctagctgtaatgctcggattaggacggccgttggcgtaggaa 1801

AACCCGTTACCTTAACTTTGGCAGTTCTATTAGGATTGGGAGTAGCAGCTGGAGTAGGTA 60

Matches 378;

Conservative

0;

Mismatches 182; Indels

12;

Local Similarity

2037

230

2097

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BASE COUNT
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AZ642336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
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1M0505M18F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0505M18 F, DNA sequence.
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Location/Qualifiers
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: CGTTGTAAAACGACGGCCAGT
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Plate: 0505 row: M column:
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

116 c 131 g 174 t
                                                                                                                                                                                                                            with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed
                                                                                                                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                              polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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Score 246.8; DB 1
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                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0152 row: C column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 641.
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University of Utah
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                                                                                                                               ggcgtcgaagggaaagaggctgaccaggggttggtttgaaggattggttcaaccaggtctc 2149
                                                                                                                                                                                                      ATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCCAAACTTAGAGAACGCCTAGATA 177
                                                                                                                                                                                                                                                                                                          ACTTATTATTCCTTAAAGAAGGAGGACTCTGTGCTGCCCTAAAAGAGGAATGTTGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAGAACTACGTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTATAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC2M0152C18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%;
63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 245.2; DB 13; Length 641; Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 223; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACTTTTGGCCCCTGCATCCTTAATAAGTTGGTAGCTTTTATTAGAGAAAG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn,D., Aoyagi,A., Barber,M., Beacorn,I., Luvus, ..., Reilly Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 493)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                        was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114) gbl pAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

103 c 89 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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     8.2%;
70.7%;
                                                                                                                                                                                                                The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia; Sciurognathi; Muridae;
  Score 242.6; DB 13; Pred. No. 4.4e-42;
No. 4.4e-42;
                    Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-2000
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FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2095 cgaaggggaaagaggctgaccaggggtggtttgaaggatggttcaacaggtctccttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2035 gatcactcaggagccatcagagactccatgaacaagcttagaaaaaagttaggagaggcgt 2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1975 ctgtttctaagagaaggtgggttatgtgcagccttaaaagaagaatgttgcttctatgta 2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1855 gagctacatgcggccatgacagaagatctccgagccttaaaggagtctgttagcaaccta 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 TTTGGCCCCTGCATCCTTAATAAGTTGGTAGCTTTTATTAGAGAAAAGGATAAATGCAGTA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 CTCACCACTCTCCTCCCACCATAACAGGACCTTTAATTACACTTATGCTTTTGCTTACT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 GACCATTCAGGAGTAATCAAAGATTCTATGGCCAAACTTAGAGAACGCCTAGATATACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 TTATTTCTTAAAGAAGGAGGACTCTGTGCTGCCCTAAAAGAAGAATGTTGTTTTTATGTT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 AAAAGAGAAAAGAGAAAGCCAACAAGGATGGTTCGAAAGCTGGTTTAATAAGTCCCCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 GAACTACGTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTATAACCAAGTTA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 CAGGTTATGGTACTAAGGCAACAATATCGGGTCCTTC 35
                                                                                             Plate: 0453 row: I column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errc
Plate: 0453 row: I column: 12
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 650)

Dunn, D., Abyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323; Conservative
                                                                               High quality sequence stop: 650
                                                                                                                                                                                                                                         84112,
                                                                                                                                                                                                                                                                            University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                   Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                            and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ620796.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse
                                                                                                                                                                                                                                                            308,
                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                            Biomedical
/organism="Mus musculus"
/strain="C57BL/6J"
                                                          Location/Qualifiers
                                          . 650
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                                                                                                                                                      Std Error:
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                                                                                                                                                                                                                                                    2030 E., SLC, UT
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1772 tcggattagggacggccgttggcgtaggaacagggacagctgccctgatcacaggaccac 1831
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                                                                                                                                                               2252 ttagagaacgagtgagtgcagtccagatcattggtacttaggcaacagtaccaaggccttc 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                            2132 gatggttcaacaggtctccttggatgaccaccctgctttctgctctgacggggcccctag 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2072: ttagaaaaaagttagagaggggtcgaaggggaaagagggctgaccaggggtggtttgaag 2131
                                                               2312 tg 2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 TAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCCTGTCCGAAGTGGTGCTGC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 CAAATCTATA-----AGAACTACGTGCAGCTATGGATATTGATCTTAGAACTA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TTACACTTATGCTTTTGCTTACTTTTTGGCCCATGCATCCTTAATAAGTTAGTAGCTTTTA 182
                                                                                                                               181 TTAGAGAAAGGATAAACGCAGTCCAAGTTATGGTACTAAGGCAACAATATCGGGTCCTTC
121 AG
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Local Similarity 67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aagaagaatgttgcttctatgtagatcactcaggagccatcagagactccatgaacaagc 2071
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                                                                                                                                                                                                                                                                                                                                                                                                         GCTGGTTTAATAAGTCCCCTTGGCTCACCACTCTCCTCTCCACTATAGCAGGACCTTTAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAAGAATGTTGTTTTATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCCAAAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAATAGAAGGGGATTAGACTTATTATTCCTTAAAGAAGGAGGACTCTGTGCTGCCTTAA 422
                                                                                                                                                                                                                                                                                                                              180
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131 c 128 g 211 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 167; Indels
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FEATURES
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                                                                                                                                                                                                                 Query Match
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                                                                                                    1574 acaggtggtgggcatgcaatactgggttaaccccctgtgtttccacctcagtcttcaacc 1633
1634 aatccaaagatttgtgtgtcatggtccaaatcgtcccccgagtgtactaccatcctgagg 1693
                                                       618 ACACAGTGTGAGCTTGCAATAACGGTCTCACTCCTTGTGTGTCTATGTCTGTTTTTAATA 559
                                                                                                                                                                                        Match 8.1%;
Local Similarity 63.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS
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AZ813042.1 GI:12982881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errc
Plate: 0080 row: E column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
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                                                                                                                                                                                                                                                                                                                  purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4
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/clone="UUGC2M0080E11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
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                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2114 accaggggtggtttgaaggatggttcaacaggttctctttggatgaccaccctgctttctg 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2054 gagactccatgaacaagcttagaaaaaagttagagaggcgtcgaaggggaaagagaggctg 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1934 tgtctgaagtggttctacagaaccggaggggattagatctgctgtttctaagagaaggtg 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2174 ctctgacggggcccctagtagtcctgctcctgt 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 CTATAGCAGGACCTTTAATTACACTTATGCTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAAGGATGGTTCGAAAGCTGGTTTAATAAGTCCCCCTTGGCTCACCACTCTCCTCCCA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTCTGTGCTGCCTTAAAAGAAGAATGTTGTTTTTTATGTTGACCATTCAGGAGTAATCA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99ttat9t9cagcettaaaagaatgattgcttctat9tagatcactcaggagccatca 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTCTGAAGTGGTGCTGCAAAATAGAAGGGGGATTAGACTTATTATTCCTTAAAGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATTGATCTTAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cagaagatctccgagccttaaaggagtctgttagcaacctagaagagtccctgacttctt 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTTAATTAAGACCCCCC------AATACTATGAAGAACTACGTGCAGCTATGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccctgatcacaggaccacagcagctagagaaaggacttggtgagctacatgcgggccatga 187:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAACTTTGGCAGTTCTATTAGGATTGGGAGTAGCAGCTGGAGTAGGTACAGGAACCGCTG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttaccctagctgtaatgctcggattagggacggccgttggcgtaggaacagggacagctg 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aagtggtccttgatgaatatgactatcggtataaccgaccaaaaagagaacccgtatccc 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCTTTTTAGATAAATTTGAACATCGG----GTCCGCTGGAAAAGAGAAACCCGTTACCT 442
                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0131 row: E column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            High quality sequence stop: 592
                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                           plasmid inserts
                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                     and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ836232 592 bp DNA GSS 20-FEB-2 2M0131E01F Mouse 10kb plasmid UUGCIM library Mus musculus clone_UUGC2M0131E01 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ836232.1 GI:13006140
                                       lass: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
2268 tgcagtccagatc 2280
                                                                                                                                                                                                                                                                                                                                                2028 ctatgtagatcactcaggagccatcagagactccatgaacaagcttagaaaaaagttaga
                                                                                                                                                                                                                                                                                                                                                                                                                                          1968 agatctgctgtttctaagagaaggtgggttatgtgcagccttaaaagagaatgttgctt 2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1908 caacctagaagagtccctgacttctttgtctgaagtggttctacagaaccgggaggggatt 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1728 ccgaccaaaaagagaacccgtatcccttaccctagctgtaatgctcggattagggacggc 1787
                                                                                                                                 442 CCCTTGGCTCACCACTCTCCTCCACTATAGCAGGACCTTTAATTACACTTATGCTTTT 501
                                                                                                                                                                                                                                                                                                                                                                                                                  262 AGACTTATTATTCCTTAAAGAAGGAGGACTCTGTGCTGCCTTAAAAGAGGAATGTCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 CAAATTAGAAGAATCTTTAACTTCCCTGTCCAAAGTGGTGCTGCAAAATAGAAGGGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ---TGAAGAACTACGTGCAGCTATGGATATTGATCTTAGAACTATAGAACAGTCTATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
                                                            acttacagttgggccttgcttaattaataggtttgttgcctttgttagagaacgagtgag 2267
                                       GCTTACTTTTGGCCCATGTATCCTTAATAAGTTAGTAGCTTTTATTAGAGAAAAGGATAAA 561
                                                                                                                                                            teettggatgaecaecetgetttetgetetgaeggggeecetagtagteetgeteetgtt 2207
                                                                                                                                                                                                                           TATACGTAAAAGAGAAAAGAGAAAGCCAACAAGGATGGTTTGAAAGCTGGTTTAATAAGTC
                                                                                                                                                                                                                                                                                                                     TTATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCTAAACTTAGAGAACGCCTAGA
                                                                                                                                                                                                                                                      9a9gcgtcgaagggaaagaggctgaccaggggtggtttgaaggatggttcaacaggtc 2147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acttggtgagctacatgcggccatgacagaagatctccgaggccttaaaggagtctgttag 1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyttygcytaggaacagygacagctyccctyatcacagyaccacagcagctagagaaagg 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCTGGAAAAGAGAACCCGTTACCTTAACTTTGGCAGTTCTATTAGGATTGGGAGTAGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTGGAGTAGGTACAGGAACTGCTGCCTTAATTAAGACCCCCCCAATACTA----- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. **

a 112 c 127 g 165 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0131E01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.9%;
65.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 234.6; DB 13;
Pred. No. 2.2e-40;
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321

Db 562 TGCAGTCCAAGTC 574

Search completed: February 23, 2002, 23:37:18 Job time: 9439 sec

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gb_est1:AW657531
gb_gss:AZ970955
gb_gss:BH059027
                                                                        gb_esr2:BF181106
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gb_gss:AZ64766
gb_esr2:BI106591
gb_esr2:BI158931
gb_gss:AZ989131
gb_gss:AZ349077
                                                                                                                                                                                                                                                             9b_9ss:AZ836232
9b_est2:BF608L55
9b_est1:BE56947
9b_est1:BE56947
9b_gss:AZ416306
9b_est2:BF159914
9b_gss:BH054319
9b_gss:BH054319
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gb_9ss: AZ642336
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gb_9ss: AZ741412
gb_9ss: AZ375836
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gb_gss:AZ356870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences: 11351937
Database length: 1077921985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query length: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search information block:
Query: US-09-171-553B-10
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                                                       gb_est2:BI082444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_gss:AZ376517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL=frame+_p2n.model -DEV-xlh
-Q=/cgn2_1/USPTO_spool/US9171553_frunat_22022002_122825_11137/app_query.fasta_1.3312
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-DELOP=6.000 -FAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR_SCORE=PCt
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR_SCORE=PCt
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2.6e-38
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2.1ae-46
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9.1e-46
1.0e-45
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6.7e-44
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AW657731 110922 MARC 1BOV BOS I AW657731 110922 MARC 1BOV BOS I AZ970955 2M0244HL6F MOUSE 10kb BH059027 RPCI-24-326G3.TJ RPCI-BH122287 RPCI-24-326G3.TJ RPCI-BH122287 RPCI-24-288P13.TJ RPCI-AZ850764 2M0152C18R MOUSE 10kb B1510666 9 602893272F1 NCI_CGAP_I AZ356870 1M0098F09F MOUSE 10kb AZ813049 1M0205M18F MOUSE 10kb AZ3763617 1M0130J20F MOUSE 10kb AZ3763617 1M0130J20F MOUSE 10kb AZ37936 1M0505M18F MOUSE 10kb AZ337993 1M0068F24R MOUSE 10kb AZ33993 1M0068F24R MOUSE 10kb AZ37936 1M0150F0KR MOUSE 10kb AZ375836 1M0129J20F MOUSE 10kb AZ375836 1M0129J20F MOUSE 10kb AZ49035 1M036P05R MOUSE 10kb AZ49035 1M036P05R MOUSE 10kb AZ49035 1M036P05R MOUSE 10kb AZ49935 1M036P05R MOUSE 10kb AZ4973847 RPCI-24-73L17.TJ RPCI-42379847 RPCI-24-73L17.TJ RPCI-42379847 RPCI-24-73L17.TJ RPCI-42379847 RPCI-24-73L17.TJ RPCI-4319847 RPCI-24-73L17.TJ RPCI-4319847 RPCI-24-398E11.TV RPCI-4316306 1M0131E01F MOUSE 9-day BE569478 601328494F1 NCI_CGAP_MAZ416306 1M0151041E MOUSE 10kb AZ416306 1M0151041E MOUSE 10kb AZ416306 1M0151041E MOUSE 10kb AZ416466 1M056P05F MOUSE 10kb AZ416466 1M0514J1EF MOUSE 10kb AZ416466 1M056P05F MOUSE 10kb AZ41646 1M056P05F MOUSE 10kb AZ41646 1M056P05F MOUSE 10kb AZ41646 1M056P05F MOUSE 10kb AZ41646 1M056P05F MOUSE 10kb AZ41648 1M056P05F MOUSE 10kb AZ41648 1M056P05F MOUSE 10kb AZ41648 1M056P05F MOUSE 10kb AZ41648 1M05
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                                                  2M0272E22F Mouse 10kb
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gb_gss:AZ887402
gb_gss:BH055839
gb_gss:AZ637496
306 nGlyAlaPheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerC
                                       BACKWARD: GTTTTCCCAGTCACGACG Plate: 94 row: E column: 1:
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Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett ,G.L., Haaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW657531 549 bp mRNA EST 110922 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e.\ Vector\ identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and -minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pooled"
/lab_host="DH10B"
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BF786434 602112966F1 NCI_CO
AZ887402 RPCI_24-176N10.TJ
BH055839 RPCI_24-93p15.TVB
AZ637496 1M0496123R Mouse
                                           52
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RPCI-24-93P16.TVB
1M0496123R Mouse
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FEATURES
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ORGANISM
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LOCUS AZ970955
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                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 leGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValVal 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 ySerArgAsnLysLeuThrLeuThrGluValSerGlyLysGlyThrCysI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrGluGinAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTr 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGGAAAAGCTCCCCCATCCCACCAACACCTTTGCAATAGTACTATGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluArgLysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpG1 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCAATCCAAAGATTTCTGTGTCATGGTCCAGCTCGTCCCCTGGGTACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGGGAAATTCAATGTGACCAAAGAGCATAGAAATCAATGTACATGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss:A2970955
                                                                                                                                                        84112,
Tel: 8
                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0244 row: H column: 16
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 754)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                             Mouse whole genome plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                High quality sequence stop: 754
                                      Class: plasmid ends
                                                                                                                                                                                                               University of Utah
                                                                                                                                                                                                                                                                                                                                ,M., Rose,M., Rose,R., and Wright,D.,Weiss,R.
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2M0244H16F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0244H16 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ970955
AZ970955.1 GI:13842182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nouse mouse
                                                                                                                                                                                                 308,
                                                                                                                                                                               USA
                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
Location/Qualifiers
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-171-553B-10 x AZ970955/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                   523 erLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPhe 539
                                                                                                                                                                                                                                                                                                                                                                                 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 TrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAs 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProLysArgGluProValSerLeuThrLeuAlaValMetLeuGlyLeuGl 473
:::|||||||||:::::|||||||||
TGGAGAAGAGACCCATTACCTTAACTTTGACAGTTCTATTAGGATTAGG 555
CCCTGTCCGAAGTGGTGCTACAGAATAGAAGGGGATTAGACTTATTATTC
                                                                                                                                                                                   pLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrS 523
                                                                                                                                                                                                                                                                                                                ln.GlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAs
                                                                                                                                                                                                                                                                                                                                                                          yThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yrHisProGluGluValValLeuAspGluTyrAspTyrArgTyrAsnArg 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGCTTGCAATACCGGTCTCATTCCTTGTGTGTCTATGTCTGATTTTAA 702
                                                                                                                             TCTTAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTT
                                                                                                                                                                                                                                                   AATACTAATGAA......GAACTACGTGCAGCTATGGATGTTGA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCATGATGATAGCTCCTTTTTAGACAAATTTGAGCATCGGGTC...CGC
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gblAFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         875.50
3.998
89.754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (female) was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptored DNA was purified and size-selected for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UUGC2M0244H16"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
3
67.213
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REFERENCE
AUTHORS
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                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuTh 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rValAspHisSerGlyAlaIleArgAspSerMetAsnLysLeuArgLysL 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGTACTAAGGCAACAATATCGGGTCCTT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetValLeuArgGlnGlnTyrGlnGlyLeu 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rGlyProLeuValValLeuLeuLeuLeuThrValGlyProCysLeuI 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTGGTTTAATAAGTCCCCCTTGGCTCACCACTCTCCTCCTCCACCATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCCAAACTTAGAGAAC 267
                                                                                                                                                                                                                                                                                     Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 326 row: G column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH059027 882 bp DNA GSS 18-JUL-2001
RPCI-24-326G3.TJ RPCI-24 Mus musculus genomic clone RPCI-24-326G3,
                                                                                                                                                                                                                                           Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Other_GSSs: RPCI-24-326G3.TV
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Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao,S., Nierman,W., Malek,J., Shatsman,S., A)
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
l (bases 1 to 882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nouse mouse
                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-326G3"
                                               /clone_lib="RPCI-24"
/sex="Male"
                                                                                                                                                                                              Location/Qualifiers
1. .882
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                                                                                                                                                                     /organism="Mus musculus'
                         type="Spleen/Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shatsman, S., Akinret, B., Levins, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gebregeorgis, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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     633 AATCTGTTGATGCATTAGAGAAATCCTTGACGTCCCTGTCAGAAGTAGTA
                                                                                                                                                                                                                                                                                          493
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SOURCE

VERSION

COMMENT

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alignment_block:
US-09-171-553B-10 x BH059027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 lyLeuThrProCysValSerThrSerValPheAsnGlnSerLysAspLeu 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 roProTyrTyrGluGlyMetAlaLysGluArgLysPheAsnValThrLys 347
542 GGAATGGGTTTAGCAGCCTTGGTTGAGGGTAGACAAGGAATTCACACCTT 591
                                                                                                                                                                                                                                                                                                                                                                462 alSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyVal 478
                                                                                                                                                                                                                                                                                                                                                                                                                   449 CCTGGAAGATGAATATATCAGTAAG.....AAGTTGAAAAGAGATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 lValLeuAspGluTyrAspTyrArgTyrAsnArgProLysArgGluProV 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 CysValMetValGlnIleValProArgValTyrTyrHisProGluGluVa 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 CAACTATTACCTTGTGCCATATCCAGTTGGTTGGTGGGCCTGTAACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 uAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAlaCysAsnThrG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 CCCACCAACACCTATGTGGTCGGACTTAATTCTGTATCCAGGACAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 rThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GlyGlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSe
                                                                                     592 CTTAAGAGAA......GCTATAAATGAAGATTTAAGCATGCTACAAA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGGCANAGACTGTTCAACCTGATTAGAGGAGCCTTTTATGCCCTTAACAG
                                                                                                                                                                                                                                                    GlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTCACCCCATGTGTATCAACTAGTGTCTTTGACCCCTCTGGTGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erHisGlnHisLeuCysTyrSerThr.ValValTyrGluGlnAlaSerGl 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAAGTGTCAGGAGCAGCCCTTGTCTCTGTACAGGGACACCTCCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGGATCCAGATGCCACTACATACTGCTGGTTATTCCTATCATCAGGCC
                                                                                                                                       yLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysG 512
                                                                                                                                                                                                                                                                                                            TCTCCATTACTCTAGCTATGTTAATGGGGGTCGGTCTTACAGA.GGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTATCATGGTTCATCTTCTATCTCGCATGTATTATTATCCTGCCTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            859.50
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JOURNAL
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                          COUNT
                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               595 rProTrpMetThrThrLeuLeuSer 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         783 TAGTCAGAGATTCTATGCAGAAATTGAGGGAAAGACTGGAAAGGGAA...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTGCAGCCTTAAAAGAAGAATGCTGCTTCTATGCAGACCACACGGGAA 782
                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 288 row: P column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel:
Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Nierman, W., Malek, J., Shatsman, S., Ak
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_GSSs: RPCI-24-288P13.TV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 774)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
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                        221
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301 838 0208
                                                                                                                                                                                                                                                                                                                                                                           BAC ends
                     a
                                                         /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                  BamH1 sites
DNA."
                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="RPCI-24-288P13"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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alignment_block:
US-09-171-553B-10 x BH122287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 rCysIleGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 alValTyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsn
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                                                                                                                                                                                                  PheTyrValAspHisSerGlyAlaIleArgAspSerMetAsnLysLeuAr 571
                                                                                                                                                                                                                                                                                                                                                                            uThrSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuL 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluAspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLe
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                                                                                                                                                                                                                                                                                         euPheLeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCys 554
                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGATCTTAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTT
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TCGAAAGCTGGGTTAATAAGTCCCCTTGGCTCACCACTCTTCTCTCCACC
                                         heGluGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAla 604
                                                                                       AGAACGCCTAGATATACGTGAAAGAGAAATAGAAAGCCAACAAGGATGGT
                                                                                                                              gLysLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyTrpP 588
                                                                                                                                                                           TTTTATGTTGACCATTCATGAGTAATCAAAGATTCTATGGCCAAACTTAG
                                                                                                                                                                                                                                                                  TATTCCTTAAAGAACGAGGACTCTGTGCTGCCCTAAAAGAAGAATGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt lyProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ... CGCTGGAGAAGAGCCCCGTTACCTTAACTTTGGCAGTTCTATTAGG
                                                                                                                                                                                                                                                                                                                                                       AACTTCCCTGTCCGAAGTGGTGCTACAAAATAGAAGGGGATTAGACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGTATCATGATGATAGCGCCTTTTTAGACAAATTTGAGCATCGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgTrpTrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
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LeuThrGlyProLeuValValLeuLeuLeuLeuLeu

ATAGCAGGACCTTTGATTACTCTTATGCTTTTGCTT 772

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COMMENT
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                                                                                                                                                                                                                                                                                ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                       BASE COUNT
    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rm. 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ351242 701 bp DNA GSS 29-SEP-2000 1M0089L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0089 row: L_column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 701) Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Duval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone UUGC1M0089L09 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                           מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732.114 gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                           adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."

149 c 134 g 206 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UUGC1M0089L09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
    89.316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                            814.00
                                                . 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sheared, adaptored mouse DNA was annealed to
Percent Identity: 67.521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
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alignment_block: us-09-171-553B-10 \times Az351242/rev
                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est2:BI151181
                                                                                                                                                        ACCESSION
                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                       KEYWORDS
                                                                                                                        VERSION
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                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 ValSerThrSerValPheAsnGlnSerLysAspLeuCysValMetValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550 LysGluGluCysCysPheTyrValAspHisSerGlyAlaIleArgAspSe 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 nLeuGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnArgA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 uAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrGlyThrA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 TTGAGCATCGGGTC...CGCTGGAGAAGAGAACCCGTTACCCTTAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 yrAspTyrArgTyrAsnArgProLysArgGluProValSer.LeuThrLe 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 nIleValProArgValTyrTyrHisProGluGluValValLeuAspGluT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    700 GTGTCTATGTCTGTTTTTAATAGTTCCAAAGATTTCTGCATTTTGGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 rMetAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArgGluA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 ATTAGAAGAATCTTTAACTTCCCTGTCCGAAGTGGTGCTACAGAATAGAA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 CTGCCTTAATTAAGACCCCCCAATACTATGAA......GAACTA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 laAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeu 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 GGCAGTTCTATTAGGATTGGGAGTAGCGGTTGGAGTAGGTACAGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 uThrValGlyProCysLeuIleAsnArgPheValAlaPheValArgGluA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 ThrLeuLeuSerAlaLeuThrGlyProLeuValValLeuLeuLeuLeuLe 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 GCCAACAAGGATGGTTCGAAAGCTGGTTTAATAAGTCCCCCTTGGCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGATTAGACTTATTCCTTAAA...GGAGGACTCTGTGCTGCCCTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAlaLeu 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            rgValSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGlyLeu 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTTTTGGCCCCTGCATCCTTAATAAGTTAGTAGCTTTTATTAGAGAAA
                                                                                                                                                                                                            602916935F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5067273 5',
                                                                                                                    BI151181.1 GI:14611182
                                                                                                                                                                               mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                             Mus musculus
                                                          house mouse.
                                                                                                                                                                                                                                                   845 bp
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alignment_block:
US-09-171-553B-10 x BI151181
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423 nGlnSerLysAspLeuCysValMetValGlnIleValProArgValTyrT
                                                                                                                                                                                                                                                                                                                  373 eGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrValValT 390
                                                                                                                                                                                                                                                                                                                                                                                                                         359 AsnLysLeuThrLeuThrGluValSerGlyLys......GlyThrCysIl 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 ysPheAsnValThrLysGluHisArgAsnGlnCysThrTrpGlySerArg 358
                                                                                                                                                                                                              390 yrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrp 406
                                                                                                                                                                                                                                                                                                                                                                            149 CAAAAACTGACCCTGACTGAAGTATCCGCGAGGAATCCAGGTCTCTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 ATTTCAACAGAACCAGCAGCCAT...ACTTCCTGCTCTTGGGGTACAGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 uCysLeuSerSerGlyProProTyrTyrGluGlyMetAlaLysGluArgL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 PheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTrpLe 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TTTTATGCCCTTAACAGAACTGATCCAAGCGCTACTGAGGACTGCTGGCT
                                                                                   TrpAlaCysAsnThrGlyLeuThrProCysValSerThrSerValPheAs 423
                                                                                                                                                              TGTCCAGAACGGAAGCTAATTACTATCTTGTACCTTCCCCGGTTGGATGG
                                                                                                                                                                                                                                                                     AGGTACCCCACCTTCCACTCACAAACACCTATGCGGACAAATTCAGTCCG 248
                                                    TGGGCTTGCAATACAGGACTTACTCCCTGTGTATCAACTAAGGTTTTTAA
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 845)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"

a 188 c 216 g 215 t 1 others
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79.861
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/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="MAGE:5067273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
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Percent Identity: 58.333
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VERSION
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                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCAGATCATACAGGAATAGTTAGAAGACTCTATGCCGAAACTGAGGAG 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ850764 641 bp DNA GSS 21-FEB-2001 2M0152C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0152C18 R, DNA sequence.
AZ850764
                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                 University of Utah Genome Center University of Utah
                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                     plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 TTGAGCATCGGGTC...CGCTGGAGAAGAGAACCCGTTACCTTAACTTTG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 nIleValProArgValTyrTyrHisProGluGluValValLeuAspGluT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 GTGTCTATGTCTGTTTTTAATAGTTCCAAAGATTTCTGCATTTTGGTTCA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 ValSerThrSerValPheAsnGlnSerLysAspLeuCysValMetValGl 433
                                                                                                                                                                                                                                                                                                                                               483 aAlaLeuIleThrGlyProGlnGlnLeuGluLysGlyLeuGlyGluLeuH 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450 yrAspTyrArgTyrAsnArgProLysArgGluProValSerLeuThrLeu 466
                                                                  517 LeuGluGluSerLeuThrSerLeuSerGluValValLeuGlnAsnArgAr 533
TTAGAAGAATCTTTAACTTCCCTGTCCGAAGTGTTGCTACAGAATAGAAG
                                                                                                                                    GTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTATAACCAAA 355
                                                                                                                                                                                                      isAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValSerAsn 516
                                                                                                                                                                                                                                                                            TGCCTTAATTAAGACCCCCCAATACTATGAA......GAACTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGTTCTATTAGGATTGGGAGTAGCGGCTGGAGTAGGTACAGGAACCGC 443
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Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with according the content of the derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. "
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3.951
89.450
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/clone="UUGC2M0152C18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACACAGGAAACAGCTATGACC
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seq_name: gb_gss:AZ813042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAACAAGGATGGTTCGAAAGCTGGTTTAATAAGTTCCCTTGGCTCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ813042 625 bp DNA GSS 20-FEB-22M0080E11F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC2M0080E11 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 625)
                                                                                                                                                                                                                            High quality sequence stop: 625
                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                    Insert Length: 10000 Std Error: Plate: 0080 row: E column: 11 Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A.
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                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                           /organism="Mus musculus
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                        /sex="Male"
                                                                                        /clone="UUGC2M0080E11"
                                                                                                                                                                                                        Locati
/note="Vector: PWD42nv; Purified genomic
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                     . 625
                                                                                                                                                                                                      on/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                    Std Error: 0.00
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                                                         172 GACCATTCAGGAGTAATCAAAGATTCTATGGCTAAACTTAGAGAACGCTT 123
574 uGluArgArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyT
                                                                                         558 ASPHisSerGlyAlaIleArgAspSerMetAsnLysLeuArgLysLysLe 574
                                                                                                                                                                                                 541 rgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrVal 557
                                                                                                                                                                     222 AAGAAGGAGGACTCTGTGCTGCCTTAAAAGAAGAATGTTGTTTTATGTT
                                                                                                                                                                                                                                                                                272 GTCTGAAGTGGTGCTGCAAAATAGAAGGGGATTAGACTTATTATTCCTTA 223
                                                                                                                                                                                                                                                                                                             524 uSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuA 541
                                                                                                                                                                                                                                                                                                                                                                                              322 AGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557 TTCTAAAGATTTCTGCATTTTGGTTCAGCTTATTCCCAGACTCTTGTATC
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ORIGIN BASE COUNT

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AUTHORS
                                                                                                                                                                                                              US-09-171-553B-10 x BI106669
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                         315 rAspProAspAlaThrSerSerCysTrpLeuCysLeuSerSerGlyProP 332
                                                                                                            299 GlnArgLeuPheSerLeuIleGlnGlyAlaPheGlnAlaIleAsnSerTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                          4 CAGAGGATGTTTAACCTAGTGAGAGGAGCCTTTTATGCCCCTTAACAGAAC
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CCTTTAATTACACTTATGCTT 2
                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1105 row: p column: 17
High quality sequence stop: 805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI106669 921 bp mRNA EST 26-JUN-2001 602893272F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5038336 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 921)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
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                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                      to: BI106669
                                                                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 211 c 229 g 232 t
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3.181
78.289
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Stem cell origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="CZECH II (feral)"
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/clone="IMAGE:5038336"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Lu29"
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Gaps: 10
Percent Identity: 53.947
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SOURCE ORGANISM VERSION KEYWORDS

Mus musculus house mouse

AZ356870.1 GI:10470556 GSS.

clone UUGC1M0098F09 F, DNA sequence

1M0098F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

GSS

02-OCT-2000

DEFINITION LOCUS

AZ356870

644 bp

ACCESSION

REFERENCE

Mammalia; Eutheria; l (bases 1 to 644)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Murinae; Mus

AUTHORS

COMMENT

University of Utah University of Utah Unpublished (2000) Contact: Robert B. plasmid inserts

Genome Center Weiss

308,

Biomedical

Polymers Research Bldg.,

20

S. 2030 E.,

SLC, ŢD JOURNAL

Mouse whole genome scaffolding with paired end reads from 10kb Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R. Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.

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833
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GA 884
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                                                                                   AACACGGGAACCGGATGCCCAACGGGGTAGCTGAGTCGGGTTTGAATCCA 882
                                                                                                                     .ArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPheAsnA 594
                                                                                                                                                                       TAGTTAGAGACTCCTATGCAGAACCTGGACAGAACGATTTCAAGCGAAGG
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FEATURES

Class: plasmid ends

quality sequence stop: 644

Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: Plate: 0098 row: F column: 09 Seg primer: CGTTGTAAAACGACGGCCAGT

Std Error: 0.00

Tel: 801 585 5606 Fax: 801 585 7177 84112, USA

source

. 644

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alignment_block:
                                                                                                                              BASE COUNT
ORIGIN
                                                                                           alignment_scores:
                      US-09-171-553B-10 x AZ356870/rev
Align seg 1/1 to reverse of: AZ356870
                                                         Percent Similarity:
                                                                               Quality:
                                                                    Ratio:
                                                        3.866
88.372
                                                                               734.50
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                                                                                                                                        133 g
 from: 1
                                                        215
2
66.512
to:
 644
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185

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136 c

190 t

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

purified. The sheared, adaptored mouse DNA was annealed to

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and continued the shared adaptors to the insert adaptors.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/).

The DNA

/note="Vector: PWD42nv; Purified genomic DNA from M.

'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/sex="Male"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/clone="UUGC1M0098F09" /db_xref="taxon:10090" /strain="C57BL/6J" organism="Mus musculus" location/Qualifiers

seq_documentation_block: seq_name: gb_gss:AZ356870

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seq_name: gb_gss:AZ376517
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    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 GAGAAGAGAACCCGTTACCTTAACTTTGGCAGTTTA.TTAGGATTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeu 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGATATACGTAAAAGAGAAAGAGAAAGCCAACAAGGATGGTTCGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGAACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGATGATAGCTCCTTTTTAGACAAATTTGAGCATCGGGTC...CGCTG
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                                                                                                                                                                                                                                                                                                                              AZ376517 610 bp DNA GSS 02-OCT-2000 1M0130J20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0130J20 F, DNA sequence.
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 610)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                         GSS.
Unpublished (2000)
                                            Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                     Mus musculus
                      plasmid inserts
                                                                       and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                 house mouse.
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 ValGlnIleValProArgValTyrTyrHisProGluGluValValLeuAs 448
                                                                                                                                                                                                                                                          465 hrLeuAlaValMetLeuGlyLeuGlyThrAlaValGlyValGlyThrGly 481
                                                                                                                                                                                                                                                                                                                   558 CAGATTTGAGCATCGGGTC...CGCTGGAGAAGAGAGCCCCGTTACCTTAA 512
                                                                                                                                                                                                                                                                                                                                                                     448 pGluTyrAspTyrArgTyrAsnArgProLysArgGluProValSerLeuT 465
                                                                                                                                                                                                                                                                                                                                                                                                                              608 GTTCAGCTTATTCCTAGACTCCTGTATCATGATGATAGCTCCTTTTTAGA 559
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uLeuHisAlaAlaMetThrGluAspLeuArgAlaLeuLysGluSerValS 515
                                                                                                                    ThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluLySGlyLeuGlyGl 498
                                                                                                                                                                                                 ACCGCTGCCTTAATTAAGACCCCCCAATACTATGAA......GA 424
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 10000 Std E
Plate: 0130 row: J column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored vector DNA, and transformed into chemically-competent E. coli Xx10-Gold (Stratagene) cells and selected for ampicillin resistance."

131 c 120 g 182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730.50
3.970
90.196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0130J20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCACTCTCCTCCACCATAGCAGGACCTTTGATTACACTTATGCTTT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spSerMetAsnLysLeuArgLysLysLeuGluArgArgArgArgGluArg 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAl 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tThrThrLeuLeuSerAlaLeuThrGlyProLeuValValLeuLeuLeuL 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAGGGGATTAGACTTATTATTCCTTAAAGAAGGAGGACTCTGTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ430249 591 bp DNA GSS 03-OCT-2000 1M0214G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0214G11 R, DNA sequence.
                                                                                                           Class: plasmid ends
High quality sequence stop: 591
                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0214 row: G column: 11
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 591)
                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
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                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg.,
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reilly
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alignment_block: US-09-171-553B-10 \times AZ430249/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 uGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGlyP 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     588 CGCTGGAAAAGAGAACCCGTTACCTTAACTTTGGCAGTTTTATTAGGATT
589 luGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeu 605
                                                                                                                                                                                                               572 sLysLeuGluArgArgArgArgGluArgGluAlaAspGlnGlyTrpPheG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 ArgProLysArgGluProValSerLeuThrLeuAlaValMetLeuGlyLe 472
                                                                                                                                                                                                                                                                                                                                                                                                                    TyrValAspHisSerGlyAlaIleArgAspSerMetAsnLysLeuArgLy 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heLeuArgGluGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPhe 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rSerLeuSerGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuP 539
                                                                                                                                                                                                                                                                                                                                                         TATGTTGACCATTCAGGAGTAATCAAAGATTCTATGGCTAAACTTAAAGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTTAAAGAAGGAGGACTCTGTGCTCCCTTAAAAAGAAGAATGTTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCCTATCCGAAGTGGTGCTGCAAAATAGAAGGGGGGTTAGACTTATTAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATCTTAGAACCATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspLeuArgAlaLeuLysGluSerValSerAsnLeuGluGluSerLeuTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptor of passage to the sheared adaptor of the passage of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.096
91.753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leMetValLeuArgGlnGlnTyrGlnGlyLeu 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 0505 row: M column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ642336 624 bp DNA GSS 1M0505M18F Mouse 10kb plasmid UUGC1M library clone UUGC1M0505M18 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Wright, D., Weiss, R. Mouse whole genome sca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B.
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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801 585 7177
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remath: 10000 Std Error: 0.00
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                        with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                         polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
   chemically-competent E. coli XL10-Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UUGC1M0505M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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   (Stratagene) cells
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   KEYWORDS
SOURCE
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US-09-171-553B-10 x AZ642336
                                                                                       ACCESSION
                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                         644 lnGlnTyrGlnGlyLeuLeuSerGlnGlyGluThrAspLeu 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 yValGlyThrGlyThrAlaAlaLeuIleThrGlyProGlnGlnLeuGluL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 lAlaPheValArgGluArgValSerAlaValGlnIleMetValLeuArgG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 ValLeuLeuLeuLeuThrValGlyProCysLeuIleAsnArgPheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         594 rgSerProTrpMetThrThrLeuLeuSerAlaLeuThrGlyProLeuVal 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 TAAAAGAGAAAGGAAAGCCAACAAGGATGGTTTGAAAGCTGGTTTAATA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 GlyAlaIleArgAspSerMetAsnLysLeuArgLysLysLeuGluArgAr 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 lyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAspHisSer 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 lValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 GAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCCTGTCCGAAGT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 LysGluSerValSerAsnLeuGluGluSerLeuThrSerLeuSerGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 ProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAlaValGl 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CCCGTTACCTTAACTTTGGCAGTTCTATTAGGATTGGGAGTAGCAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gArgArgGluArgGluAlaAspGlnGlyTrpPheGluGlyTrpPheAsnA 594
|:::||||||||||||:::::||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTAATCAAAGATTCTATGGCTAAACTTAGAGAACGCCTAGATATACG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArgAlaLeu 510
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTTTTATTAGAGAAAGGATAAACGCAGTCCAAGTTATGGTCCTAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACTTATGCTTTGCTTTTGGCCCATGCATCCTTAATAAGTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTCCCCTTGGCTCACCACTCTCCTCTCCACTATAGCAGGACCTTTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCTGTGCTTGAAAAGAAGAATGTTGTTTTTTTGTTGACCATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGCTGCAAAATAGAAGGGGATTAGACTTATTATTCCTTAAAGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTAGGTACAGGAACCGCTGCCTTAATTAAGACCCCCCAATACTATGAA.
                                                                                                                                                                                                                                                                                                                     AACAATATCGG....GTCCTTCAGGAGGTTGAAAACTCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
GSS.
house mouse
                                                      AZ337993.1 GI:10410826
                                                                                                         1m0068F24R mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1m0068F24 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....GAACTACGTGCAGCTATGGATATTGATCTTAGAACTATA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 a
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3.964
92.386
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a 116 c 131 g 174 t
                                                                                                                                                                           673 bp
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527

JOURNAL COMMENT

308,

TITLE

FEATURES

source

490

540

29-SEP-2000

genomic

440

627

ACCESSION VERSION

AZ642336

DEFINITION

SOURCE

KEYWORDS ORGANISM

REFERENCE

AUTHORS

seq_name:

100

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                               US-09-171-553B-10 x AZ337993
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                Align seg 1/1 to: AZ337993 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                          421 ValPheAsnGlnSerLysAspLeuCysValMetValGlnIleValProAr 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                            437 gValTyrTyrHisProGluGluValValLeuAspGluTyrAspTyrArgT 454
                                                                                                1 GTTTTTAATTCATCTCATGATTTTTGTGTCATGATCCAGCTGTTACCCCG
CGTATATTATCACCCTGCATCCAGTTTA....GAAGAAAGCTATGCTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            punn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 673)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     801 585 5606
801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNAV2 (gil4732114 gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                     721.50
3.607
87.719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UUGC1M0068F24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 673
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                                                                                                                                                                                                                                                                                                     Length: 228
Gaps: 3
Percent Identity: 58.772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Std Error: 0.00
                                                                                                                                                                                                to: 673
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ACCESSION
VERSION
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LOCUS AZ814037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                JOURNAL
                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                          AUTHORS
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University of Utah

University of Utah
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 632)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
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                                                                                                         plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone UUGC2M0081N06 R, DNA sequence.
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542 luGlyGlyLeuCysAlaAlaLeuLysGluGluCysCysPheTyrValAsp 558
                                                                              525 rGluValValLeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgG 542
                                                                                                                                                          141 ACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAACTTCCCTGTC 190
                                                                                                                                                                                                                                                                                               492 euGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArg 508
                                                                                                                                                                                                                                                                                                                                                                        509 AlaLeuLysGluSerValSerAsnLeuGluGluSerLeuThrSerLeuSe 525
                                                                                                                                                                                                                                                                    103 ATGAA.....GAACTACGTGCAGCTATGGATGTTGATCTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 ArgGluProValSerLeuThrLeuAlaValMetLeuGlyLeuGlyThrAl 475
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                                                        CGAAGTGGTGCTACAGAATAGAAGGGGATTAGACTTATTATTCCTTAAAG
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Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: N column: 06
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 632.
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWN42 (gil4732114 jgb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0081N06"
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length: 2000000000
  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                           11351937 seqs, 5372889281 residues
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. 1 2 3 4 4 5	Score 18.4 18.4 18.4 18.4 18.4	Query Match 92.0 92.0 92.0 92.0 92.0 92.0	Length DB 391 429 11 435 1 444 11 448 1 510 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	DB 11 10 110 110 110 110 110 110 110 110	ID BF465634 AA797871 BF565386 AA472060 BF719561 AA033199 AC512916	Description BF465634 U AA797871 v BF565386 U AA472060 v BF719561 m AA033199 m AA033199 m
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ω	18.4	92.0	435	11	BF565386	BF56
4	18.4	92.0	444	10	AA472060	AA47
Ŋ	18.4	92.0	488	11	BF719561	BF719
0	18.4	92.0	510	10	AA033199	AA033
c 7	18.4	92.0	539	13	AQ512916	AQ512
ი 8	18.4	92.0	566	10	AA121599	AA121599
	18.4	92.0	571	10	BE097309	BE097309
c 10	18.4	92.0	592	10	AW556515	AW556515
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AZ453887 1M0255N03 AZ457973 1M0261A07	1186	272	AI102103 EST211392	AZ951110 2M0215M20	A2730616 BBCT-24-1	BE650111 UI-M-BH3-	BE586605 WHE0509_G	AQ456957 HS_5151_A	AZ582584 1M0376003	BF554951 UI-R-E0-c	AA170346 ms88g09.r	BF549019 UI-R-A0-a	AQ902607 LMAJFV1_1	AV228430 AV228430	AA478651 zv19c05.r	вв362510 вв362510	T25876 ESTDIR3 CD3	BG256691 602370880	BE612516 601452020	AI735229 at08a01.x	BH051324 RPCI-24-3	W20084 zb40f01.rl	AZ777840 2M0012D10	AI013028 EST207479	AW489995 UI-M-BH3-	1921	AK019522 Mus muscu		вG075579 H3149A02-

ALIGNMENTS

LOCUS

VERSION KEYWORDS SOURCE RESULT BF465634 FEATURES COMMENT REFERENCE ACCESSION DEFINITION MEDLINE JOURNAL TITLE AUTHORS ORGANISM Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, BF465634 391 bp mRNA EST 04-DEC-2000 UI-M-CG0p-bql-h-12-0-UI.S1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bql-h-12-0-UI 3', mRNA sequence. Seq primer: M13 Forward POLYA=No. Tel: 301 443 1706 Fax: 301 443 9890 Genome Res. 6 (9), 97044477 discovery Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 391) Mus musculus EST BF465634.1 GI:11534817 BF465634 20892-9643, USA Normalization and subtraction: two approaches Bonaldo, M.F., Lennon, G. and Soares, M.B. house mouse. Location/Qualifiers 791-806 (1996) to facilitate gene Euteleostomi; Murinae; Mus. M

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gatggctctcctgccctttg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vw31h06.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1245467 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 429)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA797871.1 GI:2860826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:659155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov) for further information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop:
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/organism="Mus musculus"
/strain="0.57BL/6J"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-bql-h-12-0-UI"
/clone="UI-M-CG0p-bql-h-12-0-UI"
/clone="UI-M-CG0p-bql-h-12-0-UI"
/clone="UI-M-CG0p-bql-h-12-0-UI"
/clone="UI-BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/lab_
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100 c 123 g
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TMAGE:1245467"
                                                                                  /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                      /clone_lib="Soares_mammary_gland_NbMMG"
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Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gatggctctcctgccctttg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1798920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF565386 435 bp mRNA EST 12-DEC-2000 UI-R-BO1-ajv-e-06-0-UI.rl UI-R-BO1 Rattus norvegicus cDNA clone UI-R-BO1-ajv-e-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus
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derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"
                                                                                            hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was
                                                                                                                                                               /lab_host="DH10B (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site=1: Not I; Site=2: Eco RI; The library (UI-R-BO1) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Ronaldo "
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                                                                                                                                                                                                                                                                                                                  /clone="UI-R-BO1-ajv-e-06-0-UI"
/clone_lib="UI-R-BO1"
                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                            /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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95.0%;
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s (Pharmacia), digested with Not I and cloned into
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Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
Contact: Warra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA472060
AA472060.1 GI:2200051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:513377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
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                                                                                                                              constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                              T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
                                                                                                                                                                                                                                                                                                        /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:873897"
                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mammary gland"
/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_mammary_gland_NbMMG"
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Pred. No. 4.4e+02;
Score 18.4; DB 10;
Pred. No. 4.4e+02;
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mi36d04.rl Soares mouse
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (Dases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                         l Similarity
19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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IMAGE:3972947 5' similar to SW:BR14_HUMAN P55201 PEREGRIN ;, mRNA
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Librar
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                                                     AQ512916 539 bp DNA GSS 0
HS_5139_A2_B09_T7A RPCI-11 Human Male BAC Library H
genomic clone Plate=715 Col=18 Row=C, DNA sequence.
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AQ512916.1 GI:4745207
GSS.
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Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                     Similarity
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dul
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morrits,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone IMAGE:465607 5' similar to PTR:JC2069 JC2069 zinc-finger protein, BR140 - human ;, mRNA sequence. AA033199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. \mbox{\sc "}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10000"
/clone="IMAGE:465607"
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95.0%;
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Pred. No. 4.5e+02;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 566)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                          human
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EST.
                                                                                                                                                                                                                                                                                                                                                       zn78a06.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
cDNA clone IMAGE:564274 5', mRNA sequence.
                                                                                                                                                                                                                                Homo sapiens
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7
Class: BAC ends
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Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
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. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECORI Methylase. Size selected DNA was cloned pBACe3.6 vector at ECORI sites" a 179 c 99 g 108 t 6 others
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/clone="plate=715 Col=18 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mscares@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28HJ sev2 from Amersham High quality sequence stop: 439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE097309 571 bp mRNA EST 12-JUN-2000 UI-R-BOl-apv-g-12-0-UI.sl UI-R-BOl Rattus norvegicus cDNA clone UI-R-BOl-apv-g-12-0-UI 3', mRNA sequence.
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Fax: 319 335 9565
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                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%; Score 18.4; DB 10; Length 566; 95.0%; Pred. No. 4.5e+02; Live 0; Mismatches 1; Indels 0
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Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                   Email: est@watson.wustl.edu
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                                                         Contact: Wilson RK
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Best Local Similarity 95.08
Matches 19; Conservative
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                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 592)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H. Genome-wide expression profilling of mid-gestation placenta and minroarray.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
normalized medulla library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L0269D06-3 NIA Mouse Newborn Ovary CDNA Library Mus musculus CDNA
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
20381348
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                                                                                                                                                                                                                                 /clone="UI-R-BO1-apv-g-12-0-UI"
/clone_lib="UI-R-BO1"
                                                                                                                                                                 /organism="Rattus norvegicus"
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AW556515
                                                                                                                                                                                       /strain="Sprague-Dawley/db_xref="taxon:10116"
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Seg primer: -21M13 Forward
High quality sequence stop: 592
                                                                                                                     Location/Qualifiers
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                                              Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=GAACCG'
152 c 13
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The sequence contained an oligo-dT track that was present in the oligourcleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library or Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
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                                   /clone="L0269D06"
/clone_lib="NIA Mouse Newborn Ovary cDNA Library"
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Mational Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 18.4; DB 10; Length 592; 95.0%; Pred. No. 4.5e+02; 1ve 0; Mismatches 1; Indels 0
                                                                                            /dev_stage="Newborn Ovary"
/lab_host="DH10B"
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                     /db_xref="taxon:10090"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mEST@mail.nih.gov
                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 GATGGCTCTTCCTTTG 492
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Best Local Similarity 95.0°
Matches 19; Conservative
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TTel: 301 443 1706
Fax: 301 443 9890
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AW488316/c
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BEST 21-JUL-2000 659 bp mRNA EST 21-JUL-2000 601227645FI NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3585899 5', BE374286
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements Seg primer: M13 Forward POLYA-Yes.
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/clone_lib="NIH_BMAP_M_S4"
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                                                                                                                     /organism="Mus musculus"
                                                                                                                                                  /db_xref="taxon:10090"
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TAG_SEQ=GACTC"
166 c 143 q
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
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                                                                                        /lab_host="DH10B"
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333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Seq primer: -21M13 Forward
High quality sequence stop: 690
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Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM8746 row: j column: 12
High quality sequence stop: 586.
Location/Qualifiers
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               Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                              /strain="FVB/N"
/db_zref="asxon:10090"
/clone="IMAGE:3585899"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH108"
  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                      1. .659
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="H3149A02"
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Laboratory of Genetics
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/lab_lost="Vector: pspor: Site_1: Sal1; Site_2: NotI: This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with oligo(dT).Not primers. References include: (1) Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U. S. A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse develolpment, 2000, Development, 127: 1777-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5 day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
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Plate: LLAM10318 row: p column: 23
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Shibata, K., Itoh, M., Aizawa, K., Kitsunai, T., Tashiro, H., Ttoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tranaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Punctional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
5 (bases I to 2171)
5 (bases I to 2171)
Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Honana, K., Ishi, Y., Itoh, M., Izawa, M., Rato, H., Rawai, J., Konno, H., Rouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Rouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, H., Salto, H., Salto, H., Salto, R., Sakai, K., Sano, H., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
ItOh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome research. 10 (10), 1617-1630 (2000)
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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                            Average insert size 3.3 kb. Library enriched for full.length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

259 c 228 g 166 t
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
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Encount library was prepared and sequenced in Mouse Genome Encoclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5 GAOGAGGAAGAGCACTTTTTTTTTTTTTTTTTTYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to adapter of sequence [5'
                                                                                               Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 330-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="head"
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<1. 1477
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DSESSSSSSSSAASDRTSTTPSKQGRGKPSFSRGTFPEDSSEDTSGTENEAYSVGTGR
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QRETGRDGPERHGPSGRGNLTPHPAACDKDGQTDSAAEESSSQETSKGLGPNMSSTPA
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HGVP1PVPPLEVLKLGEQMTQEAREHLYLVLFFDNKRTWQMLPRTKLVPLGVNQDLDK
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
Yoshida,K., Yoshido,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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95.0%; Pred. No. 4.9e+02;
tive 0; Mismatches 1;
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Search completed: February 23, 2002, 23:37:21

Job time: 9442 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BI360879 388957 MA			BH097469 RPCI-24-3	AW346676 29231 MAR	AW346655 29171 MAR	AV312947 AV312947	AV289929 AV289929	BI184980 UNIP-FN-	AZ113096 RPCI-23-4	BF713588 MT-P-02-a	BT184279 INIP-FN-
SUMMARIES	ID	BI360879	AZ056887	AZ749422	BH097469	AW346676	AW346655	AV312947	AV289929	BI184980	AZ113096	BF713588	BI184279
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	Length	558	323	559	655	155	166	232	254	261	290	294	300
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13 16.4 91.1 370 15 16.4 91.1 379 16 16.4 91.1 379 17 16.4 91.1 425 18 16.4 91.1 428 20 16.4 91.1 458 21 16.4 91.1 468 22 16.4 91.1 468 23 16.4 91.1 470 24 16.4 91.1 470 25 16.4 91.1 553 26 16.4 91.1 573 27 16.4 91.1 573 30 16.4 91.1 573 31 16.4 91.1 573 32 16.4 91.1 573 31 16.4 91.1 602 32 16.4 91.1 602 33 16.4 91.1 613 34 16.4 91.1 622 35 16.4 91.1 622 36 16.4 91.1 622 37 16.4 91.1 642 38 16.4 91.1 642 39 16.4 91.1 622 31 16.4 91.1 643 31 16.4 91.1 643 32 16.4 91.1 643 33 16.4 91.1 653 34 16.4 91.1 653 35 16.4 91.1 2260 42 15.4 85.6 252
13 16.4 91.1 16.4 91.1 16.4 91.1 17 16.4 91.1 18 16.4 91.1 19 16.4 91.1 22 16.4 91.1 23 16.4 91.1 24 91.1 25 16.4 91.1 26 16.4 91.1 27 16.4 91.1 28 16.4 91.1 29 16.4 91.1 31 16.4 91.1 32 16.4 91.1 33 16.4 91.1 34 16.4 91.1 35 16.4 91.1 36 16.4 91.1 37 16.4 91.1 38 16.4 91.1 39 16.4 91.1 30 16.4 91.1 31 16.4 91.1 32 16.4 91.1 33 16.4 91.1 34 16.4 91.1 35 16.4 91.1 36 16.4 91.1 37 16.4 91.1 38 16.4 91.1 39 16.4 91.1 31 16.4 91.1 31 16.4 91.1 32 16.4 91.1 33 16.4 91.1 34 16.4 91.1 35 16.4 91.1 36 16.4 91.1 37 16.4 91.1 38 16.4 91.1 39 16.4 91.1 30 16.4 91.1 31 16.4 91.1 31 16.4 91.1 31 16.4 91.1
13 16.4 15 16.4 16 16.4 17 16.4 18 16.4 19 16.4 19 16.4 10
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ALIGNMENTS

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DHJOB electrocompetent cells (BRL Life Technologies). "
59 c 17 2 g 109 t.
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/cofderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZO56887 323 bp DNA GSS 30-MAR-2000
PPCI-23-428K7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-428K7,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                              /note="Vector: pcMv SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
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/tissue_type="pooled"
/lab_host="DH10B"
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/clone_lib="RPCI-23"
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/db_xref="taxon:9823"
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AUTHORS
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AZ749422 559 bp DNA GSS 25-JAN-2001
RPCI-24-115E19.TV RPCI-24 Mus musculus genomic clone RPCI-24-115E19
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Email: szhaoétigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: T7
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSS: RPCI-24-115E19.TJ
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 559)
                                                     Gaps
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            Score 17; DB 13; Pred. No. 2.1e+02;
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94.4%; bcc. 100.0%; Pred. No. 2... 0; Mismatches
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100.0%; Pred. No. 2...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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/clone="RPCI-24-115E19"
/clone_lib="RPCI-24"
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Best Local Similarity 100.
Matches 17; Conservative
                                                       Conservative
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      Query Match
Best Local Similarity
Matches 17; Conserva
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BH097469

ORIGIN

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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 13 row: H column: 6
Seg primer: ATTTAGGTGACACTATAG.
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Sus scrofa
Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 155)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
BH097469 655 bp DNA GSS 19-JUL-2001
RPCI-24-315L22.TV RPCI-24 Mus musculus genomic clone RPCI-24-315L22
DNA sequence.
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0
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejongémail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 315 row: L column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Spleen/Brain" /note="Vector: pTARBAC1, Site_1: BamH1; Site_2: BamH1; RPC1-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                           Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Upublished (1999)
Other_GSSs: RPCI-24-315L22.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                           Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 655)

                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AW346676
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Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research
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/clone="RPCI-24-315L22"
/clone_lib="RPCI-24"
/sex="Male"
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JOURNAL
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.9809046.e. Vector identified by cross_match with the -minscore 20
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
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1 (bases 1 to 166)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine lonpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
and Keele,J.W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AW346655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                   BACKWARD: GTTTTCCCAGTCACGACG
Plate: 13 row: B column: 12
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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source
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AV289929/c
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1.S Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayacsu, N., Hirozane, T., Hori, F., Ishiikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saitchi, T., Shiraki, T., Soque, S., Yibhata, K., Shibata, Y., Shiraki, T., Soque, Y., Sujahara, Y., Suzuki, H., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., KIKEN Mouse ESTS (Konno, H., et al. 1999)

AL Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV312947 232 bp mRNA EST 08-NOV-1999 AV312947 RIKEN full-length enriched, adult male thymus Mus musculus CDNA clone 5830407B15 3', mRNA sequence.
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suthiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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URL:http://genome.gsc.riken.go.jp/
Saski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                         /lab_host="DH10B".
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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                                                                                       /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                            /organism="Sus scrofa"
                                                                                                                                                 /tissue_type="pooled"
      Location/Qualifiers
                                                                                                                                                                                                                                                                                            39 g
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Matches 17; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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I (bases 1 to 254)

S Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishi, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadoa, K., Kagawa, I., Kai
Shii, Y., Ishikawa, T., Itoh, M., Izawa, M., Oda, R., Odazaki, Y.,
Matsuyama, T., Miki, R., Mizuno, Y., Nodamira, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Sairo, H., Sano, M., Sato, K., Shibata, K., Shipata,
Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Subahara, Y., Suzuki, H.,
Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y.,
Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
RIKEN Mouse ESTS (Konno, H., et al. 1999)

L Unpublished (1999)
                                                                                        /clone_lib="RIKEN full-length enriched, adult male thymus"
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Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSO), Yokohama Institute
The Institute of GPysical and Chemical Research (RIKEN)
T-7.22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Pred. No. 3.8e+02;
0; Mismatches 1;
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organism="Mus musculus"
                                              /db_xref="taxon:10090"
/clone="5830407B15"
                                                                                                                                 /tissue_type="thymus"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 g
                       /strain="C57BL/6J'
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94.48;
                                                                                                               /sex="male"
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house mouse.
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                                                                                                                                                                  Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M.; Kitsunai, T., Akiyama, J.; Shibata, K., Izawa, M.; Rawai, J., Y. Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. Automated filtration-based high-throughput plasmid preparation carninci, P. and Hayashizaki, Y. (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Email: genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5033430G19"
/clone_lib="RIKEN full-length enriched, 11 days pregnant adult female ovary and uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic Sciences Center and Genome Science Laboratory in
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 t
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/lab_host="multiple (Life Technologies)"
/lab_host="multiple (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter. collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
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RPCI-23-475F22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-475F22
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                   Email: dpomp@unl.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized porcine ovarian follicles library The following repetitive elements were found in this cDNA sequence: 255-304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="University of Nebraska, Lincoln Swine Selection
Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization of a normalized cDNA
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/clone_lib="UNL-P-FN"
                                                                          library from swine ovarian follicles
Unpublished (2001)
Contact: Pomp, D
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                                                                                                                                                                               Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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Email: cktuggle@iastate.edu
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BI184279
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CooRi Site_2: EcoRI; Female C57BL/61 mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

59 c 84 g 63 t
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                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SPG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 294)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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MI-P-O2-adx-e-01-1-UM.S1 MI-P-O2 Sus scrofa cDNA clone
MI-P-O2-adx-e-01-1-UM 3', mRNA sequence.
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                                                                                                                    The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-475F22_TV
                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tuggle CK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Fax: 5152942401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 17; Conserv
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The sequence contained an oligo-dr track that was present in the oligousclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pr/r3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECORI; The MI-P-02 library is derived from ovary at estrus day 5. For a detailed description of the library from which this clone was derived, please visit our web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="University of Nebraska, Lincoln Swine Selection
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "[ (bases 1 to 300) Caetano, A.R., and Pomp, D. Gaetano, A.R., Johnson, R.K. and Pomp, D. Gaetano, A.R., and sequence characterization of a normalized cDNA Unbrary from swine ovarian follicles
Unpublished (2001)
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Pred. No. 4e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MI-P-02-adx-e-01-1-UM"
/clone_lib="MI-P-02"
/lab_host="DH10B (Life Technologies)"
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TAG_SEQ=None found"
61 c 77 g 87 t
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Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
/strain="crossbreed"
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/organism="Sus scrofa"
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BI184279.1 GI:14658688
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94.4%;
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Best Local Similarity
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/dev_stage="ADULE" in the control of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Juna, Agyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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1M0029A06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0029A06 R, DNA sequence.
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/db_xref="taxon:10000"
/clone="UUGC1M0029A06" '
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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Pred. No. 4e+02;
0; Mismatches 1; Indels 0
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                             /clone="UNL-P-FN-ck-g-02-0-UNL"
/clone__lib="UNL-P-FN"
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Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 370.
Location/Qualifiers
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/db_xref="taxon:9823"
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94.48;
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Best Local Similarity 94.48
Matches 17; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blurt end-repaired with TH DNA polymerase and TH polymerase and TH polymerase and TH polymelectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of publa, 19072.11, a copy number of publa derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored weeter DNA, and transformed into chemically-competent E. coli XLl0'Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ793176 379 bp DNA GSS 16-FEB-2001
2M0046N11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/clone="UGC2M0046N11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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Pred. No. 4.2e+02;
0; Mismatches 1;
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Location/Qualifiers
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Insert Length: 10000 Std Erro
Plate: 0046 row: N column: 11
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94.48;
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/) The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TH DNA polymerase and TH polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwAc2 (gil4732114 gplAR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M011K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0111K09 R, DNA sequence.
AZ831760.1 GI:13001668
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., ISlam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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/db_xref="taxon:10090"
/clone="UUGC2M0111K09"
/scx="Male" Mouse 10kb plasmid UUGC1M library"
                                                          Laboratory Mouse DNA Resource
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Trasert Length: 10000 Std Error: C
Plate: 0111 row: K column: 09
Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA
/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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